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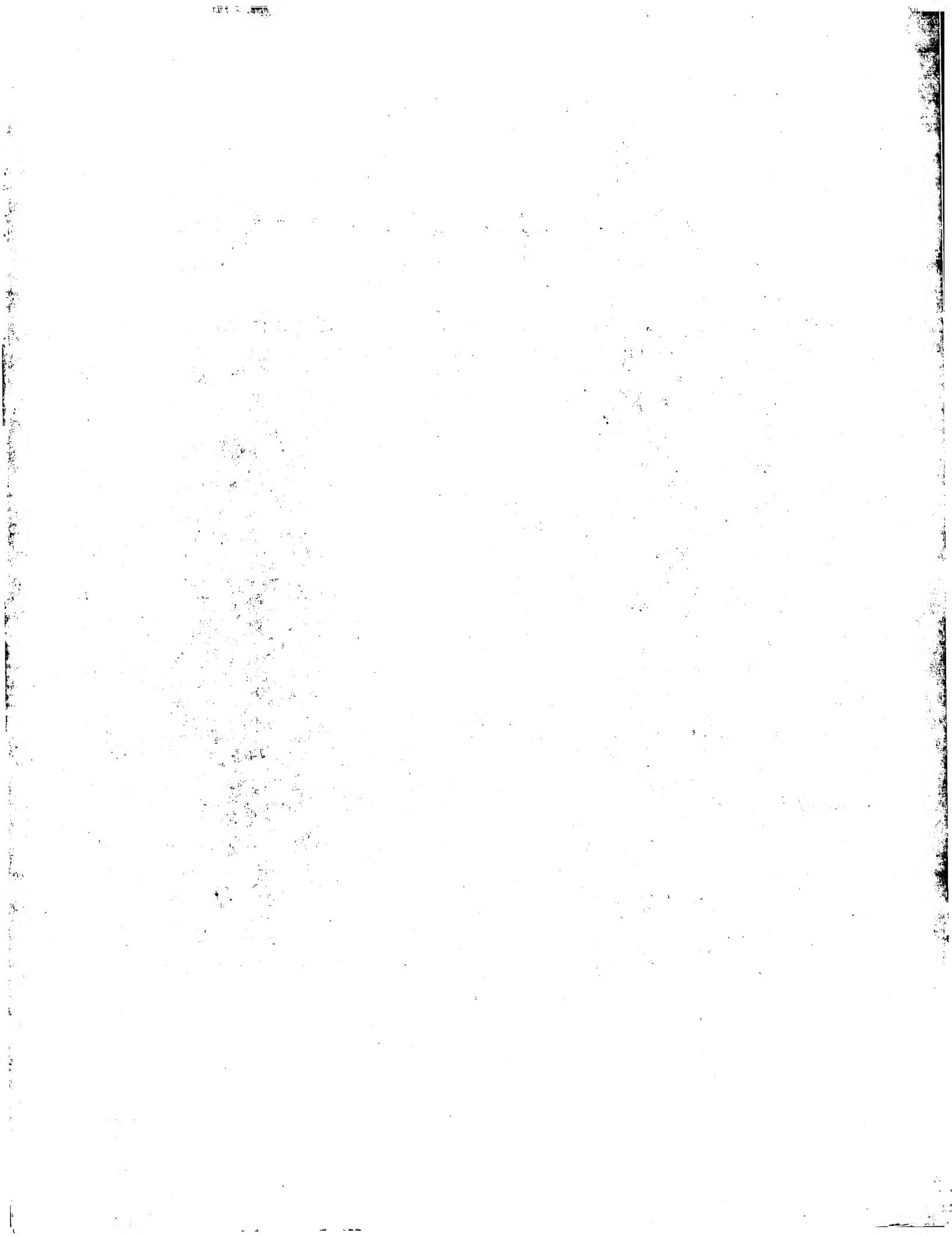
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(54) Title: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO HELICOBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS			
(57) Abstract <p>Recombinant or substantially pure preparations of <i>H. pylori</i> polypeptides are described. The nucleic acids encoding the polypeptides also are described. The <i>H. pylori</i> polypeptides are useful for diagnostics and vaccine compositions.</p>			

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**NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
HELICOBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS**

Background of the Invention

5 *Helicobacter pylori* is a gram-negative, S-shaped, microaerophilic bacterium that was discovered and cultured from a human gastric biopsy specimen. (Warren, J.R. and B. Marshall, (1983) *Lancet* 1: 1273-1275; and Marshall et al., (1984) *Microbios Lett.* 25: 83-88). *H. pylori* has been strongly linked to chronic gastritis and duodenal ulcer disease. (Rathbone et. al., (1986) *Gut* 27: 635-641). Moreover, evidence is accumulating for an 10 etiologic role of *H. pylori* in nonulcer dyspepsia, gastric ulcer disease, and gastric adenocarcinoma. (Blaser M. J., (1993) *Trends Microbiol.* 1: 255-260). Transmission of the bacteria occurs via the oral route, and the risk of infection increases with age. (Taylor, D.N. and M. J. Blaser, (1991) *Epidemiol. Rev* 13: 42-50). *H. pylori* colonizes the human 15 gastric mucosa, establishing an infection that usually persists for decades. Infection by *H. pylori* is prevalent worldwide. Developed countries have infection rates over 50% of the adult population, while developing countries have infection rates reaching 90% of the adults over the age of 20. (Hopkins R. J. and J. G. Morris (1994) *Am. J. Med.* 97: 265-277).

The bacterial factors necessary for colonization of the gastric environment, and for virulence of this pathogen, are poorly understood. Examples of the putative virulence 20 factors include the following: urease, an enzyme that may play a role in neutralizing gastric acid pH (Eaton et al., (1991) *Infect. Immunol.* 59: 2470-2475; Ferrero, R.L. and A. Lee (1991) *Microb. Ecol. Hlth. Dis.* 4: 121-134; Labigne et al., (1991) *J. Bacteriol.* 173: 1920-1931); the bacterial flagellar proteins responsible for motility across the mucous layer. (Hazell et al., (1986) *J. Inf. Dis.* 153: 658-663; Leying et al., (1992) *Mol. Microbiol.* 6: 25 2863-2874; and Haas et al., (1993) *Mol. Microbiol.* 8: 753-760); Vac A, a bacterial toxin that induces the formation of intracellular vacuoles in epithelial cells (Schmitt, W. and R. Haas, (1994) *Molecular Microbiol.* 12(2): 307-319); and several gastric tissue-specific adhesins. (Boren et al., (1993) *Science* 262: 1892-1895; Evans et al., (1993) *J. Bacteriol.* 175: 674-683; and Falk et al., (1993) *Proc. Natl. Acad. Sci. USA* 90: 2035-203).

30 Numerous therapeutic agents are currently available that eradicate *H. pylori* infections *in vitro*. (Huesca et. al., (1993) *Zbl. Bakt.* 280: 244-252; Hopkins, R. J. and J. G. Morris, supra). However, many of these treatments are suboptimally effective *in vivo* because of bacterial resistance, altered drug distribution, patient non-compliance or poor drug availability. (Hopkins, R. J. and J. G. Morris, supra). Treatment with antibiotics 35 combined with bismuth are part of the standard regime used to treat *H. pylori* infection. (Malfertheiner, P. and J. E. Dominguez-Munoz (1993) *Clinical Therapeutics* 15 Supp. B: 37-48). Recently, combinations of a proton pump inhibitors and a single antibiotic have been shown to ameliorate duodenal ulcer disease. (Malfertheiner, P. and J. E. Dominguez-Munoz supra). However, methods employing antibiotic agents can have the problem of the

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emergence of bacterial strains which are resistant to these agents. (Hopkins, R. J. and J. G. Morris, *supra*). These limitations demonstrate that new more effective methods are needed to combat *H. pylori* infections *in vivo*. In particular, the design of new vaccines that may prevent infection by this bacterium is highly desirable.

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Summary of the Invention

This invention relates to novel genes, e.g., genes encoding polypeptides such as bacterial surface proteins, from the organism *Helicobacter pylori* (*H. pylori*), and other related genes, their products, and uses thereof. The nucleic acids and peptides of the 10 present invention have utility for diagnostic and therapeutics for *H. pylori* and other *Helicobacter* species. They can also be used to detect the presence of *H. pylori* and other *Helicobacter* species in a sample; and for use in screening compounds for the ability to interfere with the *H. pylori* life cycle or to inhibit *H. pylori* infection. More specifically, 15 this invention features compositions of nucleic acids corresponding to entire coding sequences of *H. pylori* proteins, including surface or secreted proteins or parts thereof, nucleic acids capable of binding mRNA from *H. pylori* proteins to block protein translation, and methods for producing *H. pylori* proteins or parts thereof using peptide synthesis and recombinant DNA techniques. This invention also features antibodies and nucleic acids useful as probes to detect *H. pylori* infection. In addition, vaccine 20 compositions and methods for the protection or treatment of infection by *H. pylori* are within the scope of this invention.

Detailed Description of the Drawings

Figure 1 is a bar graph that depicts the antibody titer in serum of mice following 25 immunization with specific *H. pylori* antigens.

Figure 2 is a bar graph that depicts the antibody titer in mucous of mice following immunization with specific *H. pylori* antigens.

30 Figure 3 is a bar graph that depicts therapeutic immunization of *H. pylori* infected mice with specific antigens dissolved in HEPES buffer.

Figure 4 is a bar graph that depicts therapeutic immunization of *H. pylori* infected mice with specific antigens dissolved in buffer containing DOC.

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Detailed Description of the Invention

In one aspect, the invention features a recombinant or substantially pure preparation of *H. pylori* polypeptide of SEQ ID NO: 384. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide of SEQ ID NO: 384, such nucleic acid

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is contained in SEQ ID NO: 1. The *H. pylori* polypeptide sequences of the invention described herein are contained in the Sequence Listing, and the nucleic acids encoding *H. pylori* polypeptides of the invention are contained in the Sequence Listing.

- In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 384 through SEQ ID NO: 389, SEQ ID NO: 391 through SEQ ID NO: 400, SEQ ID NO: 402 through SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 411 through SEQ ID NO: 412, SEQ ID NO: 414 through SEQ ID NO: 430, SEQ ID NO: 432 through SEQ ID NO: 434, SEQ ID NO: 436 through SEQ ID NO: 441, and SEQ ID NO: 443. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 384 through SEQ ID NO: 389, SEQ ID NO: 391 through SEQ ID NO: 400, SEQ ID NO: 402 through SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 411 through SEQ ID NO: 412, SEQ ID NO: 414 through SEQ ID NO: 430, SEQ ID NO: 432 through SEQ ID NO: 434, SEQ ID NO: 436 through SEQ ID NO: 441, and SEQ ID NO: 443, such nucleic acids are contained in SEQ ID NO: 1 through SEQ ID NO: 50.

- In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 444, SEQ ID NO: 446 through SEQ ID NO: 448, SEQ ID NO: 450 through SEQ ID NO: 462, SEQ ID NO: 465 through SEQ ID NO: 466, SEQ ID NO: 468 through SEQ ID NO: 469, SEQ ID NO: 471 through SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 478 through SEQ ID NO: 479, SEQ ID NO: 481 through SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488 through SEQ ID NO: 501, and SEQ ID NO: 503 through SEQ ID NO: 506. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 444, SEQ ID NO: 446 through SEQ ID NO: 448, SEQ ID NO: 450 through SEQ ID NO: 462, SEQ ID NO: 465 through SEQ ID NO: 466, SEQ ID NO: 468 through SEQ ID NO: 469, SEQ ID NO: 471 through SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 478 through SEQ ID NO: 479, SEQ ID NO: 481 through SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488 through SEQ ID NO: 501, and SEQ ID NO: 503 through SEQ ID NO: 506, such nucleic acids are contained in SEQ ID NO: 51 through SEQ ID NO: 100.

- In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 509 through SEQ ID NO: 510, SEQ ID NO: 512 through SEQ ID NO: 514, SEQ ID NO: 516, SEQ ID NO: 518 through SEQ ID NO: 520, SEQ ID NO: 522 through SEQ ID NO: 525, SEQ ID NO: 527 through SEQ ID NO: 533, SEQ ID NO: 535 through SEQ ID NO: 537, SEQ ID NO: 539 through SEQ ID NO: 540, SEQ ID NO: 542 through SEQ ID NO: 544, SEQ ID NO: 546 through SEQ ID NO: 548, SEQ ID NO:

550, SEQ ID NO: 553 through SEQ ID NO: 556, SEQ ID NO: 558, SEQ ID NO: 560, SEQ ID NO: 562 through SEQ ID NO: 568, SEQ ID NO: 570, and SEQ ID NO: 572 through SEQ ID NO: 575. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ 5 ID NO: 509 through SEQ ID NO: 510, SEQ ID NO: 512 through SEQ ID NO: 514, SEQ ID NO: 516, SEQ ID NO: 518 through SEQ ID NO: 520, SEQ ID NO: 522 through SEQ ID NO: 525, SEQ ID NO: 527 through SEQ ID NO: 533, SEQ ID NO: 535 through SEQ ID NO: 537, SEQ ID NO: 539 through SEQ ID NO: 540, SEQ ID NO: 542 through SEQ ID NO: 544, SEQ ID NO: 546 through SEQ ID NO: 548, SEQ ID NO: 550, SEQ ID NO: 553 through SEQ ID NO: 556, SEQ ID NO: 558, SEQ ID NO: 560, SEQ ID NO: 562 through SEQ ID NO: 568, SEQ ID NO: 570, and SEQ ID NO: 572 through SEQ ID NO: 575, such nucleic acids are contained in SEQ ID NO: 101 through SEQ ID NO: 150.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 576 through SEQ ID NO: 579, SEQ ID NO: 581 through SEQ ID NO: 583, SEQ ID NO: 585 through SEQ ID NO: 593, SEQ ID NO: 596 through SEQ ID NO: 614, SEQ ID NO: 617 through SEQ ID NO: 623, SEQ ID NO: 625, SEQ ID NO: 627, SEQ ID NO: 629 through SEQ ID NO: 631, SEQ ID NO: 633, and SEQ ID NO: 635 through SEQ ID NO: 636. The invention also includes substantially pure nucleic acid 15 encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 576 through SEQ ID NO: 579, SEQ ID NO: 581 through SEQ ID NO: 583, SEQ ID NO: 585 through SEQ ID NO: 593, SEQ ID NO: 596 through SEQ ID NO: 614, SEQ ID NO: 617 through SEQ ID NO: 623, SEQ ID NO: 625, SEQ ID NO: 627, SEQ ID NO: 629 through SEQ ID NO: 631, SEQ ID NO: 633, and SEQ ID NO: 635 20 through SEQ ID NO: 636, such nucleic acids are contained in SEQ ID NO: 151 through SEQ ID NO: 200.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 638 through SEQ ID NO: 640, SEQ ID NO: 642 through SEQ ID NO: 643, SEQ ID NO: 647, SEQ ID NO: 649 through SEQ ID NO: 651, SEQ ID NO: 653 through SEQ ID NO: 661, SEQ ID NO: 663 through SEQ ID NO: 670, SEQ ID NO: 673 through SEQ ID NO: 674, SEQ ID NO: 676, SEQ ID NO: 678 through SEQ ID NO: 683, SEQ ID NO: 687 through SEQ ID NO: 692, and SEQ ID NO: 694 through SEQ ID NO: 702. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 638 through SEQ ID NO: 640, SEQ ID NO: 642 through SEQ ID NO: 643, SEQ ID NO: 647, SEQ ID NO: 649 through SEQ ID NO: 651, SEQ ID NO: 653 through SEQ ID NO: 661, SEQ ID NO: 663 through SEQ ID NO: 670, SEQ ID NO: 673 through SEQ ID NO: 674, SEQ ID NO: 676, SEQ ID NO: 678 through SEQ ID NO: 683, SEQ ID NO: 687 30 35

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through SEQ ID NO: 692, and SEQ ID NO: 694 through SEQ ID NO: 702, such nucleic acids are contained in SEQ ID NO: 201 through SEQ ID NO: 250.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 705 through SEQ ID NO: 708, SEQ ID NO: 712 through SEQ ID NO: 714, SEQ ID NO: 716 through SEQ ID NO: 722, SEQ ID NO: 725 through SEQ ID NO: 730, SEQ ID NO: 732 through SEQ ID NO: 733, SEQ ID NO: 735 through SEQ ID NO: 744, SEQ ID NO: 746 through SEQ ID NO: 752, SEQ ID NO: 755 through SEQ ID NO: 757, SEQ ID NO: 759, SEQ ID NO: 761 through SEQ ID NO: 763, and SEQ ID NO: 767 through SEQ ID NO: 770. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 705 through SEQ ID NO: 708, SEQ ID NO: 712 through SEQ ID NO: 714, SEQ ID NO: 716 through SEQ ID NO: 722, SEQ ID NO: 725 through SEQ ID NO: 730, SEQ ID NO: 732 through SEQ ID NO: 733, SEQ ID NO: 735 through SEQ ID NO: 744, SEQ ID NO: 746 through SEQ ID NO: 752, SEQ ID NO: 755 through SEQ ID NO: 757, SEQ ID NO: 759, SEQ ID NO: 761 through SEQ ID NO: 763, and SEQ ID NO: 767 through SEQ ID NO: 770, such nucleic acids are contained in SEQ ID NO: 251 through SEQ ID NO: 300.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 771 through SEQ ID NO: 773, SEQ ID NO: 775, SEQ ID NO: 777, SEQ ID NO: 779 through SEQ ID NO: 784, SEQ ID NO: 786 through SEQ ID NO: 787, SEQ ID NO: 789 through SEQ ID NO: 792, SEQ ID NO: 794, SEQ ID NO: 796, SEQ ID NO: 798 through SEQ ID NO: 805, SEQ ID NO: 807 through SEQ ID NO: 811, SEQ ID NO: 813 through SEQ ID NO: 819, SEQ ID NO: 821 through SEQ ID NO: 822, SEQ ID NO: 824 through SEQ ID NO: 826, SEQ ID NO: 828 through SEQ ID NO: 832, and SEQ ID NO: 835. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 771 through SEQ ID NO: 773, SEQ ID NO: 775, SEQ ID NO: 777, SEQ ID NO: 779 through SEQ ID NO: 784, SEQ ID NO: 786 through SEQ ID NO: 787, SEQ ID NO: 789 through SEQ ID NO: 792, SEQ ID NO: 794, SEQ ID NO: 796, SEQ ID NO: 798 through SEQ ID NO: 805, SEQ ID NO: 807 through SEQ ID NO: 811, SEQ ID NO: 813 through SEQ ID NO: 819, SEQ ID NO: 821 through SEQ ID NO: 822, SEQ ID NO: 824 through SEQ ID NO: 826, SEQ ID NO: 828 through SEQ ID NO: 832, and SEQ ID NO: 835, such nucleic acids are contained in SEQ ID NO: 301 through SEQ ID NO: 350.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 836 through SEQ ID NO: 841, SEQ ID NO: 843 through SEQ ID NO: 851, SEQ ID NO: 853, SEQ ID NO: 855 through SEQ ID NO: 857, SEQ ID NO:

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- 859 through SEQ ID NO: 862, SEQ ID NO: 866, SEQ ID NO: 868 through SEQ ID NO: 871, SEQ ID NO: 873 through SEQ ID NO: 876, and SEQ ID NO: 879. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 836 through SEQ ID NO: 841, 5 SEQ ID NO: 843 through SEQ ID NO: 851, SEQ ID NO: 853, SEQ ID NO: 855 through SEQ ID NO: 857, SEQ ID NO: 859 through SEQ ID NO: 862, SEQ ID NO: 866, SEQ ID NO: 868 through SEQ ID NO: 871, SEQ ID NO: 873 through SEQ ID NO: 876, and SEQ ID NO: 879, such nucleic acids are contained in SEQ ID NO: 351 through SEQ ID NO: 383.
- 10 In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 385, SEQ ID NO: 390, SEQ ID NO: 401, SEQ ID NO: 407, SEQ ID NO: 409 through SEQ ID NO: 410, SEQ ID NO: 413, SEQ ID NO: 431, SEQ ID NO: 435, SEQ ID NO: 442, SEQ ID NO: 445, SEQ ID NO: 449, SEQ ID NO: 463 through 15 SEQ ID NO: 464, SEQ ID NO: 467, SEQ ID NO: 470, SEQ ID NO: 474, SEQ ID NO: 476 through SEQ ID NO: 477, SEQ ID NO: 480, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 502, SEQ ID NO: 507 through SEQ ID NO: 508, SEQ ID NO: 511, SEQ ID NO: 515, SEQ ID NO: 517, SEQ ID NO: 521, SEQ ID NO: 526, SEQ ID NO: 534, SEQ ID NO: 538, SEQ ID NO: 541, SEQ ID NO: 545, SEQ ID NO: 549, SEQ ID NO: 551 through SEQ 20 ID NO: 552, SEQ ID NO: 557, SEQ ID NO: 559, SEQ ID NO: 561, SEQ ID NO: 569, SEQ ID NO: 571, SEQ ID NO: 580, SEQ ID NO: 584, SEQ ID NO: 594 through SEQ ID NO: 595, SEQ ID NO: 615 through SEQ ID NO: 616, SEQ ID NO: 624, and SEQ ID NO: 626. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 25 385, SEQ ID NO: 390, SEQ ID NO: 401, SEQ ID NO: 407, SEQ ID NO: 409 through SEQ ID NO: 410, SEQ ID NO: 413, SEQ ID NO: 431, SEQ ID NO: 435, SEQ ID NO: 442, SEQ ID NO: 445, SEQ ID NO: 449, SEQ ID NO: 463 through SEQ ID NO: 464, SEQ ID NO: 467, SEQ ID NO: 470, SEQ ID NO: 474, SEQ ID NO: 476 through SEQ ID NO: 477, SEQ ID NO: 480, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 502, SEQ ID NO: 507 30 through SEQ ID NO: 508, SEQ ID NO: 511, SEQ ID NO: 515, SEQ ID NO: 517, SEQ ID NO: 521, SEQ ID NO: 526, SEQ ID NO: 534, SEQ ID NO: 538, SEQ ID NO: 541, SEQ ID NO: 545, SEQ ID NO: 549, SEQ ID NO: 551 through SEQ ID NO: 552, SEQ ID NO: 557, SEQ ID NO: 559, SEQ ID NO: 561, SEQ ID NO: 569, SEQ ID NO: 571, SEQ ID NO: 580, SEQ ID NO: 584, SEQ ID NO: 594 through SEQ ID NO: 595, SEQ ID NO: 615 through SEQ ID NO: 616, SEQ ID NO: 624, and SEQ ID NO: 626, such nucleic acids are 35 contained in SEQ ID NO: 881 through SEQ ID NO: 930.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 628, SEQ ID NO: 632, SEQ ID NO: 634, SEQ ID NO: 637,

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SEQ ID NO: 641, SEQ ID NO: 644 through SEQ ID NO: 646, SEQ ID NO: 648, SEQ ID NO: 652, SEQ ID NO: 662, SEQ ID NO: 671 through SEQ ID NO: 672, SEQ ID NO: 675, SEQ ID NO: 677, SEQ ID NO: 684 through SEQ ID NO: 686, SEQ ID NO: 693, SEQ ID NO: 703 through SEQ ID NO: 704, SEQ ID NO: 709 through SEQ ID NO: 711, SEQ ID NO: 715, SEQ ID NO: 723 through SEQ ID NO: 724, SEQ ID NO: 731, SEQ ID NO: 734, SEQ ID NO: 745, SEQ ID NO: 753 through SEQ ID NO: 754, SEQ ID NO: 758, SEQ ID NO: 760, SEQ ID NO: 764 through SEQ ID NO: 766, SEQ ID NO: 774, SEQ ID NO: 776, SEQ ID NO: 778, SEQ ID NO: 785, SEQ ID NO: 788, SEQ ID NO: 793, SEQ ID NO: 795, SEQ ID NO: 797, SEQ ID NO: 806, SEQ ID NO: 812, SEQ ID NO: 820, SEQ ID NO: 823, and SEQ ID NO: 827. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 628, SEQ ID NO: 632, SEQ ID NO: 634, SEQ ID NO: 637, SEQ ID NO: 641, SEQ ID NO: 644 through SEQ ID NO: 646, SEQ ID NO: 648, SEQ ID NO: 652, SEQ ID NO: 662, SEQ ID NO: 671 through SEQ ID NO: 672, SEQ ID NO: 675, SEQ ID NO: 677, SEQ ID NO: 684 through SEQ ID NO: 686, SEQ ID NO: 693, SEQ ID NO: 703 through SEQ ID NO: 704, SEQ ID NO: 709 through SEQ ID NO: 711, SEQ ID NO: 715, SEQ ID NO: 723 through SEQ ID NO: 724, SEQ ID NO: 731, SEQ ID NO: 734, SEQ ID NO: 745, SEQ ID NO: 753 through SEQ ID NO: 754, SEQ ID NO: 758, SEQ ID NO: 760, SEQ ID NO: 764 through SEQ ID NO: 766, SEQ ID NO: 774, SEQ ID NO: 776, SEQ ID NO: 778, SEQ ID NO: 785, SEQ ID NO: 788, SEQ ID NO: 793, SEQ ID NO: 795, SEQ ID NO: 797, SEQ ID NO: 806, SEQ ID NO: 812, SEQ ID NO: 820, SEQ ID NO: 823, and SEQ ID NO: 827, such nucleic acids are contained in SEQ ID NO: 931 through SEQ ID NO: 980.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 833 through SEQ ID NO: 834, SEQ ID NO: 842, SEQ ID NO: 852, SEQ ID NO: 854, SEQ ID NO: 858, SEQ ID NO: 863, SEQ ID NO: 864 through SEQ ID NO: 865, SEQ ID NO: 867, SEQ ID NO: 872, SEQ ID NO: 877 through SEQ ID NO: 878, and SEQ ID NO: 880. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 833 through SEQ ID NO: 834, SEQ ID NO: 842, SEQ ID NO: 852, SEQ ID NO: 854, SEQ ID NO: 858, SEQ ID NO: 863, SEQ ID NO: 864 through SEQ ID NO: 865, SEQ ID NO: 867, SEQ ID NO: 872, SEQ ID NO: 877 through SEQ ID NO: 878, and SEQ ID NO: 880, such nucleic acids are contained in SEQ ID NO: 981 through SEQ ID NO: 994.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1446 through SEQ ID NO: 1461, SEQ ID NO: 1463, and SEQ ID NO: 1465 through SEQ ID NO: 1495. The invention also includes substantially

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pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1446 through SEQ ID NO: 1461, SEQ ID NO: 1463, and SEQ ID NO: 1465 through SEQ ID NO: 1495, such nucleic acids are contained in SEQ ID NO: 995 through SEQ ID NO: SEQ ID NO: 1010, SEQ ID NO: 1012, and SEQ ID NO: 5 1014 through SEQ ID NO: 1044.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1497 through SEQ ID NO: 1515, and SEQ ID NO: 1517 through SEQ ID NO: 1545. The invention also includes substantially pure nucleic acid 10 encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1497 through SEQ ID NO: 1515, and SEQ ID NO: 1517 through SEQ ID NO: 1545, such nucleic acids are contained in SEQ ID NO: 1046 through SEQ ID NO: 1064, and SEQ ID NO: 1066 through SEQ ID NO: 1094.

In another aspect, the invention features a recombinant or substantially pure 15 preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1546 through SEQ ID NO: 1595. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1546 through SEQ ID NO: 1595, such nucleic acids are contained in SEQ ID NO: 1095 through SEQ ID NO: 1144.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1596 through SEQ ID NO: 1617, SEQ ID NO: 1620 through SEQ ID NO: 1645. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1596 through SEQ ID NO: 1617, SEQ ID NO: 1620 through SEQ ID NO: 1645, such nucleic acids are contained in SEQ ID NO: 1145 through SEQ ID NO: 1166, and SEQ ID 20 25 NO: 1169 through SEQ ID NO: 1194.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1646 through SEQ ID NO: 1681, and SEQ ID NO: 1683 through SEQ ID NO: 1695. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1646 through SEQ ID NO: 1681, and SEQ ID NO: 1683 through SEQ ID NO: 1695, such nucleic acids are contained in SEQ ID NO: 1195 through SEQ ID 30 35 NO: 1230, and SEQ ID NO: 1232 through SEQ ID NO: 1244.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1696 through SEQ ID NO: 1745. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group

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consisting of *H. pylori* polypeptides SEQ ID NO: 1696 through SEQ ID NO: 1745, such nucleic acids are contained in SEQ ID NO: 1245 through SEQ ID NO: 1294.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1746 through SEQ ID NO: 1783, and SEQ ID NO: 1786 through SEQ ID NO: 1795. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1746 through SEQ ID NO: 1783, and SEQ ID NO: 1786 through SEQ ID NO: 1795, such nucleic acids are contained in SEQ ID NO: 1295 through SEQ ID NO: 1332, and SEQ ID NO: 1335 through SEQ ID NO: 1344.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1796 through SEQ ID NO: 1817, SEQ ID NO: 1819, SEQ ID NO: 1821, SEQ ID NO: 1823 through SEQ ID NO: 1836, and SEQ ID NO: 1838 through SEQ ID NO: 1845. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1796 through SEQ ID NO: 1817, SEQ ID NO: 1819, SEQ ID NO: 1821, SEQ ID NO: 1823 through SEQ ID NO: 1836, and SEQ ID NO: 1838 through SEQ ID NO: 1845, such nucleic acids are contained in SEQ ID NO: 1345 through SEQ ID NO: 1366, SEQ ID NO: 1368, SEQ ID NO: 1370, SEQ ID NO: 1372 through SEQ ID NO: 1385, and SEQ ID NO: 1387 through SEQ ID NO: 1394.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1846 through SEQ ID NO: 1896. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1846 through SEQ ID NO: 1896, such nucleic acids are contained in SEQ ID NO: 1395 through SEQ ID NO: 1445.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of the invention as set forth in the Sequence Listing. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of the invention as set forth in the Sequence Listing. It should be understood that this invention encompasses each of the *H. pylori* polypeptides and nucleic acids encoding such polypeptides as identified in the Sequence Listing by a given sequence identification number. For example, a representative *H. pylori* polypeptide is contained in SEQ ID NO: 1450. Therefore, this invention encompasses a recombinant or substantially pure preparation of an *H. pylori* polypeptide of SEQ ID NO: 1450. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide of SEQ ID NO: 1450.

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In another aspect, the invention pertains to any individual *H. pylori* polypeptide member or nucleic acid encoding such member from the above-identified groups of *H. pylori* polypeptides (e.g., SEQ ID NO: 1546 through SEQ ID NO: 1595) or nucleic acids (e.g., SEQ ID NO: 1095-SEQ ID NO: 1144), as well as any subgroups from within the
5 above-identified groups. Furthermore, the subgroups can preferably consists of 1, 3, 5, 10,
15, 20, 30 or 40 members of any of the groups identified above, as well as any
combinations thereof. For example, the group consisting of *H. pylori* polypeptides SEQ ID
NO: 1846 through SEQ ID NO: 1896 can be divided into one or more subgroups as
follows: SEQ ID NO: 1846-SEQ ID NO: 1860; SEQ ID NO: 1861-SEQ ID NO: 1875;
10 SEQ ID NO: 1876-SEQ ID NO: 1885; SEQ ID NO: 1886-SEQ ID NO: 1896; or any
combinations thereof.

Particularly preferred is an isolated nucleic acid comprising a nucleotide sequence
encoding an *H. pylori* cell envelope polypeptide or a fragment thereof. Such nucleic acid is
selected from the group consisting of SEQ ID NO: 1020, SEQ ID NO: 1021, SEQ ID NO:
15 1036, SEQ ID NO: 1050, SEQ ID NO: 1071, SEQ ID NO: 1101, SEQ ID NO: 1135, SEQ
ID NO: 1276, SEQ ID NO: 1150, SEQ ID NO: 1187, SEQ ID NO: 1192, SEQ ID NO:
1361, SEQ ID NO: 1379, SEQ ID NO: 1399, SEQ ID NO: 1403, SEQ ID NO: 1400, SEQ
ID NO: 1189, SEQ ID NO: 1002, SEQ ID NO: 1213, SEQ ID NO: 1214, SEQ ID NO:
1215, SEQ ID NO: 1234, SEQ ID NO: 1236, SEQ ID NO: 1237, SEQ ID NO: 1224, SEQ
20 ID NO: 1251, SEQ ID NO: 1262, SEQ ID NO: 1149, SEQ ID NO: 1220, SEQ ID NO:
1240, SEQ ID NO: 1164, SEQ ID NO: 1165, SEQ ID NO: 1404, SEQ ID NO: 1144, SEQ
ID NO: 1182, SEQ ID NO: 1157, SEQ ID NO: 1160, SEQ ID NO: 1300, SEQ ID NO:
1321, SEQ ID NO: 1323, SEQ ID NO: 1329, SEQ ID NO: 1332, SEQ ID NO: 1345, SEQ
ID NO: 1358, SEQ ID NO: 1375, SEQ ID NO: 1417, SEQ ID NO: 1283, SEQ ID NO:
25 1335, SEQ ID NO: 1368, SEQ ID NO: 1179, SEQ ID NO: 1255, SEQ ID NO: 1258, SEQ
ID NO: 1044, SEQ ID NO: 1273, SEQ ID NO: 1219, SEQ ID NO: 1274, SEQ ID NO:
1210, SEQ ID NO: 1422, SEQ ID NO: 1302, SEQ ID NO: 1308, SEQ ID NO: 1310, SEQ
ID NO: 1331, SEQ ID NO: 1432. SEQ ID NO: 1052, SEQ ID NO: 1091, SEQ ID NO:
1421, SEQ ID NO: 1069. SEQ ID NO: 1005, SEQ ID NO: 1007, SEQ ID NO: 1166, SEQ
30 ID NO: 1177, SEQ ID NO: 1193. SEQ ID NO: 1206, SEQ ID NO: 1207, SEQ ID NO:
1304, SEQ ID NO: 1305. SEQ ID NO: 1346, SEQ ID NO: 1348, SEQ ID NO: 1350, SEQ
ID NO: 1032, SEQ ID NO: 1053. SEQ ID NO: 1081, SEQ ID NO: 1124, SEQ ID NO:
1382, SEQ ID NO: 1437. SEQ ID NO: 1263, SEQ ID NO: 1173, SEQ ID NO: 1405, SEQ
ID NO: 1406, SEQ ID NO: 1410. SEQ ID NO: 1086, SEQ ID NO: 1322, SEQ ID NO:
35 1266, SEQ ID NO: 1282, SEQ ID NO: 1271, SEQ ID NO: 1208, SEQ ID NO: 1126, SEQ
ID NO: 1270, SEQ ID NO: 1278, SEQ ID NO: 1419, SEQ ID NO: 1125, SEQ ID NO:
1181, SEQ ID NO: 1416, SEQ ID NO: 1096, SEQ ID NO: 1082, SEQ ID NO: 1146, SEQ
ID NO: 1145, SEQ ID NO: 1108, SEQ ID NO: 1148, SEQ ID NO: 1337, SEQ ID NO:
1338, SEQ ID NO: 1424, SEQ ID NO: 1000, SEQ ID NO: 1027, SEQ ID NO: 1175, SEQ

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ID NO: 1330, SEQ ID NO: 217, SEQ ID NO: 217, SEQ ID NO: 367, SEQ ID NO: 911, SEQ ID NO: 944, SEQ ID NO: 18, SEQ ID NO: 107, SEQ ID NO: 894, SEQ ID NO: 943, SEQ ID NO: 203, SEQ ID NO: 85, SEQ ID NO: 290, SEQ ID NO: 5, SEQ ID NO: 199, SEQ ID NO: 992, SEQ ID NO: 934, SEQ ID NO: 899, SEQ ID NO: 302, SEQ ID
5 NO: 215, SEQ ID NO: 893, SEQ ID NO: 984, SEQ ID NO: 97, SEQ ID NO: 22, SEQ ID NO: 49, SEQ ID NO: 309, SEQ ID NO: 150, SEQ ID NO: 240, SEQ ID NO: 957, SEQ ID NO: 57, SEQ ID NO: 2, SEQ ID NO: 92, SEQ ID NO: 255, SEQ ID NO: 164, SEQ ID NO: 201, SEQ ID NO: 278, SEQ ID NO: 245, SEQ ID NO: 921, SEQ ID NO: 896, SEQ ID NO: 248, SEQ ID NO: 159, SEQ ID NO: 979, SEQ ID NO: 194, SEQ ID NO: 194, SEQ
10 ID NO: 946, SEQ ID NO: 916, SEQ ID NO: 76, SEQ ID NO: 905, SEQ ID NO: 914, SEQ ID NO: 931, SEQ ID NO: 50, SEQ ID NO: 250, SEQ ID NO: 969, SEQ ID NO: 66, SEQ ID NO: 275, SEQ ID NO: 330, SEQ ID NO: 204, SEQ ID NO: 383, SEQ ID NO: 303, SEQ ID NO: 70, SEQ ID NO: 983, SEQ ID NO: 972, SEQ ID NO: 929, SEQ ID NO: 972, SEQ ID NO: 936, SEQ ID NO: 267, SEQ ID NO: 197, SEQ ID NO: 55, SEQ ID NO: 54,
15 SEQ ID NO: 210, SEQ ID NO: 90, SEQ ID NO: 15, SEQ ID NO: 913, SEQ ID NO: 227, SEQ ID NO: 79, SEQ ID NO: 191, SEQ ID NO: 238, SEQ ID NO: 274, SEQ ID NO: 27, SEQ ID NO: 258, SEQ ID NO: 295, SEQ ID NO: 10, SEQ ID NO: 160, SEQ ID NO: 225, SEQ ID NO: 964, SEQ ID NO: 166, SEQ ID NO: 56, SEQ ID NO: 980, SEQ ID NO: 903, SEQ ID NO: 261, SEQ ID NO: 71, SEQ ID NO: 955, SEQ ID NO: 361, SEQ ID NO: 58,
20 SEQ ID NO: 114, SEQ ID NO: 940, SEQ ID NO: 960, SEQ ID NO: 144, SEQ ID NO: 362, SEQ ID NO: 40, SEQ ID NO: 285, SEQ ID NO: 11, SEQ ID NO: 161, SEQ ID NO: 974, SEQ ID NO: 111, SEQ ID NO: 316, SEQ ID NO: 257, SEQ ID NO: 78, SEQ ID NO: 966, SEQ ID NO: 352, SEQ ID NO: 981, SEQ ID NO: 158, SEQ ID NO: 989, SEQ ID NO: 963, SEQ ID NO: 48, SEQ ID NO: 68, SEQ ID NO: 135, SEQ ID NO: 910, SEQ ID
25 NO: 236, SEQ ID NO: 241, SEQ ID NO: 949, SEQ ID NO: 945, SEQ ID NO: 207, SEQ ID NO: 977, SEQ ID NO: 978, SEQ ID NO: 994, SEQ ID NO: 163, SEQ ID NO: 256, SEQ ID NO: 287, SEQ ID NO: 184, SEQ ID NO: 45, SEQ ID NO: 136, SEQ ID NO: 214, SEQ ID NO: 16, SEQ ID NO: 192, SEQ ID NO: 373, SEQ ID NO: 892, SEQ ID NO: 239, SEQ ID NO: 34, SEQ ID NO: 340, SEQ ID NO: 41, SEQ ID NO: 332, SEQ ID NO: 134,
30 and SEQ ID NO: 330.

In one embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* flagella-associated polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1020, SEQ ID NO: 1021, SEQ ID NO: 1036, SEQ ID NO: 1050, SEQ ID NO: 1071, SEQ ID NO: 1101, SEQ ID NO: 1135, SEQ ID NO: 1276, SEQ ID NO: 1150, SEQ ID NO: 1187, SEQ ID NO: 1192, SEQ ID NO: 1361, SEQ ID NO: 1379, SEQ ID NO: 1399, SEQ ID NO: 1403, SEQ ID NO: 1400, SEQ ID NO: 1189, SEQ ID NO: 217, SEQ ID NO: 367, SEQ ID NO: 911, SEQ ID NO: 944, SEQ ID NO: 18, SEQ ID NO: 107, SEQ ID NO: 894, SEQ ID NO: 943, SEQ ID NO:

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203, SEQ ID NO: 85, SEQ ID NO: 290, SEQ ID NO: 5, SEQ ID NO: 199, SEQ ID NO:
992, SEQ ID NO: 934, SEQ ID NO: 899, SEQ ID NO: 302, and SEQ ID NO: 215.

In another embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* inner membrane polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1002, SEQ ID NO: 1213, SEQ ID NO: 1214, SEQ ID NO: 1215, SEQ ID NO: 1234, SEQ ID NO: 1236, SEQ ID NO: 1237, SEQ ID NO: 1224, SEQ ID NO: 1251, SEQ ID NO: 1262, SEQ ID NO: 1149, SEQ ID NO: 1220, SEQ ID NO: 1240, SEQ ID NO: 1164, SEQ ID NO: 1165, SEQ ID NO: 1404, SEQ ID NO: 1144, SEQ ID NO: 1182, SEQ ID NO: 1157, SEQ ID NO: 1160, SEQ ID NO: 1300, SEQ ID NO: 1321, SEQ ID NO: 1323, SEQ ID NO: 1329, SEQ ID NO: 1332, SEQ ID NO: 1345, SEQ ID NO: 1358, SEQ ID NO: 1375, SEQ ID NO: 1417, SEQ ID NO: 1283, SEQ ID NO: 1335, SEQ ID NO: 1368, SEQ ID NO: 1179, SEQ ID NO: 1255, SEQ ID NO: 1258, SEQ ID NO: 1044, SEQ ID NO: 1273, SEQ ID NO: 893, SEQ ID NO: 984, SEQ ID NO: 97, SEQ ID NO: 22, SEQ ID NO: 49, SEQ ID NO: 309, SEQ ID NO: 150, SEQ ID NO: 240, SEQ ID NO: 957, SEQ ID NO: 57, SEQ ID NO: 2, SEQ ID NO: 92, SEQ ID NO: 255, SEQ ID NO: 164, SEQ ID NO: 201, SEQ ID NO: 278, SEQ ID NO: 245, SEQ ID NO: 921, SEQ ID NO: 896, SEQ ID NO: 248, SEQ ID NO: 159, SEQ ID NO: 979, SEQ ID NO: 194, SEQ ID NO: 194, SEQ ID NO: 946, SEQ ID NO: 916, SEQ ID NO: 76, SEQ ID NO: 905, SEQ ID NO: 914, SEQ ID NO: 931, SEQ ID NO: 50, SEQ ID NO: 250, SEQ ID NO: 969, SEQ ID NO: 66, SEQ ID NO: 275, SEQ ID NO: 330, SEQ ID NO: 204, SEQ ID NO: 383, SEQ ID NO: 303, SEQ ID NO: 70, SEQ ID NO: 983, SEQ ID NO: 972, SEQ ID NO: 929, SEQ ID NO: 972, SEQ ID NO: 936, SEQ ID NO: 267, SEQ ID NO: 197, SEQ ID NO: 55, SEQ ID NO: 54, and SEQ ID NO: 210.

In yet another embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* transporter polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1219, SEQ ID NO: 1274, SEQ ID NO: 1210, SEQ ID NO: 1422, SEQ ID NO: 1302, SEQ ID NO: 1308, SEQ ID NO: 1310, SEQ ID NO: 1331, SEQ ID NO: 1432, SEQ ID NO: 1052, SEQ ID NO: 1091, SEQ ID NO: 1421, SEQ ID NO: 1069, SEQ ID NO: 1005, SEQ ID NO: 1007, SEQ ID NO: 1166, SEQ ID NO: 1177, SEQ ID NO: 1193, SEQ ID NO: 1206, SEQ ID NO: 1207, SEQ ID NO: 1304, SEQ ID NO: 1305, SEQ ID NO: 1346, SEQ ID NO: 1348, SEQ ID NO: 1350, SEQ ID NO: 1032, SEQ ID NO: 1053, SEQ ID NO: 1081, SEQ ID NO: 1124, SEQ ID NO: 1382, SEQ ID NO: 1437, SEQ ID NO: 1263, SEQ ID NO: 90, SEQ ID NO: 15, SEQ ID NO: 913, SEQ ID NO: 227, SEQ ID NO: 79, SEQ ID NO: 191, SEQ ID NO: 238, SEQ ID NO: 274, SEQ ID NO: 27, SEQ ID NO: 258, SEQ ID NO: 295, SEQ ID NO: 10, SEQ ID NO: 160, SEQ ID NO: 225, SEQ ID NO: 964, SEQ ID NO: 166, SEQ ID NO: 56, SEQ ID NO: 980, SEQ ID NO: 903, SEQ ID NO: 261, SEQ ID NO: 71, SEQ ID NO: 955, SEQ ID NO: 361, SEQ ID NO: 58, SEQ ID NO: 114, SEQ ID NO: 940, SEQ ID NO: 960, SEQ ID NO: 144, SEQ ID NO: 362, SEQ ID NO: 40, SEQ ID NO: 285, SEQ ID NO: 11, SEQ

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ID NO: 161, SEQ ID NO: 974, SEQ ID NO: 111, SEQ ID NO: 316, SEQ ID NO: 257, SEQ ID NO: 78, and SEQ ID NO: 966.

In yet a further embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* outer membrane polypeptide or a fragment thereof encoded by the
5 nucleic acid selected from the group consisting of SEQ ID NO: 1173, SEQ ID NO: 1405, SEQ ID NO: 1406, SEQ ID NO: 1410, SEQ ID NO: 1086, SEQ ID NO: 1322, SEQ ID NO: 1266, SEQ ID NO: 1282, SEQ ID NO: 1271, SEQ ID NO: 1208, SEQ ID NO: 1126, SEQ ID NO: 1270, SEQ ID NO: 1278, SEQ ID NO: 1419, SEQ ID NO: 1125, SEQ ID NO: 1181, SEQ ID NO: 1416, SEQ ID NO: 1096, SEQ ID NO: 1082, SEQ ID NO: 1146,
10 SEQ ID NO: 1145, SEQ ID NO: 1108, SEQ ID NO: 1148, SEQ ID NO: 1337, SEQ ID NO: 1338, SEQ ID NO: 1424, SEQ ID NO: 1000, SEQ ID NO: 1027, SEQ ID NO: 1175, SEQ ID NO: 1330, SEQ ID NO: 352, SEQ ID NO: 981, SEQ ID NO: 158, SEQ ID NO: 989, SEQ ID NO: 963, SEQ ID NO: 48, SEQ ID NO: 68, SEQ ID NO: 135, SEQ ID NO: 910, SEQ ID NO: 236, SEQ ID NO: 241, SEQ ID NO: 949, SEQ ID NO: 945, SEQ ID NO: 207, and SEQ ID NO: 977.

Particularly preferred is an isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* cytoplasmic polypeptide or a fragment thereof. Such nucleic acid is selected from the group consisting of SEQ ID NO: 1147, SEQ ID NO: 1288, SEQ ID NO: 1324, SEQ ID NO: 1363, SEQ ID NO: 997, SEQ ID NO: 1015, SEQ ID NO: 1084, SEQ
20 ID NO: 1094, SEQ ID NO: 1099, SEQ ID NO: 1229, SEQ ID NO: 1250, SEQ ID NO: 1268, SEQ ID NO: 1293, SEQ ID NO: 1339, SEQ ID NO: 1408, SEQ ID NO: 1429, SEQ ID NO: 1434, SEQ ID NO: 1228, SEQ ID NO: 1031, SEQ ID NO: 1034, SEQ ID NO: 1008, SEQ ID NO: 1061, SEQ ID NO: 1064, SEQ ID NO: 1191, SEQ ID NO: 1217, SEQ ID NO: 1365, SEQ ID NO: 1394, SEQ ID NO: 1414, SEQ ID NO: 1415, SEQ ID NO:
25 1435, SEQ ID NO: 1058, SEQ ID NO: 1059, SEQ ID NO: 1080, SEQ ID NO: 1128, SEQ ID NO: 1133, SEQ ID NO: 1211, SEQ ID NO: 1252, SEQ ID NO: 1253, SEQ ID NO: 1286, SEQ ID NO: 1289, SEQ ID NO: 1291, SEQ ID NO: 1303, SEQ ID NO: 1396, SEQ ID NO: 996, SEQ ID NO: 1095. SEQ ID NO: 1156, SEQ ID NO: 1158, SEQ ID NO: 1159, SEQ ID NO: 1277, SEQ ID NO: 1038, SEQ ID NO: 1257, SEQ ID NO: 1357, SEQ ID NO: 1436, SEQ ID NO: 1047. SEQ ID NO: 1055, SEQ ID NO: SEQ ID NO: 1141, SEQ ID NO: 1227, SEQ ID NO: 1327. SEQ ID NO: 1412, SEQ ID NO: 1003, SEQ ID NO: 1087, SEQ ID NO: 1116. SEQ ID NO: 1130, SEQ ID NO: 1132, SEQ ID NO: 1185, SEQ ID NO: 1188, SEQ ID NO: 1198. SEQ ID NO: 1218, SEQ ID NO: 1244, SEQ ID NO: 1306, SEQ ID NO: 1325, SEQ ID NO: 1397, SEQ ID NO: 1398, SEQ ID NO: 1407, SEQ
30 ID NO: 1433, SEQ ID NO: 1216. SEQ ID NO: 1239, SEQ ID NO: 1362, SEQ ID NO: 1017, SEQ ID NO: 1019, SEQ ID NO: 1360, SEQ ID NO: 1423, SEQ ID NO: 1425, SEQ ID NO: 1374, SEQ ID NO: 1028. SEQ ID NO: 1037, SEQ ID NO: 1077, SEQ ID NO: 1115, SEQ ID NO: 1232, SEQ ID NO: 1241, SEQ ID NO: 1267, SEQ ID NO: 1163, SEQ ID NO: 1068, SEQ ID NO: 1025, SEQ ID NO: 1042, SEQ ID NO: 1046, SEQ ID NO:

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1056, SEQ ID NO: 1039, SEQ ID NO: 1072, SEQ ID NO: 1073, SEQ ID NO: 1092, SEQ
ID NO: 1100, SEQ ID NO: 1102, SEQ ID NO: 1103, SEQ ID NO: 1104, SEQ ID NO:
1111, SEQ ID NO: 1119, SEQ ID NO: 1136, SEQ ID NO: 1137, SEQ ID NO: 1140, SEQ
ID NO: 1142, SEQ ID NO: 1233, SEQ ID NO: 1238, SEQ ID NO: 1243, SEQ ID NO:
5 1245, SEQ ID NO: 1247, SEQ ID NO: 1249, SEQ ID NO: 1261, SEQ ID NO: 1269, SEQ
ID NO: 1279, SEQ ID NO: 1284, SEQ ID NO: 1290, SEQ ID NO: 1297, SEQ ID NO:
1328, SEQ ID NO: 1370, SEQ ID NO: 1372, SEQ ID NO: 1377, SEQ ID NO: 1383, SEQ
ID NO: 1384, SEQ ID NO: 1385, SEQ ID NO: 1388, SEQ ID NO: 1401, SEQ ID NO:
1402, SEQ ID NO: 1418, SEQ ID NO: 1420, SEQ ID NO: 1427, SEQ ID NO: 1070, SEQ
10 ID NO: 1151, SEQ ID NO: 1176, SEQ ID NO: 999, SEQ ID NO: 1006, SEQ ID NO: 1012,
SEQ ID NO: 1018, SEQ ID NO: 1030, SEQ ID NO: 1033, SEQ ID NO: 1041, SEQ ID
NO: 1049, SEQ ID NO: 1054, SEQ ID NO: 1057, SEQ ID NO: 1090, SEQ ID NO: 1097,
SEQ ID NO: 1129, SEQ ID NO: 1139, SEQ ID NO: 1143, SEQ ID NO: 1152, SEQ ID
NO: 1153, SEQ ID NO: 1155, SEQ ID NO: 1161, SEQ ID NO: 1162, SEQ ID NO: 1169,
15 SEQ ID NO: 1170, SEQ ID NO: 1171, SEQ ID NO: 1180, SEQ ID NO: 1194, SEQ ID
NO: 1195, SEQ ID NO: 1199, SEQ ID NO: 1200, SEQ ID NO: 1201, SEQ ID NO: 1202,
SEQ ID NO: 1205, SEQ ID NO: 1312, SEQ ID NO: 1336, SEQ ID NO: 1349, SEQ ID
NO: 1355, SEQ ID NO: 1359, SEQ ID NO: 1413, SEQ ID NO: 1426, SEQ ID NO: 1430,
SEQ ID NO: 882, SEQ ID NO: 382, SEQ ID NO: 130, SEQ ID NO: 230, SEQ ID NO:
20 269, SEQ ID NO: 312, SEQ ID NO: 211, SEQ ID NO: 959, SEQ ID NO: 938, SEQ ID
NO: 110, SEQ ID NO: 244, SEQ ID NO: 328, SEQ ID NO: 235, SEQ ID NO: 315, SEQ
ID NO: 296, SEQ ID NO: 976, SEQ ID NO: 321, SEQ ID NO: 43, SEQ ID NO: 281, SEQ
ID NO: 326, SEQ ID NO: 272, SEQ ID NO: 344, SEQ ID NO: 139, SEQ ID NO: 30, SEQ
ID NO: 220, SEQ ID NO: 364, SEQ ID NO: 369, SEQ ID NO: 372, SEQ ID NO: 991,
25 SEQ ID NO: 128, SEQ ID NO: 347, SEQ ID NO: 52, SEQ ID NO: 12, SEQ ID NO: 247,
SEQ ID NO: 64, SEQ ID NO: 101, SEQ ID NO: 338, SEQ ID NO: 83, SEQ ID NO: 46,
SEQ ID NO: 348, SEQ ID NO: 223, SEQ ID NO: 39, SEQ ID NO: 232, SEQ ID NO: 168,
SEQ ID NO: 65, SEQ ID NO: 952, SEQ ID NO: 341, SEQ ID NO: 69, SEQ ID NO: 924,
SEQ ID NO: 4, SEQ ID NO: 197, SEQ ID NO: 313, SEQ ID NO: 119, SEQ ID NO: 188,
30 SEQ ID NO: 956, SEQ ID NO: 935, SEQ ID NO: 246, SEQ ID NO: 196, SEQ ID NO:
376, SEQ ID NO: 172, SEQ ID NO: 25, SEQ ID NO: 126, SEQ ID NO: 951, SEQ ID NO:
147, SEQ ID NO: 895, SEQ ID NO: 14, SEQ ID NO: 154, SEQ ID NO: 277, SEQ ID NO:
363, SEQ ID NO: 342, SEQ ID NO: 378, SEQ ID NO: 130, SEQ ID NO: 198, SEQ ID
NO: 243, SEQ ID NO: 19, SEQ ID NO: 9, SEQ ID NO: 149, SEQ ID NO: 167, SEQ ID
35 NO: 349, SEQ ID NO: 209, SEQ ID NO: 990, SEQ ID NO: 185, SEQ ID NO: 883, SEQ
ID NO: 8, SEQ ID NO: 887, SEQ ID NO: 350, SEQ ID NO: 987, SEQ ID NO: 63, SEQ ID
NO: 249, SEQ ID NO: 118, SEQ ID NO: 132, SEQ ID NO: 47, SEQ ID NO: 106, SEQ ID
NO: 324, SEQ ID NO: 155, SEQ ID NO: 121, SEQ ID NO: 153, SEQ ID NO: 87, SEQ ID
NO: 986, SEQ ID NO: 262, SEQ ID NO: 333, SEQ ID NO: 36, SEQ ID NO: 982, SEQ ID

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NO: 180, SEQ ID NO: 84, SEQ ID NO: 900, SEQ ID NO: 20, SEQ ID NO: 7, SEQ ID NO:
61, SEQ ID NO: 253, SEQ ID NO: 120, SEQ ID NO: 268, SEQ ID NO: 299, SEQ ID NO:
942, SEQ ID NO: 173, SEQ ID NO: 187, SEQ ID NO: 187, SEQ ID NO: 234, SEQ ID
NO: 112, SEQ ID NO: 324, SEQ ID NO: 971, SEQ ID NO: 62, SEQ ID NO: 308, SEQ ID
5 NO: 74, SEQ ID NO: 1, SEQ ID NO: 266, SEQ ID NO: 337, SEQ ID NO: 93, SEQ ID NO:
44, SEQ ID NO: 335, SEQ ID NO: 368, SEQ ID NO: 208, SEQ ID NO: 358, SEQ ID NO:
923, SEQ ID NO: 310, SEQ ID NO: 26, SEQ ID NO: 279, SEQ ID NO: 890, SEQ ID NO:
325, SEQ ID NO: 109, SEQ ID NO: 143, SEQ ID NO: 918, SEQ ID NO: 252, SEQ ID
NO: 953, SEQ ID NO: 902, SEQ ID NO: 174, SEQ ID NO: 73, SEQ ID NO: 898, SEQ ID
10 NO: 300, SEQ ID NO: 356, SEQ ID NO: 298, SEQ ID NO: 354, SEQ ID NO: 138, SEQ
ID NO: 319, SEQ ID NO: 80, SEQ ID NO: 933, SEQ ID NO: 891, SEQ ID NO: 366, SEQ
ID NO: 113, SEQ ID NO: 320, SEQ ID NO: 915, SEQ ID NO: 351, SEQ ID NO: 162,
SEQ ID NO: 965, SEQ ID NO: 67, SEQ ID NO: 314, SEQ ID NO: 904, SEQ ID NO: 345,
SEQ ID NO: 374, SEQ ID NO: 962, SEQ ID NO: 270, SEQ ID NO: 186, SEQ ID NO: 60,
15 SEQ ID NO: 379, SEQ ID NO: 889, SEQ ID NO: 967, SEQ ID NO: 973, SEQ ID NO:
280, SEQ ID NO: 170, SEQ ID NO: 985, and SEQ ID NO: 932.

In one embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in energy conversion encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1147, SEQ ID NO:
20 1288, SEQ ID NO: 1324, SEQ ID NO: 1363, SEQ ID NO: 882, SEQ ID NO: 382, SEQ ID
NO: 130, and SEQ ID NO: 230.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in amino acid metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 997, SEQ
25 ID NO: 1015, SEQ ID NO: 1084, SEQ ID NO: 1094, SEQ ID NO: 1099, SEQ ID NO:
1229, SEQ ID NO: 1250, SEQ ID NO: 1268, SEQ ID NO: 1293, SEQ ID NO: 1339, SEQ
ID NO: 1408, SEQ ID NO: 1429, SEQ ID NO: 1434, SEQ ID NO: 1228, SEQ ID NO:
1031, SEQ ID NO: 1034, SEQ ID NO: 1008, SEQ ID NO: 269, SEQ ID NO: 312, SEQ ID
NO: 211, SEQ ID NO: 959, SEQ ID NO: 938, SEQ ID NO: 110, SEQ ID NO: 244, SEQ
30 ID NO: 328, SEQ ID NO: 235, SEQ ID NO: 315, SEQ ID NO: 296, SEQ ID NO: 976,
SEQ ID NO: 321, SEQ ID NO: 43, SEQ ID NO: 281, SEQ ID NO: 326, and SEQ ID NO:
272.

In yet another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in nucleotide metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1061, SEQ
35 ID NO: 1064, SEQ ID NO: 1191, SEQ ID NO: 1217, SEQ ID NO: 1365, SEQ ID NO:
1394, SEQ ID NO: 1414, SEQ ID NO: 1415, SEQ ID NO: 1435, SEQ ID NO: 1058, SEQ
ID NO: 1059, SEQ ID NO: 344, SEQ ID NO: 139, SEQ ID NO: 30, SEQ ID NO: 220,

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SEQ ID NO: 364, SEQ ID NO: 369, SEQ ID NO: 372, SEQ ID NO: 991, SEQ ID NO: 128, SEQ ID NO: 347, and SEQ ID NO: 52.

In yet a further embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in carbohydrate

5 metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1080, SEQ ID NO: 1128, SEQ ID NO: 1133, SEQ ID NO: 1211, SEQ ID NO: 1252, SEQ ID NO: 1253, SEQ ID NO: 1286, SEQ ID NO: 1289, SEQ ID NO: 1291, SEQ ID NO: 1303, SEQ ID NO: 1396, SEQ ID NO: 996, SEQ ID NO: 12, SEQ ID NO: 247, SEQ ID NO: 64, SEQ ID NO: 101, SEQ ID NO: 338, SEQ ID NO: 83, SEQ ID NO: 46, SEQ ID NO: 348, SEQ ID NO: 223, SEQ ID NO: 39, SEQ ID NO: 232, and SEQ ID NO: 168.

10 In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in cofactor metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1095, SEQ ID NO: 1156, SEQ ID NO: 1158, SEQ ID NO: 1159, SEQ ID NO: 1277, SEQ ID NO: 1038, SEQ ID NO: 65, SEQ ID NO: 952, SEQ ID NO: 341, SEQ ID NO: 69, SEQ ID NO: 924, and SEQ ID NO: 4.

15 In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in lipid metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1257, SEQ ID NO: 1357, SEQ ID NO: 1436, SEQ ID NO: 197, SEQ ID NO: 313, and SEQ ID NO: 119.

20 In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in mRNA translation and ribosome biogenesis encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1047, SEQ ID NO: 1055, SEQ ID NO: 1141, SEQ ID NO: 1227, SEQ ID NO: 1327, SEQ ID NO: 1412, SEQ ID NO: 188, SEQ ID NO: 956, SEQ ID NO: 935, SEQ ID NO: 246, SEQ ID NO: 196, and SEQ ID NO: 376.

25 In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in genome replication, transcription, recombination and repair encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1003, SEQ ID NO: 1087, SEQ ID NO: 1116, SEQ ID NO: 1130, SEQ ID NO: 1132, SEQ ID NO: 1185, SEQ ID NO: 1188, SEQ ID NO: 1198, SEQ ID NO: 1218, SEQ ID NO: 1244, SEQ ID NO: 1306, SEQ ID NO: 1325, SEQ ID NO: 1397, SEQ ID NO: 1398, SEQ ID NO: 1407, SEQ ID NO: 1433, SEQ ID NO: 172, SEQ ID NO: 25, SEQ ID NO: 126, SEQ ID NO: 951, SEQ ID NO: 147, SEQ ID NO: 895, SEQ ID NO: 14, SEQ ID NO: 154, SEQ ID NO: 277, SEQ ID NO: 363, SEQ ID NO: 342, SEQ ID NO: 378, SEQ ID NO: 130, SEQ ID NO: 198, SEQ ID NO: 243, SEQ ID NO: 19, and SEQ ID NO: 9.

30 In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in outer membrane or cell wall

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biosynthesis encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1216, SEQ ID NO: 1239, SEQ ID NO: 1362, SEQ ID NO: 1017, SEQ ID NO: 1019, SEQ ID NO: 1360, SEQ ID NO: 149, SEQ ID NO: 167, SEQ ID NO: 349, SEQ ID NO: 209, SEQ ID NO: 990, SEQ ID NO: 185, SEQ ID NO: 883, and SEQ ID NO: 8.

5 In yet another embodiment, the *H. pylori* cytoplasmic polypeptide is an *H. pylori* chaperone polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1423, SEQ ID NO: 1425, SEQ ID NO: 1374, SEQ ID NO: 887, SEQ ID NO: 350, and SEQ ID NO: 987.

Particularly preferred is an isolated nucleic acid comprising a nucleotide sequence
10 encoding an *H. pylori* secreted or periplasmic polypeptide or a fragment thereof. Such nucleic acid is selected from the group consisting of SEQ ID NO: 1004, SEQ ID NO: 1138, SEQ ID NO: 1067, SEQ ID NO: 1078, SEQ ID NO: 1314, SEQ ID NO: 1319, SEQ ID NO: 1378, SEQ ID NO: 1105, SEQ ID NO: 1114, SEQ ID NO: 1118, SEQ ID NO: 1120, SEQ ID NO: 1123, SEQ ID NO: 1127, SEQ ID NO: 1212, SEQ ID NO: 1223, SEQ ID NO: 1225, SEQ ID NO: 1246, SEQ ID NO: 1248, SEQ ID NO: 1259, SEQ ID NO: 1264, SEQ ID NO: 1265, SEQ ID NO: 1281, SEQ ID NO: 1285, SEQ ID NO: 1294, SEQ ID NO: 1298, SEQ ID NO: 1299, SEQ ID NO: 1315, SEQ ID NO: 1316, SEQ ID NO: 1317, SEQ ID NO: 1318, SEQ ID NO: 1344, SEQ ID NO: 1351, SEQ ID NO: 1353, SEQ ID NO: 1373, SEQ ID NO: 1380, SEQ ID NO: 1387, SEQ ID NO: 1389, SEQ ID NO: 1393, SEQ ID NO: 1411, SEQ ID NO: 1428, SEQ ID NO: 1431, SEQ ID NO: 1439, SEQ ID NO: 1043, SEQ ID NO: 1183, SEQ ID NO: 1184, SEQ ID NO: 1196, SEQ ID NO: 1197, SEQ ID NO: 1203, SEQ ID NO: 995, SEQ ID NO: 998, SEQ ID NO: 1001, SEQ ID NO: 1022, SEQ ID NO: 1023, SEQ ID NO: 1029, SEQ ID NO: 1040, SEQ ID NO: 1051, SEQ ID NO: 1062, SEQ ID NO: 1154, SEQ ID NO: 1320, SEQ ID NO: 1075, SEQ ID NO: 1106, SEQ ID NO: 1109, SEQ ID NO: 1134, SEQ ID NO: 1221, SEQ ID NO: 1226, SEQ ID NO: 1235, SEQ ID NO: 1301, SEQ ID NO: 1311, SEQ ID NO: 1326, SEQ ID NO: 1341, SEQ ID NO: 1354, SEQ ID NO: 1364, SEQ ID NO: 1366, SEQ ID NO: 1376, SEQ ID NO: 1391, SEQ ID NO: 1395, SEQ ID NO: 1445, SEQ ID NO: 1079, SEQ ID NO: 1186, SEQ ID NO: 1010, SEQ ID NO: 1016, SEQ ID NO: 1172, SEQ ID NO: 1174, SEQ ID NO: 117, SEQ ID NO: 254, SEQ ID NO: 24, SEQ ID NO: 242, SEQ ID NO: 950, SEQ ID NO: 263, SEQ ID NO: 286, SEQ ID NO: 947, SEQ ID NO: 51, SEQ ID NO: 177, SEQ ID NO: 156, SEQ ID NO: 190, SEQ ID NO: 375, SEQ ID NO: 222, SEQ ID NO: 21, SEQ ID NO: 912, SEQ ID NO: 148, SEQ ID NO: 202, SEQ ID NO: 224, SEQ ID NO: 112, SEQ ID NO: 32, SEQ ID NO: 339, SEQ ID NO: 182, SEQ ID NO: 228, SEQ ID NO: 152, SEQ ID NO: 219, SEQ ID NO: 137, SEQ ID NO: 318, SEQ ID NO: 141, SEQ ID NO: 165, SEQ ID NO: 334, SEQ ID NO: 13, SEQ ID NO: 297, SEQ ID NO: 35, SEQ ID NO: 216, SEQ ID NO: 908, SEQ ID NO: 124, SEQ ID NO: 75, SEQ ID NO: 927, SEQ ID NO: 221, SEQ ID NO: 178, SEQ ID NO: 169, SEQ ID NO: 293, SEQ ID NO: 289, SEQ ID NO: 926, SEQ ID NO: 948, SEQ ID NO: 115, SEQ ID NO: 251, SEQ ID NO: 345, SEQ

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- ID NO: 17, SEQ ID NO: 920, SEQ ID NO: 95, SEQ ID NO: 86, SEQ ID NO: 360, SEQ ID NO: 271, SEQ ID NO: 970, SEQ ID NO: 288, SEQ ID NO: 282, SEQ ID NO: 98, SEQ ID NO: 29, SEQ ID NO: 317, SEQ ID NO: 343, SEQ ID NO: 291, SEQ ID NO: 108, SEQ ID NO: 377, SEQ ID NO: 305, SEQ ID NO: 305, SEQ ID NO: 100, SEQ ID NO: 988, SEQ ID NO: 212, SEQ ID NO: 884, SEQ ID NO: 37, SEQ ID NO: 968, SEQ ID NO: 975, SEQ ID NO: 237, SEQ ID NO: 335, SEQ ID NO: 260, SEQ ID NO: 370, SEQ ID NO: 91, SEQ ID NO: 276, SEQ ID NO: 311, SEQ ID NO: 173, SEQ ID NO: 102, SEQ ID NO: 304, SEQ ID NO: 380, SEQ ID NO: 127, SEQ ID NO: 993, SEQ ID NO: 925, SEQ ID NO: 181, and SEQ ID NO: 171.
- Particularly preferred is an isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* surface or membrane polypeptide or a fragment thereof. Such nucleic acid is selected from the group consisting of SEQ ID NO: 1060, SEQ ID NO: 1110, SEQ ID NO: 1112, SEQ ID NO: 1230, SEQ ID NO: 1260, SEQ ID NO: 1280, SEQ ID NO: 1292, SEQ ID NO: 1296, SEQ ID NO: 1307, SEQ ID NO: 1442, SEQ ID NO: 1444, SEQ ID NO: 1122, SEQ ID NO: 1254, SEQ ID NO: 1256, SEQ ID NO: 1272, SEQ ID NO: 1275, SEQ ID NO: 1309, SEQ ID NO: 1313, SEQ ID NO: 1347, SEQ ID NO: 1352, SEQ ID NO: 1356, SEQ ID NO: 1438, SEQ ID NO: 1441, SEQ ID NO: 1009, SEQ ID NO: 1026, SEQ ID NO: 1048, SEQ ID NO: 1063, SEQ ID NO: 1190, SEQ ID NO: 1083, SEQ ID NO: 1113, SEQ ID NO: 1222, SEQ ID NO: 1295, SEQ ID NO: 1343, SEQ ID NO: 1392, SEQ ID NO: 1443, SEQ ID NO: 1085, SEQ ID NO: 1093, SEQ ID NO: 1117, SEQ ID NO: 1121, SEQ ID NO: 1131, SEQ ID NO: 1287, SEQ ID NO: 1440, SEQ ID NO: 1209, SEQ ID NO: 1342, SEQ ID NO: 1381, SEQ ID NO: 1390, SEQ ID NO: 1409, SEQ ID NO: 1035, SEQ ID NO: 1014, SEQ ID NO: 1088, SEQ ID NO: 1242, SEQ ID NO: 1178, SEQ ID NO: 1089, SEQ ID NO: 1340, SEQ ID NO: 1074, SEQ ID NO: 1107, SEQ ID NO: 1204, SEQ ID NO: 1066, SEQ ID NO: 381, SEQ ID NO: 229, SEQ ID NO: 323, SEQ ID NO: 371, SEQ ID NO: 284, SEQ ID NO: 116, SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 907, SEQ ID NO: 193, SEQ ID NO: 145, SEQ ID NO: 59, SEQ ID NO: 322, SEQ ID NO: 94, SEQ ID NO: 306, SEQ ID NO: 939, SEQ ID NO: 205, SEQ ID NO: 123, SEQ ID NO: 906, SEQ ID NO: 928, SEQ ID NO: 346, SEQ ID NO: 129, SEQ ID NO: 307, SEQ ID NO: 133, SEQ ID NO: 131, SEQ ID NO: 886, SEQ ID NO: 179, SEQ ID NO: 104, SEQ ID NO: 213, SEQ ID NO: 359, SEQ ID NO: 140, SEQ ID NO: 146, SEQ ID NO: 327, SEQ ID NO: 365, SEQ ID NO: 33, SEQ ID NO: 331, SEQ ID NO: 175, SEQ ID NO: 200, SEQ ID NO: 292, SEQ ID NO: 23, SEQ ID NO: 336, SEQ ID NO: 301, SEQ ID NO: 28, SEQ ID NO: 941, SEQ ID NO: 103, SEQ ID NO: 231, SEQ ID NO: 176, SEQ ID NO: 31, SEQ ID NO: 917, SEQ ID NO: 151, SEQ ID NO: 922, SEQ ID NO: 265, SEQ ID NO: 142, SEQ ID NO: 259, SEQ ID NO: 122, SEQ ID NO: 206, SEQ ID NO: 96, SEQ ID NO: 353, SEQ ID NO: 38, SEQ ID NO: 89, SEQ ID NO: 77, SEQ ID NO: 954, SEQ ID NO: 264, SEQ ID NO: 937, SEQ ID NO: 226, SEQ ID NO: 283, SEQ ID NO: 88,

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SEQ ID NO: 125, SEQ ID NO: 183, SEQ ID NO: 195, SEQ ID NO: 81, SEQ ID NO: 901, SEQ ID NO: 82, SEQ ID NO: 42, SEQ ID NO: 881, and SEQ ID NO: 885.

In one embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least one membrane

- 5 spanning region encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1060, SEQ ID NO: 1110, SEQ ID NO: 1112, SEQ ID NO: 1230, SEQ ID NO: 1260, SEQ ID NO: 1280, SEQ ID NO: 1292, SEQ ID NO: 1296, SEQ ID NO: 1307, SEQ ID NO: 1442, SEQ ID NO: 1444, SEQ ID NO: 381, SEQ ID NO: 229, SEQ ID NO: 323, SEQ ID NO: 371, SEQ ID NO: 284, SEQ ID NO: 116, SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 907, SEQ ID NO: 193, SEQ ID NO: 145, SEQ ID NO: 59, SEQ ID NO: 322, SEQ ID NO: 94, SEQ ID NO: 306, and SEQ ID NO: 881.

- 10 In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least two membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1122, SEQ ID NO: 1254, SEQ ID NO: 1256, SEQ ID NO: 1272, SEQ ID NO: 1275, SEQ ID NO: 1309, SEQ ID NO: 1313, SEQ ID NO: 1347, SEQ ID NO: 1352, SEQ ID NO: 1356, SEQ ID NO: 1438, SEQ ID NO: 1441, SEQ ID NO: 1009, SEQ ID NO: 1026, SEQ ID NO: 1048, SEQ ID NO: 1063, SEQ ID NO: 1190, SEQ ID NO: 939, SEQ ID NO: 205, SEQ ID NO: 123, SEQ ID NO: 906, SEQ ID NO: 928, SEQ ID NO: 346, SEQ ID NO: 129, SEQ ID NO: 307, SEQ ID NO: 133, SEQ ID NO: 131, SEQ ID NO: 886, SEQ ID NO: 179, SEQ ID NO: 104, SEQ ID NO: 213, SEQ ID NO: 359, SEQ ID NO: 140, SEQ ID NO: 146, SEQ ID NO: 327, and SEQ ID NO: 365.

- 15 In yet another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least three membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1083, SEQ ID NO: 1113, SEQ ID NO: 1222, SEQ ID NO: 1295, SEQ ID NO: 1343, SEQ ID NO: 1392, SEQ ID NO: 1443, SEQ ID NO: 33, SEQ ID NO: 331, SEQ ID NO: 175, SEQ ID NO: 200, SEQ ID NO: 292, SEQ ID NO: 23, and SEQ ID NO: 336.

- 20 In yet a further embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least four membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1085, SEQ ID NO: 1093, SEQ ID NO: 1117, SEQ ID NO: 1121, SEQ ID NO: 1131, SEQ ID NO: 1287, SEQ ID NO: 1440, SEQ ID NO: 1209, SEQ ID NO: 301, SEQ ID NO: 28, SEQ ID NO: 941, SEQ ID NO: 103, SEQ ID NO: 231, SEQ ID NO: 176, SEQ ID NO: 31, SEQ ID NO: 917, SEQ ID NO: 151, and SEQ ID NO: 922.

- 25 In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least five membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1342, SEQ ID NO: 1381, SEQ ID NO: 1390, SEQ ID NO: 1409, SEQ ID

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NO: 1035, SEQ ID NO: 265, SEQ ID NO: 142, SEQ ID NO: 259, SEQ ID NO: 122, SEQ ID NO: 206, and SEQ ID NO: 885.

In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least six membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1014, SEQ ID NO: 1088, SEQ ID NO: 1242, SEQ ID NO: 1178, SEQ ID NO: 96, SEQ ID NO: 353, SEQ ID NO: 38, SEQ ID NO: 89, SEQ ID NO: 77, SEQ ID NO: 954, SEQ ID NO: 264.

In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least seven membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1089, SEQ ID NO: 1340, SEQ ID NO: 1074, SEQ ID NO: 1107, SEQ ID NO: 1204, SEQ ID NO: 1066, SEQ ID NO: 937, SEQ ID NO: 226, SEQ ID NO: 283, SEQ ID NO: 88, SEQ ID NO: 125, SEQ ID NO: 183, SEQ ID NO: 195, SEQ ID NO: 81, SEQ ID NO: 901, SEQ ID NO: 82, and SEQ ID NO: 42.

Particularly preferred is a purified or isolated *H. pylori* cell envelope polypeptide or a fragment thereof, wherein the polypeptide is selected from the group consisting of SEQ ID NO: 1471, SEQ ID NO: 1472, SEQ ID NO: 1487, SEQ ID NO: 1501, SEQ ID NO: 1522, SEQ ID NO: 1552, SEQ ID NO: 1586, SEQ ID NO: 1727, SEQ ID NO: 1601, SEQ ID NO: 1638, SEQ ID NO: 1643, SEQ ID NO: 1812, SEQ ID NO: 1830, SEQ ID NO: 1850, SEQ ID NO: 1854, SEQ ID NO: 1851, SEQ ID NO: 1640, SEQ ID NO: 1453, SEQ ID NO: 1664, SEQ ID NO: 1665, SEQ ID NO: 1666, SEQ ID NO: 1685, SEQ ID NO: 1687, SEQ ID NO: 1688, SEQ ID NO: 1675, SEQ ID NO: 1702, SEQ ID NO: 1713, SEQ ID NO: 1600, SEQ ID NO: 1671, SEQ ID NO: 1691, SEQ ID NO: 1615, SEQ ID NO: 1616, SEQ ID NO: 1855, SEQ ID NO: 1595, SEQ ID NO: 1633, SEQ ID NO: 1608, SEQ ID NO: 1611, SEQ ID NO: 1751, SEQ ID NO: 1772, SEQ ID NO: 1774, SEQ ID NO: 1780, SEQ ID NO: 1783, SEQ ID NO: 1796, SEQ ID NO: 1809, SEQ ID NO: 1826, SEQ ID NO: 1868, SEQ ID NO: 1734, SEQ ID NO: 1786, SEQ ID NO: 1819, SEQ ID NO: 1630, SEQ ID NO: 1706, SEQ ID NO: 1709, SEQ ID NO: 1495, SEQ ID NO: 1724, SEQ ID NO: 1670, SEQ ID NO: 1725, SEQ ID NO: 1661, SEQ ID NO: 1873, SEQ ID NO: 1753, SEQ ID NO: 1759, SEQ ID NO: 1761, SEQ ID NO: 1782, SEQ ID NO: 1883, SEQ ID NO: 1503, SEQ ID NO: 1542, SEQ ID NO: 1872, SEQ ID NO: 1520, SEQ ID NO: 1456, SEQ ID NO: 1458, SEQ ID NO: 1617, SEQ ID NO: 1628, SEQ ID NO: 1644, SEQ ID NO: 1657, SEQ ID NO: 1658, SEQ ID NO: 1755, SEQ ID NO: 1756, SEQ ID NO: 1797, SEQ ID NO: 1799, SEQ ID NO: 1801, SEQ ID NO: 1483, SEQ ID NO: 1504, SEQ ID NO: 1532, SEQ ID NO: 1575, SEQ ID NO: 1833, SEQ ID NO: 1888, SEQ ID NO: 1714, SEQ ID NO: 1624, SEQ ID NO: 1856, SEQ ID NO: 1857, SEQ ID NO: 1861, SEQ ID NO: 1537, SEQ ID NO: 1773, SEQ ID NO: 1717, SEQ ID NO: 1733, SEQ ID NO: 1722, SEQ ID NO: 1659, SEQ ID NO: 1577, SEQ ID NO: 1721, SEQ ID NO: 1729, SEQ

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- ID NO: 1870, SEQ ID NO: 1576, SEQ ID NO: 1632, SEQ ID NO: 1867, SEQ ID NO:
1547, SEQ ID NO: 1533, SEQ ID NO: 1597, SEQ ID NO: 1596, SEQ ID NO: 1559, SEQ
ID NO: 1599, SEQ ID NO: 1788, SEQ ID NO: 1789, SEQ ID NO: 1875, SEQ ID NO:
1451, SEQ ID NO: 1478, SEQ ID NO: 1626, SEQ ID NO: 1781, SEQ ID NO: 660, SEQ
5 ID NO: 660, SEQ ID NO: 855, SEQ ID NO: 534, SEQ ID NO: 675, SEQ ID NO: 404,
SEQ ID NO: 518, SEQ ID NO: 464, SEQ ID NO: 672, SEQ ID NO: 640, SEQ ID NO:
490, SEQ ID NO: 755, SEQ ID NO: 389, SEQ ID NO: 635, SEQ ID NO: 877, SEQ ID
NO: 637, SEQ ID NO: 477, SEQ ID NO: 772, SEQ ID NO: 658, SEQ ID NO: 463, SEQ
ID NO: 852, SEQ ID NO: 503, SEQ ID NO: 411, SEQ ID NO: 441, SEQ ID NO: 782,
10 SEQ ID NO: 575, SEQ ID NO: 691, SEQ ID NO: 724, SEQ ID NO: 452, SEQ ID NO:
386, SEQ ID NO: 497, SEQ ID NO: 712, SEQ ID NO: 591, SEQ ID NO: 638, SEQ ID
NO: 740, SEQ ID NO: 697, SEQ ID NO: 569, SEQ ID NO: 470, SEQ ID NO: 700, SEQ
ID NO: 586, SEQ ID NO: 823, SEQ ID NO: 627, SEQ ID NO: 627, SEQ ID NO: 684,
SEQ ID NO: 551, SEQ ID NO: 478, SEQ ID NO: 508, SEQ ID NO: 545, SEQ ID NO:
15 628, SEQ ID NO: 443, SEQ ID NO: 702, SEQ ID NO: 776, SEQ ID NO: 461, SEQ ID
NO: 737, SEQ ID NO: 809, SEQ ID NO: 642, SEQ ID NO: 879, SEQ ID NO: 773, SEQ
ID NO: 468, SEQ ID NO: 842, SEQ ID NO: 788, SEQ ID NO: 624, SEQ ID NO: 788,
SEQ ID NO: 644, SEQ ID NO: 727, SEQ ID NO: 631, SEQ ID NO: 450, SEQ ID NO:
448, SEQ ID NO: 653, SEQ ID NO: 495, SEQ ID NO: 400, SEQ ID NO: 541, SEQ ID
20 NO: 673, SEQ ID NO: 482, SEQ ID NO: 622, SEQ ID NO: 689, SEQ ID NO: 736, SEQ
ID NO: 417, SEQ ID NO: 716, SEQ ID NO: 762, SEQ ID NO: 395, SEQ ID NO: 587,
SEQ ID NO: 669, SEQ ID NO: 758, SEQ ID NO: 593, SEQ ID NO: 451, SEQ ID NO:
827, SEQ ID NO: 502, SEQ ID NO: 719, SEQ ID NO: 469, SEQ ID NO: 715, SEQ ID
NO: 847, SEQ ID NO: 453, SEQ ID NO: 527, SEQ ID NO: 652, SEQ ID NO: 745, SEQ
25 ID NO: 567, SEQ ID NO: 848, SEQ ID NO: 430, SEQ ID NO: 748, SEQ ID NO: 396,
SEQ ID NO: 588, SEQ ID NO: 795, SEQ ID NO: 523, SEQ ID NO: 791, SEQ ID NO:
714, SEQ ID NO: 481, SEQ ID NO: 765, SEQ ID NO: 837, SEQ ID NO: 833, SEQ ID
NO: 585, SEQ ID NO: 865, SEQ ID NO: 764, SEQ ID NO: 440, SEQ ID NO: 465, SEQ
ID NO: 555, SEQ ID NO: 526, SEQ ID NO: 687, SEQ ID NO: 692, SEQ ID NO: 693,
30 SEQ ID NO: 677, SEQ ID NO: 649, SEQ ID NO: 812, SEQ ID NO: 820, SEQ ID NO:
880, SEQ ID NO: 590, SEQ ID NO: 713, SEQ ID NO: 750, SEQ ID NO: 613, SEQ ID NO:
437, SEQ ID NO: 556, SEQ ID NO: 657, SEQ ID NO: 402, SEQ ID NO: 623, SEQ ID
NO: 862, SEQ ID NO: 449, SEQ ID NO: 690, SEQ ID NO: 424, SEQ ID NO: 821, SEQ
ID NO: 432, SEQ ID NO: 811, SEQ ID NO: 554, and SEQ ID NO: 809.
- 35 In one embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is
an *H. pylori* flagella-associated polypeptide or a fragment thereof selected from the group
consisting of SEQ ID NO: 1471, SEQ ID NO: 1472, SEQ ID NO: 1487, SEQ ID NO: 1501,
SEQ ID NO: 1522, SEQ ID NO: 1552, SEQ ID NO: 1586, SEQ ID NO: 1727, SEQ ID
NO: 1601, SEQ ID NO: 1638, SEQ ID NO: 1643, SEQ ID NO: 1812, SEQ ID NO: 1830,

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SEQ ID NO: 1850, SEQ ID NO: 1854, SEQ ID NO: 1851, SEQ ID NO: 1640, SEQ ID NO: 660, SEQ ID NO: 660, SEQ ID NO: 855, SEQ ID NO: 534, SEQ ID NO: 675, SEQ ID NO: 404, SEQ ID NO: 518, SEQ ID NO: 464, SEQ ID NO: 672, SEQ ID NO: 640, SEQ ID NO: 490, SEQ ID NO: 755, SEQ ID NO: 389, SEQ ID NO: 635, SEQ ID NO: 877, SEQ ID NO: 637, SEQ ID NO: 477, SEQ ID NO: 772, and SEQ ID NO: 658.

In another embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* inner membrane polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1453, SEQ ID NO: 1664, SEQ ID NO: 1665, SEQ ID NO: 1666, SEQ ID NO: 1685, SEQ ID NO: 1687, SEQ ID NO: 1688, SEQ ID NO: 1675, SEQ ID NO: 1702, SEQ ID NO: 1713, SEQ ID NO: 1600, SEQ ID NO: 1671, SEQ ID NO: 1691, SEQ ID NO: 1615, SEQ ID NO: 1616, SEQ ID NO: 1855, SEQ ID NO: 1595, SEQ ID NO: 1633, SEQ ID NO: 1608, SEQ ID NO: 1611, SEQ ID NO: 1751, SEQ ID NO: 1772, SEQ ID NO: 1774, SEQ ID NO: 1780, SEQ ID NO: 1783, SEQ ID NO: 1796, SEQ ID NO: 1809, SEQ ID NO: 1826, SEQ ID NO: 1868, SEQ ID NO: 1734, SEQ ID NO: 1786, SEQ ID NO: 1819, SEQ ID NO: 1630, SEQ ID NO: 1706, SEQ ID NO: 1709, SEQ ID NO: 1495, SEQ ID NO: 1724, SEQ ID NO: 463, SEQ ID NO: 852, SEQ ID NO: 503, SEQ ID NO: 411, SEQ ID NO: 441, SEQ ID NO: 782, SEQ ID NO: 575, SEQ ID NO: 691, SEQ ID NO: 724, SEQ ID NO: 452, SEQ ID NO: 386, SEQ ID NO: 497, SEQ ID NO: 712, SEQ ID NO: 591, SEQ ID NO: 638, SEQ ID NO: 740, SEQ ID NO: 697, SEQ ID NO: 569, SEQ ID NO: 470, SEQ ID NO: 700, SEQ ID NO: 586, SEQ ID NO: 823, SEQ ID NO: 627, SEQ ID NO: 627, SEQ ID NO: 684, SEQ ID NO: 551, SEQ ID NO: 478, SEQ ID NO: 508, SEQ ID NO: 545, SEQ ID NO: 628, SEQ ID NO: 443, SEQ ID NO: 702, SEQ ID NO: 776, SEQ ID NO: 461, SEQ ID NO: 737, SEQ ID NO: 809, SEQ ID NO: 642, SEQ ID NO: 879, SEQ ID NO: 773, SEQ ID NO: 468, SEQ ID NO: 842, SEQ ID NO: 788, SEQ ID NO: 624, SEQ ID NO: 788, SEQ ID NO: 644, SEQ ID NO: 727, SEQ ID NO: 631, SEQ ID NO: 450, SEQ ID NO: 448, and SEQ ID NO: 653.

In yet another embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* transporter polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1670, SEQ ID NO: 1725, SEQ ID NO: 1661, SEQ ID NO: 1873, SEQ ID NO: 1753, SEQ ID NO: 1759, SEQ ID NO: 1761, SEQ ID NO: 1782, SEQ ID NO: 1883, SEQ ID NO: 1503, SEQ ID NO: 1542, SEQ ID NO: 1872, SEQ ID NO: 1520, SEQ ID NO: 1456, SEQ ID NO: 1458, SEQ ID NO: 1617, SEQ ID NO: 1628, SEQ ID NO: 1644, SEQ ID NO: 1657, SEQ ID NO: 1658, SEQ ID NO: 1755, SEQ ID NO: 1756, SEQ ID NO: 1797, SEQ ID NO: 1799, SEQ ID NO: 1801, SEQ ID NO: 1483, SEQ ID NO: 1504, SEQ ID NO: 1532, SEQ ID NO: 1575, SEQ ID NO: 1833, SEQ ID NO: 1888, SEQ ID NO: 1714, SEQ ID NO: 495, SEQ ID NO: 400, SEQ ID NO: 541, SEQ ID NO: 673, SEQ ID NO: 482, SEQ ID NO: 622, SEQ ID NO: 689, SEQ ID NO: 736, SEQ ID NO: 417, SEQ ID NO: 716, SEQ ID NO: 762, SEQ ID NO: 395, SEQ ID NO: 587, SEQ ID NO: 669, SEQ ID NO: 758, SEQ ID NO: 593, SEQ ID NO: 451, SEQ ID NO: 827,

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SEQ ID NO: 502, SEQ ID NO: 719, SEQ ID NO: 469, SEQ ID NO: 715, SEQ ID NO: 847, SEQ ID NO: 453, SEQ ID NO: 527, SEQ ID NO: 652, SEQ ID NO: 745, SEQ ID NO: 567, SEQ ID NO: 848, SEQ ID NO: 430, SEQ ID NO: 748, SEQ ID NO: 396, SEQ ID NO: 588, SEQ ID NO: 795, SEQ ID NO: 523, SEQ ID NO: 791, SEQ ID NO: 714,
5 SEQ ID NO: 481, and SEQ ID NO: 765.

In another embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* outer membrane polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1624, SEQ ID NO: 1856, SEQ ID NO: 1857, SEQ ID NO: 1861, SEQ ID NO: 1537, SEQ ID NO: 1773, SEQ ID NO: 1717, SEQ ID NO: 1733,
10 SEQ ID NO: 1722, SEQ ID NO: 1659, SEQ ID NO: 1577, SEQ ID NO: 1721, SEQ ID NO: 1729, SEQ ID NO: 1870, SEQ ID NO: 1576, SEQ ID NO: 1632, SEQ ID NO: 1867, SEQ ID NO: 1547, SEQ ID NO: 1533, SEQ ID NO: 1597, SEQ ID NO: 1596, SEQ ID NO: 1559, SEQ ID NO: 1599, SEQ ID NO: 1788, SEQ ID NO: 1789, SEQ ID NO: 1875, SEQ ID NO: 1451, SEQ ID NO: 1478, SEQ ID NO: 1626, SEQ ID NO: 1781, SEQ ID NO: 837, SEQ ID NO: 833, SEQ ID NO: 585, SEQ ID NO: 865, SEQ ID NO: 764, SEQ ID NO: 440, SEQ ID NO: 465, SEQ ID NO: 555, SEQ ID NO: 526, SEQ ID NO: 687,
15 SEQ ID NO: 692, SEQ ID NO: 693, SEQ ID NO: 677, SEQ ID NO: 649, and SEQ ID NO: 812.

Particularly preferred is a purified or isolated *H. pylori* cytoplasmic polypeptide or a fragment thereof, wherein the polypeptide is selected from the group consisting of SEQ ID NO: 1598, SEQ ID NO: 1739, SEQ ID NO: 1775, SEQ ID NO: 1814, SEQ ID NO: 1448, SEQ ID NO: 1466, SEQ ID NO: 1535, SEQ ID NO: 1545, SEQ ID NO: 1550, SEQ ID NO: 1680, SEQ ID NO: 1701, SEQ ID NO: 1719, SEQ ID NO: 1744, SEQ ID NO: 1790, SEQ ID NO: 1859, SEQ ID NO: 1880, SEQ ID NO: 1885, SEQ ID NO: 1679, SEQ ID NO: 1482, SEQ ID NO: 1485, SEQ ID NO: 1459, SEQ ID NO: 1512, SEQ ID NO: 1515, SEQ ID NO: 1642, SEQ ID NO: 1668, SEQ ID NO: 1816, SEQ ID NO: 1845, SEQ ID NO: 1865, SEQ ID NO: 1866, SEQ ID NO: 1886, SEQ ID NO: 1509, SEQ ID NO: 1510, SEQ ID NO: 1531, SEQ ID NO: 1579, SEQ ID NO: 1584, SEQ ID NO: 1662, SEQ ID NO: 1703, SEQ ID NO: 1704, SEQ ID NO: 1737, SEQ ID NO: 1740, SEQ ID NO: 1742, SEQ ID NO: 1754, SEQ ID NO: 1847, SEQ ID NO: 1447, SEQ ID NO: 1546, SEQ ID NO: 1607, SEQ ID NO: 1609, SEQ ID NO: 1610, SEQ ID NO: 1728, SEQ ID NO: 1489, SEQ ID NO: 1708, SEQ ID NO: 1808, SEQ ID NO: 1887, SEQ ID NO: 1498, SEQ ID NO: 1506, SEQ ID NO: 1592, SEQ ID NO: 1678, SEQ ID NO: 1778, SEQ ID NO: 1863, SEQ ID NO: 1454, SEQ ID NO: 1538, SEQ ID NO: 1567, SEQ ID NO: 1581, SEQ ID NO: 1583, SEQ ID NO: 1636, SEQ ID NO: 1639, SEQ ID NO: 1649, SEQ ID NO: 1669, SEQ ID NO: 1695, SEQ ID NO: 1757, SEQ ID NO: 1776, SEQ ID NO: 1848, SEQ ID NO: 1849, SEQ ID NO: 1858, SEQ ID NO: 1884, SEQ ID NO: 1667, SEQ ID NO: 1690, SEQ ID NO: 1813, SEQ ID NO: 1468, SEQ ID NO: 1470, SEQ ID NO: 1811, SEQ ID NO: 1874, SEQ ID NO: 1876, SEQ ID NO: 1825, SEQ ID NO: 1479, SEQ ID NO: 1488,

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SEQ ID NO: 1528, SEQ ID NO: 1566, SEQ ID NO: 1683, SEQ ID NO: 1692, SEQ ID NO: 1718, SEQ ID NO: 1614, SEQ ID NO: 1519, SEQ ID NO: 1476, SEQ ID NO: 1493, SEQ ID NO: 1497, SEQ ID NO: 1507, SEQ ID NO: 1490, SEQ ID NO: 1523, SEQ ID NO: 1524, SEQ ID NO: 1543, SEQ ID NO: 1551, SEQ ID NO: 1553, SEQ ID NO: 1554,
5 SEQ ID NO: 1555, SEQ ID NO: 1562, SEQ ID NO: 1570, SEQ ID NO: 1587, SEQ ID NO: 1588, SEQ ID NO: 1591, SEQ ID NO: 1593, SEQ ID NO: 1684, SEQ ID NO: 1689, SEQ ID NO: 1694, SEQ ID NO: 1696, SEQ ID NO: 1698, SEQ ID NO: 1700, SEQ ID NO: 1712, SEQ ID NO: 1720, SEQ ID NO: 1730, SEQ ID NO: 1735, SEQ ID NO: 1741, SEQ ID NO: 1748, SEQ ID NO: 1779, SEQ ID NO: 1821, SEQ ID NO: 1823, SEQ ID NO: 1828, SEQ ID NO: 1834, SEQ ID NO: 1835, SEQ ID NO: 1836, SEQ ID NO: 1839, SEQ ID NO: 1852, SEQ ID NO: 1853, SEQ ID NO: 1869, SEQ ID NO: 1871, SEQ ID NO: 1878, SEQ ID NO: 1521, SEQ ID NO: 1602, SEQ ID NO: 1627, SEQ ID NO: 1450, SEQ ID NO: 1457, SEQ ID NO: 1463, SEQ ID NO: 1469, SEQ ID NO: 1481, SEQ ID NO: 1484, SEQ ID NO: 1492, SEQ ID NO: 1500, SEQ ID NO: 1505, SEQ ID NO: 1508,
10 SEQ ID NO: 1541, SEQ ID NO: 1548, SEQ ID NO: 1580, SEQ ID NO: 1590, SEQ ID NO: 1594, SEQ ID NO: 1603, SEQ ID NO: 1604, SEQ ID NO: 1606, SEQ ID NO: 1612, SEQ ID NO: 1613, SEQ ID NO: 1620, SEQ ID NO: 1621, SEQ ID NO: 1622, SEQ ID NO: 1631, SEQ ID NO: 1645, SEQ ID NO: 1646, SEQ ID NO: 1650, SEQ ID NO: 1651, SEQ ID NO: 1652, SEQ ID NO: 1653, SEQ ID NO: 1656, SEQ ID NO: 1763, SEQ ID NO: 1787, SEQ ID NO: 1800, SEQ ID NO: 1806, SEQ ID NO: 1810, SEQ ID NO: 1864, SEQ ID NO: 1877, SEQ ID NO: 1881, SEQ ID NO: 390, SEQ ID NO: 876, SEQ ID NO: 547, SEQ ID NO: 678, SEQ ID NO: 729, SEQ ID NO: 786, SEQ ID NO: 654, SEQ ID NO: 734, SEQ ID NO: 646, SEQ ID NO: 522, SEQ ID NO: 696, SEQ ID NO: 807, SEQ ID NO: 683, SEQ ID NO: 790, SEQ ID NO: 763, SEQ ID NO: 806, SEQ ID NO: 799,
15 SEQ ID NO: 434, SEQ ID NO: 743, SEQ ID NO: 804, SEQ ID NO: 733, SEQ ID NO: 826, SEQ ID NO: 562, SEQ ID NO: 420, SEQ ID NO: 664, SEQ ID NO: 850, SEQ ID NO: 857, SEQ ID NO: 861, SEQ ID NO: 872, SEQ ID NO: 544, SEQ ID NO: 830, SEQ ID NO: 446, SEQ ID NO: 397, SEQ ID NO: 699, SEQ ID NO: 459, SEQ ID NO: 509, SEQ ID NO: 818, SEQ ID NO: 488, SEQ ID NO: 438, SEQ ID NO: 831, SEQ ID NO:
20 30 SEQ ID NO: 667, SEQ ID NO: 429, SEQ ID NO: 680, SEQ ID NO: 597, SEQ ID NO: 460, SEQ ID NO: 709, SEQ ID NO: 822, SEQ ID NO: 466, SEQ ID NO: 584, SEQ ID NO: 388, SEQ ID NO: 631, SEQ ID NO: 787, SEQ ID NO: 532, SEQ ID NO: 619, SEQ ID NO: 723, SEQ ID NO: 641, SEQ ID NO: 698, SEQ ID NO: 630, SEQ ID NO: 869, SEQ ID NO: 601, SEQ ID NO: 415, SEQ ID NO: 542, SEQ ID NO: 704, SEQ ID NO: 572, SEQ ID NO: 467, SEQ ID NO: 399, SEQ ID NO: 579, SEQ ID NO: 739, SEQ ID NO: 849, SEQ ID NO: 824, SEQ ID NO: 871, SEQ ID NO: 547, SEQ ID NO: 633, SEQ ID NO: 695,
25 35 SEQ ID NO: 405, SEQ ID NO: 394, SEQ ID NO: 761, SEQ ID NO: 574, SEQ ID NO: 596, SEQ ID NO: 832, SEQ ID NO: 651, SEQ ID NO: 867, SEQ ID NO: 614, SEQ ID NO: 401, SEQ ID NO: 393, SEQ ID NO: 413, SEQ ID NO: 835, SEQ ID NO: 863, SEQ

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- ID NO: 458, SEQ ID NO: 701, SEQ ID NO: 531, SEQ ID NO: 550, SEQ ID NO: 439,
SEQ ID NO: 516, SEQ ID NO: 802, SEQ ID NO: 581, SEQ ID NO: 535, SEQ ID NO:
578, SEQ ID NO: 492, SEQ ID NO: 858, SEQ ID NO: 720, SEQ ID NO: 813, SEQ ID
NO: 426, SEQ ID NO: 834, SEQ ID NO: 609, SEQ ID NO: 489, SEQ ID NO: 480, SEQ
5 ID NO: 406, SEQ ID NO: 392, SEQ ID NO: 456, SEQ ID NO: 707, SEQ ID NO: 533,
SEQ ID NO: 728, SEQ ID NO: 769, SEQ ID NO: 671, SEQ ID NO: 602, SEQ ID NO:
618, SEQ ID NO: 618, SEQ ID NO: 682, SEQ ID NO: 524, SEQ ID NO: 802, SEQ ID
NO: 785, SEQ ID NO: 457, SEQ ID NO: 781, SEQ ID NO: 473, SEQ ID NO: 384, SEQ
ID NO: 726, SEQ ID NO: 817, SEQ ID NO: 498, SEQ ID NO: 436, SEQ ID NO: 815,
10 SEQ ID NO: 856, SEQ ID NO: 650, SEQ ID NO: 844, SEQ ID NO: 580, SEQ ID NO:
783, SEQ ID NO: 416, SEQ ID NO: 741, SEQ ID NO: 442, SEQ ID NO: 803, SEQ ID
NO: 520, SEQ ID NO: 566, SEQ ID NO: 557, SEQ ID NO: 706, SEQ ID NO: 710, SEQ
ID NO: 487, SEQ ID NO: 603, SEQ ID NO: 472, SEQ ID NO: 476, SEQ ID NO: 770,
SEQ ID NO: 841, SEQ ID NO: 768, SEQ ID NO: 839, SEQ ID NO: 560, SEQ ID NO:
15 796, SEQ ID NO: 483, SEQ ID NO: 634, SEQ ID NO: 445, SEQ ID NO: 853, SEQ ID
NO: 525, SEQ ID NO: 798, SEQ ID NO: 549, SEQ ID NO: 836, SEQ ID NO: 589, SEQ
ID NO: 760, SEQ ID NO: 462, SEQ ID NO: 789, SEQ ID NO: 507, SEQ ID NO: 828,
SEQ ID NO: 866, SEQ ID NO: 754, SEQ ID NO: 730, SEQ ID NO: 617, SEQ ID NO:
455, SEQ ID NO: 873, SEQ ID NO: 435, SEQ ID NO: 766, SEQ ID NO: 793, SEQ ID
20 NO: 742, SEQ ID NO: 599, SEQ ID NO: 854, and SEQ ID NO: 632.

In one embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in energy conversion selected from the group consisting of SEQ ID NO: 1598, SEQ ID NO: 1739, SEQ ID NO: 1775, SEQ ID NO: 1814, SEQ ID NO: 390, SEQ ID NO: 876, SEQ ID NO: 547, and SEQ ID NO: 678.

- 25 In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in amino acid metabolism selected from the group consisting of SEQ ID NO: 1448, SEQ ID NO: 1466, SEQ ID NO:
1535, SEQ ID NO: 1545, SEQ ID NO: 1550, SEQ ID NO: 1680, SEQ ID NO: 1701, SEQ
ID NO: 1719, SEQ ID NO: 1744, SEQ ID NO: 1790, SEQ ID NO: 1859, SEQ ID NO:
30 1880, SEQ ID NO: 1885, SEQ ID NO: 1679, SEQ ID NO: 1482, SEQ ID NO: 1485, SEQ
ID NO: 1459, SEQ ID NO: 729, SEQ ID NO: 786, SEQ ID NO: 654, SEQ ID NO: 734,
SEQ ID NO: 646, SEQ ID NO: 522, SEQ ID NO: 696, SEQ ID NO: 807, SEQ ID NO:
683, SEQ ID NO: 790, SEQ ID NO: 763, SEQ ID NO: 806, SEQ ID NO: 799, SEQ ID
NO: 434, SEQ ID NO: 743, SEQ ID NO: 804, and SEQ ID NO: 733.

- 35 In yet another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in nucleotide metabolism selected from the group consisting of SEQ ID NO: 1512, SEQ ID NO: 1515, SEQ ID NO:
1642, SEQ ID NO: 1668, SEQ ID NO: 1816, SEQ ID NO: 1845, SEQ ID NO: 1865, SEQ
ID NO: 1866, SEQ ID NO: 1886, SEQ ID NO: 1509, SEQ ID NO: 1510, SEQ ID NO: 826,

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SEQ ID NO: 562, SEQ ID NO: 420, SEQ ID NO: 664, SEQ ID NO: 850, SEQ ID NO: 857, SEQ ID NO: 861, SEQ ID NO: 872, SEQ ID NO: 544, SEQ ID NO: 830, and SEQ ID NO: 446.

In yet a further embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in carbohydrate metabolism selected from the group consisting of SEQ ID NO: 1531, SEQ ID NO: 1579, SEQ ID NO: 1584, SEQ ID NO: 1662, SEQ ID NO: 1703, SEQ ID NO: 1704, SEQ ID NO: 1737, SEQ ID NO: 1740, SEQ ID NO: 1742, SEQ ID NO: 1754, SEQ ID NO: 1847, SEQ ID NO: 1447, SEQ ID NO: 397, SEQ ID NO: 699, SEQ ID NO: 459, SEQ ID NO: 509, SEQ ID NO: 818, SEQ ID NO: 488, SEQ ID NO: 438, SEQ ID NO: 831, SEQ ID NO: 667, SEQ ID NO: 429, SEQ ID NO: 680, and SEQ ID NO: 597.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in cofactor metabolism selected from the group consisting of SEQ ID NO: 1546, SEQ ID NO: 1607, SEQ ID NO: 1609, SEQ ID NO: 1610, SEQ ID NO: 1728, SEQ ID NO: 1489, SEQ ID NO: 460, SEQ ID NO: 709, SEQ ID NO: 822, SEQ ID NO: 466, SEQ ID NO: 584, and SEQ ID NO: 388.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in lipid metabolism selected from the group consisting of SEQ ID NO: 1708, SEQ ID NO: 1808, SEQ ID NO: 1887, SEQ ID NO: 631, SEQ ID NO: 787, and SEQ ID NO: 532.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in mRNA translation and ribosome biogenesis selected from the group consisting of SEQ ID NO: 1498, SEQ ID NO: 1506, SEQ ID NO: 1592, SEQ ID NO: 1678, SEQ ID NO: 1778, SEQ ID NO: 1863, SEQ ID NO: 619, SEQ ID NO: 723, SEQ ID NO: 641, SEQ ID NO: 698, SEQ ID NO: 630, and SEQ ID NO: 869.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in genome replication, transcription, recombination and repair selected from the group consisting of SEQ ID NO: 1454, SEQ ID NO: 1538, SEQ ID NO: 1567, SEQ ID NO: 1581, SEQ ID NO: 1583, SEQ ID NO: 1636, SEQ ID NO: 1639, SEQ ID NO: 1649, SEQ ID NO: 1669, SEQ ID NO: 1695, SEQ ID NO: 1757, SEQ ID NO: 1776, SEQ ID NO: 1848, SEQ ID NO: 1849, SEQ ID NO: 1858, SEQ ID NO: 1884, SEQ ID NO: 601, SEQ ID NO: 415, SEQ ID NO: 542, SEQ ID NO: 704, SEQ ID NO: 572, SEQ ID NO: 467, SEQ ID NO: 399, SEQ ID NO: 579, SEQ ID NO: 739, SEQ ID NO: 849, SEQ ID NO: 824, SEQ ID NO: 871, SEQ ID NO: 547, SEQ ID NO: 633, SEQ ID NO: 695, SEQ ID NO: 405, SEQ ID NO: 394, and SEQ ID NO: 761.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in outer membrane or cell wall

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biosynthesis selected from the group consisting of SEQ ID NO: 1667, SEQ ID NO: 1690, SEQ ID NO: 1813, SEQ ID NO: 1468, SEQ ID NO: 1470, SEQ ID NO: 1811, SEQ ID NO: 574, SEQ ID NO: 596, SEQ ID NO: 832, SEQ ID NO: 651, SEQ ID NO: 867, SEQ ID NO: 614, SEQ ID NO: 401, and SEQ ID NO: 393.

5 In yet another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* chaperone polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1874, SEQ ID NO: 1876, SEQ ID NO: 1825, SEQ ID NO: 413, SEQ ID NO: 835, and SEQ ID NO: 863.

Particularly preferred is a purified or isolated *H. pylori* secreted or periplasmic polypeptide or a fragment thereof, wherein the polypeptide is selected from the group consisting of SEQ ID NO: 1455, SEQ ID NO: 1589, SEQ ID NO: 1518, SEQ ID NO: 1529, SEQ ID NO: 1765, SEQ ID NO: 1770, SEQ ID NO: 1829, SEQ ID NO: 1556, SEQ ID NO: 1565, SEQ ID NO: 1569, SEQ ID NO: 1571, SEQ ID NO: 1574, SEQ ID NO: 1578, SEQ ID NO: 1663, SEQ ID NO: 1674, SEQ ID NO: 1676, SEQ ID NO: 1697, SEQ ID NO: 1699, SEQ ID NO: 1710, SEQ ID NO: 1715, SEQ ID NO: 1716, SEQ ID NO: 1732, SEQ ID NO: 1736, SEQ ID NO: 1745, SEQ ID NO: 1749, SEQ ID NO: 1750, SEQ ID NO: 1766, SEQ ID NO: 1767, SEQ ID NO: 1768, SEQ ID NO: 1769, SEQ ID NO: 1795, SEQ ID NO: 1802, SEQ ID NO: 1804, SEQ ID NO: 1824, SEQ ID NO: 1831, SEQ ID NO: 1838, SEQ ID NO: 1840, SEQ ID NO: 1844, SEQ ID NO: 1862, SEQ ID NO: 1879, SEQ ID NO: 1882, SEQ ID NO: 1890, SEQ ID NO: 1494, SEQ ID NO: 1634, SEQ ID NO: 1635, SEQ ID NO: 1647, SEQ ID NO: 1648, SEQ ID NO: 1654, SEQ ID NO: 1446, SEQ ID NO: 1449, SEQ ID NO: 1452, SEQ ID NO: 1473, SEQ ID NO: 1474, SEQ ID NO: 1480, SEQ ID NO: 1491, SEQ ID NO: 1502, SEQ ID NO: 1513, SEQ ID NO: 1605, SEQ ID NO: 1771, SEQ ID NO: 1526, SEQ ID NO: 1557, SEQ ID NO: 1560, SEQ ID NO: 1585, SEQ ID NO: 1672, SEQ ID NO: 1677, SEQ ID NO: 1686, SEQ ID NO: 1752, SEQ ID NO: 1762, SEQ ID NO: 1777, SEQ ID NO: 1792, SEQ ID NO: 1805, SEQ ID NO: 1815, SEQ ID NO: 1817, SEQ ID NO: 1827, SEQ ID NO: 1842, SEQ ID NO: 1846, SEQ ID NO: 1896, SEQ ID NO: 1530, SEQ ID NO: 1637, SEQ ID NO: 1461, SEQ ID NO: 1467, SEQ ID NO: 1623, SEQ ID NO: 1625, SEQ ID NO: 530, SEQ ID NO: 708, SEQ ID NO: 414, SEQ ID NO: 694, SEQ ID NO: 703, SEQ ID NO: 721, SEQ ID NO: 749, SEQ ID NO: 685, SEQ ID NO: 444, SEQ ID NO: 606, SEQ ID NO: 582, SEQ ID NO: 621, SEQ ID NO: 868, SEQ ID NO: 666, SEQ ID NO: 408, SEQ ID NO: 538, SEQ ID NO: 573, SEQ ID NO: 639, SEQ ID NO: 668, SEQ ID NO: 524, SEQ ID NO: 422, SEQ ID NO: 819, SEQ ID NO: 611, SEQ ID NO: 674, SEQ ID NO: 577, SEQ ID NO: 663, SEQ ID NO: 558, SEQ ID NO: 794, SEQ ID NO: 564, SEQ ID NO: 592, SEQ ID NO: 814, SEQ ID NO: 398, SEQ ID NO: 767, SEQ ID NO: 425, SEQ ID NO: 659, SEQ ID NO: 517, SEQ ID NO: 539, SEQ ID NO: 475, SEQ ID NO: 615, SEQ ID NO: 665, SEQ ID NO: 607, SEQ ID NO: 598, SEQ ID NO: 759, SEQ ID NO: 752, SEQ ID NO: 595, SEQ ID NO: 686, SEQ ID NO: 528, SEQ ID NO: 705, SEQ ID NO: 828, SEQ ID

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NO: 403, SEQ ID NO: 561, SEQ ID NO: 500, SEQ ID NO: 491, SEQ ID NO: 846, SEQ ID NO: 732, SEQ ID NO: 778, SEQ ID NO: 751, SEQ ID NO: 744, SEQ ID NO: 504, SEQ ID NO: 419, SEQ ID NO: 792, SEQ ID NO: 825, SEQ ID NO: 756, SEQ ID NO: 519, SEQ ID NO: 870, SEQ ID NO: 777, SEQ ID NO: 808, SEQ ID NO: 506, SEQ ID NO: 864, SEQ ID NO: 655, SEQ ID NO: 407, SEQ ID NO: 427, SEQ ID NO: 774, SEQ ID NO: 797, SEQ ID NO: 688, SEQ ID NO: 815, SEQ ID NO: 718, SEQ ID NO: 859, SEQ ID NO: 775, SEQ ID NO: 874, SEQ ID NO: 543, SEQ ID NO: 878, SEQ ID NO: 594, SEQ ID NO: 610, and SEQ ID NO: 600.

Particularly preferred is a purified or isolated *H. pylori* surface or membrane polypeptide or a fragment thereof, wherein the polypeptide is selected from the group consisting of SEQ ID NO: 1511, SEQ ID NO: 1561, SEQ ID NO: 1563, SEQ ID NO: 1681, SEQ ID NO: 1711, SEQ ID NO: 1731, SEQ ID NO: 1743, SEQ ID NO: 1747, SEQ ID NO: 1758, SEQ ID NO: 1893, SEQ ID NO: 1895, SEQ ID NO: 1573, SEQ ID NO: 1705, SEQ ID NO: 1707, SEQ ID NO: 1723, SEQ ID NO: 1726, SEQ ID NO: 1760, SEQ ID NO: 1764, SEQ ID NO: 1798, SEQ ID NO: 1803, SEQ ID NO: 1807, SEQ ID NO: 1889, SEQ ID NO: 1892, SEQ ID NO: 1460, SEQ ID NO: 1477, SEQ ID NO: 1499, SEQ ID NO: 1514, SEQ ID NO: 1641, SEQ ID NO: 1534, SEQ ID NO: 1564, SEQ ID NO: 1673, SEQ ID NO: 1746, SEQ ID NO: 1794, SEQ ID NO: 1843, SEQ ID NO: 1894, SEQ ID NO: 1536, SEQ ID NO: 1544, SEQ ID NO: 1568, SEQ ID NO: 1572, SEQ ID NO: 1582, SEQ ID NO: 1738, SEQ ID NO: 1891, SEQ ID NO: 1660, SEQ ID NO: 1793, SEQ ID NO: 1832, SEQ ID NO: 1841, SEQ ID NO: 1860, SEQ ID NO: 1486, SEQ ID NO: 1465, SEQ ID NO: 1539, SEQ ID NO: 1693, SEQ ID NO: 1629, SEQ ID NO: 1540, SEQ ID NO: 1791, SEQ ID NO: 1525, SEQ ID NO: 1558, SEQ ID NO: 1655, SEQ ID NO: 1517, SEQ ID NO: 875, SEQ ID NO: 676, SEQ ID NO: 801, SEQ ID NO: 860, SEQ ID NO: 747, SEQ ID NO: 529, SEQ ID NO: 387, SEQ ID NO: 391, SEQ ID NO: 515, SEQ ID NO: 625, SEQ ID NO: 568, SEQ ID NO: 454, SEQ ID NO: 800, SEQ ID NO: 499, SEQ ID NO: 779, SEQ ID NO: 648, SEQ ID NO: 643, SEQ ID NO: 537, SEQ ID NO: 511, SEQ ID NO: 616, SEQ ID NO: 829, SEQ ID NO: 546, SEQ ID NO: 780, SEQ ID NO: 553, SEQ ID NO: 549, SEQ ID NO: 410, SEQ ID NO: 608, SEQ ID NO: 513, SEQ ID NO: 656, SEQ ID NO: 845, SEQ ID NO: 563, SEQ ID NO: 570, SEQ ID NO: 805, SEQ ID NO: 851, SEQ ID NO: 423, SEQ ID NO: 810, SEQ ID NO: 604, SEQ ID NO: 636, SEQ ID NO: 757, SEQ ID NO: 412, SEQ ID NO: 816, SEQ ID NO: 771, SEQ ID NO: 418, SEQ ID NO: 662, SEQ ID NO: 512, SEQ ID NO: 679, SEQ ID NO: 605, SEQ ID NO: 421, SEQ ID NO: 552, SEQ ID NO: 576, SEQ ID NO: 571, SEQ ID NO: 725, SEQ ID NO: 565, SEQ ID NO: 717, SEQ ID NO: 536, SEQ ID NO: 647, SEQ ID NO: 501, SEQ ID NO: 838, SEQ ID NO: 428, SEQ ID NO: 494, SEQ ID NO: 479, SEQ ID NO: 711, SEQ ID NO: 722, SEQ ID NO: 645, SEQ ID NO: 670, SEQ ID NO: 746, SEQ ID NO: 493, SEQ ID NO: 540, SEQ ID NO: 612, SEQ ID NO: 629, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 433, SEQ ID NO: 385, and SEQ ID NO: 409.

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- In one embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least one membrane spanning region selected from the group consisting of SEQ ID NO: 1511, SEQ ID NO: 1561, SEQ ID NO: 1563, SEQ ID NO: 1681, SEQ ID NO: 1711, SEQ ID NO: 1731, SEQ ID NO: 1743, SEQ ID NO: 1747, SEQ ID NO: 1758, SEQ ID NO: 1893, SEQ ID NO: 1895, SEQ ID NO: 875, SEQ ID NO: 676, SEQ ID NO: 801, SEQ ID NO: 860, SEQ ID NO: 747, SEQ ID NO: 529, SEQ ID NO: 387, SEQ ID NO: 391, SEQ ID NO: 515, SEQ ID NO: 625, SEQ ID NO: 568, SEQ ID NO: 454, SEQ ID NO: 800, SEQ ID NO: 499, SEQ ID NO: 779, and SEQ ID NO: 385.
- 10 In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least two membrane spanning regions selected from the group consisting of SEQ ID NO: 1573, SEQ ID NO: 1705, SEQ ID NO: 1707, SEQ ID NO: 1723, SEQ ID NO: 1726, SEQ ID NO: 1760, SEQ ID NO: 1764, SEQ ID NO: 1798, SEQ ID NO: 1803, SEQ ID NO: 1807, SEQ ID NO: 1889, SEQ ID NO: 1892, SEQ ID NO: 1460, SEQ ID NO: 1477, SEQ ID NO: 1499, SEQ ID NO: 1514, SEQ ID NO: 1641, SEQ ID NO: 648, SEQ ID NO: 643, SEQ ID NO: 537, SEQ ID NO: 511, SEQ ID NO: 616, SEQ ID NO: 829, SEQ ID NO: 546, SEQ ID NO: 780, SEQ ID NO: 553, SEQ ID NO: 549, SEQ ID NO: 410, SEQ ID NO: 608, SEQ ID NO: 513, SEQ ID NO: 656, SEQ ID NO: 845, SEQ ID NO: 563, SEQ ID NO: 570, SEQ ID NO: 805, and SEQ ID NO: 851.
- 15 In yet another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least three membrane spanning regions selected from the group consisting of SEQ ID NO: 1534, SEQ ID NO: 1564, SEQ ID NO: 1673, SEQ ID NO: 1746, SEQ ID NO: 1794, SEQ ID NO: 1843, SEQ ID NO: 1894, SEQ ID NO: 423, SEQ ID NO: 810, SEQ ID NO: 604, SEQ ID NO: 636, SEQ ID NO: 757, SEQ ID NO: 412, and SEQ ID NO: 816.
- 20 In yet a further embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least four membrane spanning regions selected from the group consisting of SEQ ID NO: 1536, SEQ ID NO: 1544, SEQ ID NO: 1568, SEQ ID NO: 1572, SEQ ID NO: 1582, SEQ ID NO: 1738, SEQ ID NO: 1891, SEQ ID NO: 1660, SEQ ID NO: 771, SEQ ID NO: 418, SEQ ID NO: 662, SEQ ID NO: 512, SEQ ID NO: 679, SEQ ID NO: 605, SEQ ID NO: 421, SEQ ID NO: 552, SEQ ID NO: 576, SEQ ID NO: 571.
- 25 In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least five membrane spanning regions selected from the group consisting of SEQ ID NO: 1793, SEQ ID NO: 1832, SEQ ID NO: 1841, SEQ ID NO: 1860, SEQ ID NO: 1486, SEQ ID NO: 725, SEQ ID NO: 565, SEQ ID NO: 717, SEQ ID NO: 536, SEQ ID NO: 647, and SEQ ID NO: 409.

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In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least six membrane spanning regions selected from the group consisting of SEQ ID NO: 1465, SEQ ID NO: 1539, SEQ ID NO: 1693, SEQ ID NO: 1629, SEQ ID NO: 501, SEQ ID NO: 838, 5 SEQ ID NO: 428, SEQ ID NO: 494, SEQ ID NO: 479, SEQ ID NO: 711, and SEQ ID NO: 722.

In yet another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least seven membrane spanning regions selected from the group consisting of SEQ ID NO: 1540, SEQ 10 ID NO: 1791, SEQ ID NO: 1525, SEQ ID NO: 1558, SEQ ID NO: 1655, SEQ ID NO: 1517, SEQ ID NO: 645, SEQ ID NO: 670, SEQ ID NO: 746, SEQ ID NO: 493, SEQ ID NO: 540, SEQ ID NO: 612, SEQ ID NO: 629, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, and SEQ ID NO: 433.

In another aspect, the invention pertains to any individual *H. pylori* polypeptide member or nucleic acid encoding such a member from the above-identified groups of *H. pylori* polypeptides.

In another aspect, the invention features nucleic acids capable of binding mRNA of *H. pylori*. Such nucleic acid is capable of acting as antisense nucleic acid to control the translation of mRNA of *H. pylori*. A further aspect features a nucleic acid which is capable 20 of binding specifically to an *H. pylori* nucleic acid. These nucleic acids are also referred to herein as complements and have utility as probes and as capture reagents.

In another aspect, the invention features an expression system comprising an open reading frame corresponding to *H. pylori* nucleic acid. The nucleic acid further comprises a control sequence compatible with an intended host. The expression system is useful for 25 making polypeptides corresponding to *H. pylori* nucleic acid.

In another aspect, the invention features a cell transformed with the expression system to produce *H. pylori* polypeptides.

In another aspect, the invention features a method of generating antibodies against *H. pylori* polypeptides which are capable of binding specifically to *H. pylori* polypeptides. 30 Such antibodies have utility as reagents for immunoassays to evaluate the abundance and distribution of *H. pylori*-specific antigens.

In another aspect, the invention features a method of generating vaccines for immunizing an individual against *H. pylori*. The method includes: immunizing a subject with an *H. pylori* polypeptide, e.g., a surface or secreted polypeptide, or active portion 35 thereof, and a pharmaceutically acceptable carrier. Such vaccines have therapeutic and prophylactic utilities.

In another aspect, the invention provides a method for generating a vaccine comprising a modified immunogenic *H. pylori* polypeptide, e.g., a surface or secreted polypeptide, or active portion thereof, and a pharmacologically acceptable carrier.

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In another aspect, the invention features a method of evaluating a compound, e.g. a polypeptide, e.g., a fragment of a host cell polypeptide, for the ability to bind an *H. pylori* polypeptide. The method includes: contacting the candidate compound with an *H. pylori* polypeptide and determining if the compound binds or otherwise interacts with an *H. pylori* polypeptide. Compounds which bind *H. pylori* are candidates as activators or inhibitors of the bacterial life cycle. These assays can be performed *in vitro* or *in vivo*.

5 In another aspect, the invention features a method of evaluating a compound, e.g. a polypeptide, e.g., a fragment of a host cell polypeptide, for the ability to bind an *H. pylori* nucleic acid, e.g., DNA or RNA. The method includes: contacting the candidate
10 compound with an *H. pylori* nucleic acid and determining if the compound binds or otherwise interacts with an *H. pylori* polypeptide. Compounds which bind *H. pylori* are candidates as activators or inhibitors of the bacterial life cycle. These assays can be performed *in vitro* or *in vivo*.

15 The invention features *H. pylori* polypeptides, preferably a substantially pure preparation of an *H. pylori* polypeptide, or a recombinant *H. pylori* polypeptide. In preferred embodiments: the polypeptide has biological activity; the polypeptide has an amino acid sequence at least 60%, 70%, 80%, 90%, 95%, 98%, or 99% identical to an amino acid sequence of the invention contained in the Sequence Listing, preferably it has about 65% sequence identity with an amino acid sequence of the invention contained in the
20 Sequence Listing, and most preferably it has about 92% to about 99% sequence identity with an amino acid sequence of the invention contained in the Sequence Listing; the polypeptide has an amino acid sequence essentially the same as an amino acid sequence of the invention contained in the Sequence Listing; the polypeptide is at least 5, 10, 20, 50, 100, or 150 amino acid residues in length; the polypeptide includes at least 5, preferably at
25 least 10, more preferably at least 20, more preferably at least 50, 100, or 150 contiguous amino acid residues of the invention contained in the Sequence Listing. In yet another preferred embodiment, the amino acid sequence which differs in sequence identity by about 7% to about 8% from the *H. pylori* amino acid sequences of the invention contained in the Sequence Listing is also encompassed by the invention.

30 In preferred embodiments: the *H. pylori* polypeptide is encoded by a nucleic acid of the invention contained in the Sequence Listing, or by a nucleic acid having at least 60%, 70%, 80%, 90%, 95%, 98%, or 99% homology with a nucleic acid of the invention contained in the Sequence Listing.

35 In a preferred embodiment, the subject *H. pylori* polypeptide differs in amino acid sequence at 1, 2, 3, 5, 10 or more residues from a sequence of the invention contained in the Sequence Listing. The differences, however, are such that the *H. pylori* polypeptide exhibits an *H. pylori* biological activity, e.g., the *H. pylori* polypeptide retains a biological activity of a naturally occurring *H. pylori* enzyme.

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In preferred embodiments, the polypeptide includes all or a fragment of an amino acid sequence of the invention contained in the Sequence Listing; fused, in reading frame, to additional amino acid residues, preferably to residues encoded by genomic DNA 5' or 3' to the genomic DNA which encodes a sequence of the invention contained in the Sequence Listing.

5 In yet other preferred embodiments, the *H. pylori* polypeptide is a recombinant fusion protein having a first *H. pylori* polypeptide portion and a second polypeptide portion, e.g., a second polypeptide portion having an amino acid sequence unrelated to *H. pylori*. The second polypeptide portion can be, e.g., any of glutathione-S-transferase, a
10 DNA binding domain, or a polymerase activating domain. In preferred embodiment the fusion protein can be used in a two-hybrid assay.

Polypeptides of the invention include those which arise as a result of alternative transcription events, alternative RNA splicing events, and alternative translational and posttranslational events.

15 The invention also encompasses an immunogenic component which includes an *H. pylori* polypeptide in an immunogenic preparation; the immunogenic component being capable of eliciting an immune response specific for the *H. pylori* polypeptide, e.g., a humoral response, an antibody response, or a cellular response. In preferred embodiments, the immunogenic component comprises at least one antigenic determinant from a
20 polypeptide of the invention contained in the Sequence Listing.

In another aspect, the invention provides a substantially pure nucleic acid having a nucleotide sequence which encodes an *H. pylori* polypeptide. In preferred embodiments: the encoded polypeptide has biological activity; the encoded polypeptide has an amino acid sequence at least 60%, 70%, 80%, 90%, 95%, 98%, or 99% homologous to an amino acid
25 sequence of the invention contained in the Sequence Listing; the encoded polypeptide has an amino acid sequence essentially the same as an amino acid sequence of the invention contained in the Sequence Listing; the encoded polypeptide is at least 5, 10, 20, 50, 100, or 150 amino acids in length; the encoded polypeptide comprises at least 5, preferably at least 10, more preferably at least 20, more preferably at least 50, 100, or 150 contiguous amino
30 acids of the invention contained in the Sequence Listing.

In preferred embodiments: the nucleic acid of the invention is that contained in the Sequence Listing; the nucleic acid is at least 60%, 70%, 80%, 90%, 95%, 98%, or 99% homologous with a nucleic acid sequence of the invention contained in the Sequence Listing.

35 In a preferred embodiment, the encoded *H. pylori* polypeptide differs (e.g., by amino acid substitution, addition or deletion of at least one amino acid residue) in amino acid sequence at 1, 2, 3, 5, 10 or more residues, from a sequence of the invention contained in the Sequence Listing. The differences, however, are such that: the *H. pylori* encoded

polypeptide exhibits a *H. pylori* biological activity, e.g., the encoded *H. pylori* enzyme retains a biological activity of a naturally occurring *H. pylori*.

In preferred embodiments, the encoded polypeptide includes all or a fragment of an amino acid sequence of the invention contained in the Sequence Listing; fused, in reading frame, to additional amino acid residues, preferably to residues encoded by genomic DNA 5' or 3' to the genomic DNA which encodes a sequence of the invention contained in the Sequence Listing.

10 In preferred embodiments, the subject *H. pylori* nucleic acid will include a transcriptional regulatory sequence, e.g. at least one of a transcriptional promoter or transcriptional enhancer sequence, operably linked to the *H. pylori* gene sequence, e.g., to render the *H. pylori* gene sequence suitable for expression in a recombinant host cell.

15 In yet a further preferred embodiment, the nucleic acid which encodes an *H. pylori* polypeptide of the invention, hybridizes under stringent conditions to a nucleic acid probe corresponding to at least 8 consecutive nucleotides of the invention contained in the Sequence Listing; more preferably to at least 12 consecutive nucleotides of the invention contained in the Sequence Listing; more preferably to at least 20 consecutive nucleotides of the invention contained in the Sequence Listing; more preferably to at least 40 consecutive nucleotides of the invention contained in the Sequence Listing.

20 In a preferred embodiment, the nucleic acid encodes a peptide which differs by at least one amino acid residue from the sequences of the invention contained in the Sequence Listing.

25 In a preferred embodiment, the nucleic acid differs by at least one nucleotide from a nucleotide sequence of the invention contained in the Sequence Listing which encodes amino acids of the invention contained in the Sequence Listing.

30 In another aspect, the invention encompasses: a vector including a nucleic acid which encodes an *H. pylori* polypeptide or an *H. pylori* polypeptide variant as described herein; a host cell transfected with the vector; and a method of producing a recombinant *H. pylori* polypeptide or *H. pylori* polypeptide variant; including culturing the cell, e.g., in a cell culture medium, and isolating the *H. pylori* or *H. pylori* polypeptide variant, e.g., from the cell or from the cell culture medium.

35 In another aspect, the invention features, a purified recombinant nucleic acid having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, or 99% homology with a sequence of the invention contained in the Sequence Listing.

The invention also provides a probe or primer which includes a substantially purified oligonucleotide. The oligonucleotide includes a region of nucleotide sequence which hybridizes under stringent conditions to at least 10 consecutive nucleotides of sense or antisense sequence of the invention contained in the Sequence Listing, or naturally occurring mutants thereof. In preferred embodiments, the probe or primer further includes a label group attached thereto. The label group can be, e.g., a radioisotope, a fluorescent

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compound, an enzyme, and/or an enzyme co-factor. Preferably the oligonucleotide is at least 10 and less than 20, 30, 50, 100, or 150 nucleotides in length.

The invention further provides nucleic acids, e.g., RNA or DNA, encoding a polypeptide of the invention. This includes double stranded nucleic acids as well as coding and antisense single strands.

The *H. pylori* strain, from which genomic sequences have been sequenced, has been deposited in the American Type Culture Collection(ATCC # 55679) as strain HP-J99.

Included in the invention are: allelic variations; natural mutants; induced mutants; proteins encoded by DNA that hybridizes under high or low stringency conditions to a nucleic acid which encodes a polypeptide of the invention contained in the Sequence Listing (for definitions of high and low stringency see Current Protocols in Molecular Biology, John Wiley & Sons, New York, 1989, 6.3.1 - 6.3.6, hereby incorporated by reference); and, polypeptides specifically bound by antisera to *H. pylori* polypeptides, especially by antisera to an active site or binding domain of *H. pylori* polypeptide. The invention also includes fragments, preferably biologically active fragments. These and other polypeptides are also referred to herein as *H. pylori* polypeptide analogs or variants.

Putative functions have been determined for several of the *H. pylori* polypeptides of the invention, as shown in Table 1.

Accordingly, uses of the claimed *H. pylori* polypeptides in these identified functions are also within the scope of the invention.

In addition, the present invention encompasses *H. pylori* polypeptides characterized as shown in Table 1 below, including: *H. pylori* cell envelope proteins, *H. pylori* periplasmic/secreted proteins, *H. pylori* cytoplasmic proteins, and other *H. pylori* surface and membrane proteins. Members of these groups were identified by BLAST homology searches and by searches for secretion signal or transmembrane protein motifs. (Polypeptides in the same row of Table 1, i.e., rows 1 and 3, or rows 2 and 4, are related to one another as described in Table 3 below.)

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TABLE 1

TABLE OF FUNCTIONAL GROUPS					
ORF Name	nt	aa	ORF Name	nt	aa
	SeqID	SeqID		SeqID	SeqID
Row	#	#	#	#	#
1	2		3	4	
A. CELL ENVELOPE					
A.1. Flagella-associated					
01gp10401orf1	1020	1471	26588588.aa	217	660
01gp10401orf5	1021	1472	26588588.aa	217	660
02ae11612orf21	1036	1487	6288949.aa	367	855
02ce10213orf7	1050	1501	22692187.aa	911	534
02ge20116orf34	1071	1522	29454837.aa	944	675
04ge11713orf5	1101	1552	1171928.aa	18	404
04ge11713orf5	1101	1552	21699087.aa	107	518
05ep20322orf11	1135	1586	16219090.aa	894	464
12ge20305orf11	1276	1727	29298130.aa	943	672
06cp20302orf12	1150	1601	25525277.aa	203	640
07ge20415orf27	1187	1638	19557055.aa	85	490
07ge20415orf27	1187	1638	36111066.aa	290	755
07ge31107orf2	1192	1643	104792.aa	5	389
29zp10241orf6	1361	1812	24882763.aa	199	635
hp2e10911orf5	1379	1830	917152.aa	992	877
hp3e11122orf1	1399	1850	25478375.aa	934	637
hp3e11168orf2	1403	1854	16984442.aa	899	477
hpe11122orf5	1400	1851	3942217.aa	302	772
07ge20415orf34	1189	1640	26380318.aa	215	658
A.2. Inner membrane proteins					
01ce11016orf1	1002	1453			
09ap11406orf14	1213	1664	16131887.aa	893	463
09ap11406orf15	1214	1665	6093906.aa	984	852
09ap11406orf5	1215	1666	2082012.aa	97	503
11ce11603orf16	1234	1685	1204418.aa	22	411
11ce11603orf16	1234	1685	14455461.aa	49	441
11ce11603orf25	1236	1687	4035783.aa	309	782
11ce11603orf6	1237	1688	23915877.aa	150	575
09cp10502orf22	1224	1675	30730068.aa	240	691
09cp10502orf22	1224	1675	3385833.aa	957	724
11gp10904orf29	1251	1702	14713512.aa	57	452
12ap10324orf2	1262	1713	10353192.aa	2	386
06cp20302orf10	1149	1600	203192.aa	92	497
09ap20802orf5	1220	1671	32704686.aa	255	712
11ge10309orf14	1240	1691	24222885.aa	164	591
11ge10309orf14	1240	1691	2548562.aa	201	638
06gp10409orf7	1164	1615	34666680.aa	278	740
06gp10409orf8	1165	1616	3203142.aa	245	697

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hp3e11168orf29	1404	1855	23853165.aa	921	569
06cp11118orf6	1144	1595	16412593.aa	896	470
06cp11118orf6	1144	1595	32236462.aa	248	700
07ee20513orf28	1182	1633	24132293.aa	159	586
07ee20513orf28	1182	1633	486075.aa	979	823
06ep10306orf12	1157	1608	24651083.aa	194	627
06ep10306orf3	1160	1611	24651083.aa	194	627
06ep10306orf3	1160	1611	30089217.aa	946	684
13ep12003orf20	1300	1751	23493756.aa	916	551
14ge10705orf11	1321	1772	17086587.aa	76	478
14ge10705orf11	1321	1772	21486677.aa	905	508
14ge10705orf11	1321	1772	23468781.aa	914	545
14ge10705orf11	1321	1772	24708129.aa	931	628
14gp11820orf13	1323	1774	14494077.aa	50	443
14gp11820orf13	1323	1774	3242337.aa	250	702
14gp11820orf13	1323	1774	3962777.aa	969	776
14gp12015orf12	1329	1780	15824052.aa	66	461
14gp12015orf12	1329	1780	34489543.aa	275	737
14gp12015orf16	1332	1783	4698838.aa	330	809
27ze10351orf17	1345	1796	25605166.aa	204	642
29zp10241orf14	1358	1809	9776562.aa	383	879
hplp13947orf2	1375	1826	3953143.aa	303	773
hp4p11352orf4	1417	1868	16406265.aa	70	468
13ap11517orf20	1283	1734	5267037.aa	983	842
16ae10113orf1	1335	1786	423131.aa	972	788
hplp13922orf22	1368	1819	24611590.aa	929	624
07ee11620orf2	1179	1630	423131.aa	972	788
12ae10622orf9	1255	1706	259665.aa	936	644
12ae10622orf9	1255	1706	34097707.aa	267	727
12ae11404orf15	1258	1709	24806290.aa	197	631
02ce10213orf14	1044	1495	14645905.aa	55	450
12ge10305orf15	1273	1724	14642202.aa	54	448
01xe21717orf18	1024	1475	26261040.aa	210	653
A.3. Transporters					
09ap20802orf27	1219	1670	20032561.aa	90	495
12ge10305orf16	1274	1725	11132778.aa	15	400
09ae11601orf14	1210	1661	23439633.aa	913	541
09ae11601orf14	1210	1661	29302003.aa	227	673
hp5e11726orf7	1422	1873	179677.aa	79	482
14ce11113orf1	1302	1753	24609593.aa	191	622
14cp10119orf12	1308	1759	30662792.aa	238	689
14cp10119orf15	1310	1761	34427317.aa	274	736
14gp12015orf14	1331	1782	12617677.aa	27	417
hp5e15440orf16	1432	1883	33203192.aa	258	716
hp5e15440orf16	1432	1883	36573502.aa	295	762
02ce11022orf7	1052	1503	1071890.aa	10	395
04ep10811orf4	1091	1542	24215.aa	160	587

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04ep10811orf4	1091	1542	289711.aa	225	669
hp5e11726orf4	1421	1872	36203402.aa	964	758
02ge20116orf28	1069	1520	24238762.aa	166	593
01ce11513orf21	1005	1456	1464715.aa	56	451
01ce11513orf21	1005	1456	4882763.aa	980	827
01ce11618orf10	1007	1458	207817.aa	903	502
06gp11202orf7	1166	1617	33399142.aa	261	719
07cp21714orf13	1177	1628	16406581.aa	71	469
07gp11807orf25	1193	1644	3319687.aa	955	715
07gp11807orf8	1206	1657	5875152.aa	361	847
07gp11807orf9	1207	1658	14714687.aa	58	453
14ce20219orf1	1304	1755	22441050.aa	114	527
14ce20219orf2	1305	1756	26258562.aa	940	652
27ze10351orf18	1346	1797	35345228.aa	960	745
27ze10351orf24	1348	1799	23728388.aa	144	567
27ze10351orf29	1350	1801	5878208.aa	362	848
02ae11611orf11	1032	1483	13726562.aa	40	430
02ae11611orf11	1032	1483	35428912.aa	285	748
02ce11022orf8	1053	1504	10723412.aa	11	396
02ce11022orf8	1053	1504	24218968.aa	161	588
02ce11022orf8	1053	1504	4455467.aa	974	795
03ee11215orf29	1081	1532	22265691.aa	111	523
05cp11911orf41	1124	1575	4338438.aa	316	791
hp2p10625orf28	1382	1833	32952.aa	257	714
hp5p15641orf12	1437	1888	17787558.aa	78	481
12ap10324orf3	1263	1714	3906712.aa	966	765
A.4. Outer membrane proteins					
07ap80601orf8	1173	1624	5083193.aa	352	837
hp3e11168orf30	1405	1856	4960952.aa	981	833
hp3p10156orf12	1406	1857	24104558.aa	158	585
hp4e13394orf2	1410	1861	7116626.aa	989	865
04ce11617orf2	1086	1537	36126938.aa	963	764
14ge10705orf5	1322	1773	1431462.aa	48	440
14ge10705orf5	1322	1773	16225006.aa	68	465
12ap10324orf7	1266	1717	23531562.aa	135	555
13ae10712orf9	1282	1733	22379952.aa	910	526
12ge10305orf1	1271	1722	30478562.aa	236	687
12ge10305orf1	1271	1722	31250333.aa	241	692
07gp31516orf4	1208	1659	31262.aa	949	693
05cp20518orf33	1126	1577	29479681.aa	945	677
12ap11614orf8	1270	1721	26054702.aa	207	649
12ge20305orf2	1278	1729	4721061.aa	977	812
A.5. Other cell envelope proteins					
hp4p11352orf9	1419	1870	4821082.aa	978	820
05cp20518orf3	1125	1576	978477.aa	994	880
07ee20513orf14	1181	1632	24220627.aa	163	590
hp4p11352orf2	1416	1867	32705252.aa	256	713

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hp4p11352orf2	1416	1867	35445843.aa	287	750
04ge11713orf11	1096	1547	24427340.aa	184	613
03ee11215orf30	1082	1533	1416312.aa	45	437
06cp11722orf15	1146	1597	23535937.aa	136	556
06cp11722orf15	1146	1597	26366312.aa	214	657
06cp11722orf12	1145	1596	114505.aa	16	402
05ae20220orf32	1108	1559	2461062.aa	192	623
06cp11722orf21	1148	1599	6828218.aa	373	862
16ae10508orf13	1337	1788	14642217.aa	892	449
16ae10508orf14	1338	1789	30703183.aa	239	690
hp5e12982orf14	1424	1875	1365943.aa	34	424
01ae22001orf2	1000	1451	4826401.aa	340	821
01xe21717orf5	1027	1478	1385937.aa	41	432
01xe21717orf5	1027	1478	4714375.aa	332	811
07ce10203orf22	1175	1626	23526667.aa	134	554
14gp12015orf13	1330	1781	4698838.aa	330	809
B. CYTOPLASAMIC PROTEINS					
B.1. Proteins involved in energy conversion					
06cp11722orf16	1147	1598	10553192.aa	882	390
13ee10216orf55	1288	1739	914087.aa	382	876
14gp11820orf20	1324	1775	23475342.aa	130	547
hp1p11244orf7	1363	1814	29500075.aa	230	678
B.2. Proteins involved in amino acid metabolism					
01ae12021orf1	997	1448	34109763.aa	269	729
01ee11621orf6	1015	1466	4177212.aa	312	786
03ge31106orf1	1084	1535	26301059.aa	211	654
04ep71403orf15	1094	1545	34194093.aa	959	734
04ge11713orf37	1099	1550	25992137.aa	938	646
09gp10903orf3	1229	1680	21976637.aa	110	522
11gp10904orf27	1250	1701	31681556.aa	244	696
12ap11614orf4	1268	1719	45914063.aa	328	807
13ee12016orf10	1293	1744	30082267.aa	235	683
16ae10508orf21	1339	1790	429192.aa	315	790
hp3p10349orf16	1408	1859	36594167.aa	296	763
hp5e15211orf22	1429	1880	4578469.aa	976	806
hp5e15440orf19	1434	1885	4492217.aa	321	799
09cp10713orf29	1228	1679	1408.aa	43	434
02ae11611orf1	1031	1482	35269000.aa	281	743
02ae11612orf13	1034	1485	4570262.aa	326	804
01ce11618orf18	1008	1459	34189716.aa	272	733
B.3. Proteins involved in nucleotide metabolism					
02cp20821orf10	1061	1512	4882652.aa	344	826
02ep30607orf10	1064	1515	23598962.aa	139	562
07ge20415orf6	1191	1642	12897656.aa	30	420
09ap20802orf1	1217	1668	2738378.aa	220	664
hp1p13852orf5	1365	1816	598933.aa	364	850
hp3e11024orf24	1394	1845	6517040.aa	369	857

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hp4e14535orf3	1414	1865	677088.aa	372	861
hp4e14535orf4	1415	1866	867183.aa	991	872
hp5e15440orf21	1435	1886	23442642.aa	128	544
02cp11822orf22	1058	1509	4895327.aa	347	830
02cp11822orf26	1059	1510	14574201.aa	52	446
B.4. Proteins involved in carbohydrate metabolism					
03ee11215orf26	1080	1531	10737627.aa	12	397
05cp20518orf5	1128	1579	32144532.aa	247	699
05cp20518orf64	1133	1584	15807794.aa	64	459
09ae11601orf3	1211	1662	2149041.aa	101	509
11gp11422orf1	1252	1703	4787562.aa	338	818
11gp11422orf2	1253	1704	19541302.aa	83	488
13ee10216orf43	1286	1737	14257751.aa	46	438
13ee10216orf56	1289	1740	4897177.aa	348	831
13ee10216orf9	1291	1742	2855006.aa	223	667
14ce11519orf2	1303	1754	13723593.aa	39	429
hp3e11060orf11	1396	1847	29557266.aa	232	680
01ae11421orf1	996	1447	24300682.aa	168	597
B.5. Proteins involved in cofactor metabolism					
04ge10816orf2	1095	1546	1581937.aa	65	460
06ee10709orf5	1156	1607	3261306.aa	952	709
06ep10306orf13	1158	1609	485375.aa	341	822
06ep10306orf14	1159	1610	16251627.aa	69	466
12ge20305orf14	1277	1728	24089437.aa	924	584
02ae11612orf26	1038	1489	10407625.aa	4	388
B.6. Proteins involved in lipid metabolism					
12ae11404orf14	1257	1708	24806290.aa	197	631
29zp10241orf11	1357	1808	422937.aa	313	787
hp5e15440orf22	1436	1887	22667967.aa	119	532
B.7. Proteins involved in mRNA translation and ribosome biogenesis					
02ce10213orf2	1047	1498	24500088.aa	188	619
02cp11404orf11	1055	1506	33601578.aa	956	723
06ce10515orf4	1141	1592	25595387.aa	935	641
09cp10713orf28	1227	1678	32036462.aa	246	698
14gp11820orf5	1327	1778	24803280.aa	196	630
hp4e14522orf11	1412	1863	785437.aa	376	869
B.8. Proteins involved in genome replication, transcription, recombination& repair					
01ce11016orf14	1003	1454	24396937.aa	172	601
04ce11617orf27	1087	1538	12520952.aa	25	415
05ap11505orf1	1116	1567	23440814.aa	126	542
05cp20518orf56	1130	1581	32431687.aa	951	704
05cp20518orf63	1132	1583	23880087.aa	147	572
07ge11504orf4	1185	1636	16305252.aa	895	467
07ge20415orf30	1188	1639	10745275.aa	14	399
07gp11807orf35	1198	1649	24036302.aa	154	579

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09ap20802orf22	1218	1669	34574062.aa	277	739
09ap20802orf22	1218	1669	5879160.aa	363	849
11ge10309orf51	1244	1695	487750.aa	342	824
14ce21516orf1	1306	1757	85786.aa	378	871
14gp11820orf27	1325	1776	23475342.aa	130	547
hp3e11060orf2	1397	1848	24818802.aa	198	633
hp3e11060orf9	1398	1849	3166040.aa	243	695
hp3p10156orf8	1407	1858	11719687.aa	19	405
hp5e15440orf18	1433	1884	10677187.aa	9	394
hp5e15440orf18	1433	1884	36523442.aa	761	
B.9. Proteins involved in outer membrane or cell wall biosynthesis					
09ap11406orf8	1216	1667	23912807.aa	149	574
09ap11406orf8	1216	1667	24298127.aa	167	596
11ep12011orf9	1239	1690	495312.aa	349	832
29zp10241orf7	1362	1813	26197187.aa	209	651
01ep30520orf16	1017	1468	7225666.aa	990	867
01ep30520orf27	1019	1470	24441412.aa	185	614
01ep30520orf27	1019	1470	11253.aa	883	401
29zp10241orf4	1360	1811	10675632.aa	8	393
B.10. Chaperones					
hp5e12982orf13	1423	1874	12343763.aa	887	413
hp5e15211orf10	1425	1876	50253.aa	350	835
hp1p13947orf1	1374	1825	6845425.aa	987	863
B.11 Other cytoplasmic proteins					
01xe21717orf9	1028	1479	156587.aa	63	458
02ae11612orf25	1037	1488	32422343.aa	249	701
03ee11215orf10	1077	1528	22542803.aa	118	531
05ae20220orf99	1115	1566	23492181.aa	132	550
11ce10917orf14	1232	1683	14313885.aa	47	439
11ge10309orf15	1241	1692	21647676.aa	106	516
12ap11614orf2	1267	1718	4562712.aa	324	802
06ge10115orf15	1163	1614	24070250.aa	155	581
02ge20116orf22	1068	1519	22704567.aa	121	535
02ge20116orf22	1068	1519	24003758.aa	153	578
02ge20116orf22	1068	1519	19626250.aa	87	492
02cp11404orf9	1056	1507	6517192.aa	986	858
03ae10516orf11	1072	1523	33476715.aa	262	720
03ae10516orf11	1072	1523	4726503.aa	333	813
03ap21820orf10	1073	1524	13673328.aa	36	426
04ep71403orf10	1092	1543	50062.aa	982	834
04gp11213orf36	1102	1553	24414687.aa	180	609
04gp11213orf60	1103	1554	19556290.aa	84	489
05ae10307orf1	1104	1555	17497107.aa	900	480
05ae20220orf54	1111	1562	1179838.aa	20	406
05cp11911orf11	1119	1570	10664078.aa	7	392
05gp11901orf20	1136	1587	15039062.aa	61	456

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05gp11901orf24	1137	1588	32600912.aa	253	707
06ae11405orf10	1140	1591	22687687.aa	120	533
06ce11002orf2	1142	1593	34099062.aa	268	728
11ce10917orf9	1233	1684	391313.aa	299	769
11cp12006orf17	1238	1689	291700.aa	942	671
11ge10309orf25	1243	1694	24406401.aa	173	602
11ge10309orf56	1245	1696	24495312.aa	187	618
11ge10309orf66	1247	1698	24495312.aa	187	618
11gp10904orf12	1249	1700	29844512.aa	234	682
12ae11404orf9	1261	1712	22303918.aa	112	524
12ap11614orf6	1269	1720	4562712.aa	324	802
12ge20305orf30	1279	1730	4095342.aa	971	785
13ap11517orf31	1284	1735	15126875.aa	62	457
13ee10216orf82	1290	1741	4035262.aa	308	781
13ee12016orf24	1297	1748	16459375.aa	74	473
14gp12015orf1	1328	1779	10009666.aa	1	384
hp1p13922orf30	1370	1821	34089087.aa	266	726
hp1p13939orf13	1372	1823	4766691.aa	337	817
hp2e10911orf25	1377	1828	2035936.aa	93	498
hp2p10625orf30	1383	1834	1411681.aa	44	436
hp2p10625orf7	1384	1835	4740887.aa	335	815
hp2p10625orf8	1385	1836	6495137.aa	368	856
hp3e10349orf18	1388	1839	260941.aa	208	650
hp3e11168orf14	1401	1852	5325005.aa	358	844
hp3e11168orf15	1402	1853	24039587.aa	923	580
hp4p11352orf8	1418	1869	4040928.aa	310	783
hp4p13402orf1	1420	1871	1256885.aa	26	416
hp5e15211orf15	1427	1878	35156938.aa	279	741
02ge20116orf33	1070	1521	14480927.aa	890	442
06cp20302orf8	1151	1602	4569693.aa	325	803
07ce11409orf4	1176	1627	21742157.aa	109	520
01ae12021orf8	999	1450	23646885.aa	143	566
01ce11513orf24	1006	1457	23539006.aa	918	557
01cp11710orf27	1012	1463	32595137.aa	252	706
01ep30520orf20	1018	1469	32627125.aa	953	710
02ae11211orf19	1030	1481	19537968.aa	902	487
02ae11611orf5	1033	1484	24407533.aa	174	603
02ce10114orf1	1041	1492	16440842.aa	73	472
02ce10213orf32	1049	1500	16839562.aa	898	476
02ce11220orf2	1054	1505	3930468.aa	300	770
02cp11721orf13	1057	1508	5265957.aa	356	841
04ep10811orf1	1090	1541	3907042.aa	298	768
04ge11713orf27	1097	1548	5111308.aa	354	839
05cp20518orf50	1129	1580	23573294.aa	138	560
06ae11020orf2	1139	1590	4486092.aa	319	796
06ce11002orf8	1143	1594	194415.aa	80	483
06cp30603orf11	1152	1603	24824087.aa	933	634

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06ee10207orf2	1153	1604	14572133.aa	891	445
06ee10709orf17	1155	1606	6136430.aa	366	853
06ep11108orf20	1161	1612	22370182.aa	113	525
06ge10115orf12	1162	1613	4491093.aa	320	798
07ap11111orf3	1169	1620	23490686.aa	915	549
07ap80601orf10	1170	1621	5078593.aa	351	836
07ap80601orf12	1171	1622	24219012.aa	162	589
07ee20513orf1	1180	1631	36520792.aa	965	760
07gp11807orf28	1194	1645	16100038.aa	67	462
07gp11807orf29	1195	1646	42683.aa	314	789
07gp11807orf38	1199	1650	214812.aa	904	507
07gp11807orf41	1200	1651	4882842.aa	345	828
07gp11807orf42	1201	1652	719606.aa	374	866
07gp11807orf44	1202	1653	35949212.aa	962	754
07gp11807orf54	1205	1656	34161500.aa	270	730
14cp10923orf1	1312	1763	24492192.aa	186	617
16ae10508orf10	1336	1787	14864452.aa	60	455
27ze10351orf25	1349	1800	875042.aa	379	873
29gp10119orf6	1355	1806	14094816.aa	889	435
29zp10241orf18	1359	1810	3906937.aa	967	766
hp4e14535orf2	1413	1864	43490713.aa	973	793
hp5e15211orf13	1426	1877	35163962.aa	280	742
hp5e15211orf29	1430	1881	24329712.aa	170	599
			625277.aa	985	854
			24816915.aa	932	632

C. SECRETED OR PERIPLASMIC PROTEINS**C.1. Secreted or periplasmic proteins**

01ce11016orf19	1004	1455	22460468.aa	117	530
05gp11901orf25	1138	1589	32609403.aa	254	708
02ge20116orf20	1067	1518	12505125.aa	24	414
03ee11215orf15	1078	1529	3157067.aa	242	694
14cp10923orf3	1314	1765	3242952.aa	950	703
14ee11217orf1	1319	1770	33595708.aa	263	721
14ee11217orf1	1319	1770	35442513.aa	286	749
hp2e10911orf30	1378	1829	30100332.aa	947	685
05ae20220orf124	1105	1556	14570443.aa	51	444
05ae20220orf92	1114	1565	24410643.aa	177	606
05ap21216orf7	1118	1569	24078837.aa	156	582
05cp11911orf12	1120	1571	24609431.aa	190	621
05cp11911orf27	1123	1574	783432.aa	375	868
05cp20518orf41	1127	1578	2843912.aa	222	666
09ae11601orf4	1212	1663	11876471.aa	21	408
09cp10502orf17	1223	1674	23438887.aa	912	538
09cp10713orf25	1225	1676	23912707.aa	148	573
11ge10309orf63	1246	1697	25501501.aa	202	639
11ge10309orf9	1248	1699	289077.aa	224	668
12ae11404orf3	1259	1710	22303918.aa	112	524

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12ap10324orf4	1264	1715	13178562.aa	32	422
12ap10324orf5	1265	1716	4805318.aa	339	819
13ae10712orf4	1281	1732	24416083.aa	182	611
13ap11517orf7	1285	1736	29386577.aa	228	674
13ee12016orf15	1294	1745	23958179.aa	152	577
13ee12016orf5	1298	1749	272058.aa	219	663
13ee12016orf8	1299	1750	23564012.aa	137	558
14cp10923orf8	1315	1766	4414000.aa	318	794
14cp11121orf6	1316	1767	23631292.aa	141	564
14ee10308orf8	1317	1768	24230058.aa	165	592
14ee10308orf9	1318	1769	4728193.aa	334	814
16ep10117orf8	1344	1795	10742963.aa	13	398
27ze10351orf5	1351	1802	3906963.aa	297	767
29ge10111orf1	1353	1804	1367157.aa	35	425
hp1p13939orf9	1373	1824	26423583.aa	216	659
hp2e11858orf5	1380	1831	21687842.aa	908	517
hp3e10349orf17	1387	1838	23439055.aa	124	539
hp3e10349orf24	1389	1840	16603418.aa	75	475
hp3e11024orf22	1393	1844	2445812.aa	927	615
hp3e11024orf22	1393	1844	2774062.aa	221	665
hp4e13394orf5	1411	1862	24411011.aa	178	607
hp5e15211orf21	1428	1879	24328910.aa	169	598
hp5e15276orf14	1431	1882	36335436.aa	293	759
hp5p15641orf8	1439	1890	35837767.aa	289	752
02ce10213orf11	1043	1494	24276587.aa	926	595
07ge11504orf2	1183	1634	30283516.aa	948	686
07ge11504orf3	1184	1635	22447252.aa	115	528
07gp11807orf32	1196	1647	32462543.aa	251	705
07gp11807orf33	1197	1648	4882842.aa	345	828
07gp11807orf48	1203	1654	116018.aa	17	403
01ae11403orf1	995	1446	23594838.aa	920	561
01ae12021orf7	998	1449	20415937.aa	95	500
01ce10516orf2	1001	1452	1962590.aa	86	491
01gp11016orf14	1022	1473	5869090.aa	360	846
01xe21717orf12	1023	1474	34179577.aa	271	732
02ae11211orf10	1029	1480	3987580.aa	970	778
02ae11612orf4	1040	1491	35704718.aa	288	751
02ce10216orf1	1051	1502	35336707.aa	282	744
02cp20821orf12	1062	1513	20836042.aa	98	504
02cp20821orf12	1062	1513	12698442.aa	29	419
06ee10709orf16	1154	1605	4339708.aa	317	792
14ep11115orf1	1320	1771	4882318.aa	343	825
C.2. Proteins likely to be secreted or periplasmic					
03ap21820orf5	1075	1526	36131282.aa	291	756
05ae20220orf24	1106	1557	21720017.aa	108	519
05ae20220orf50	1109	1560	80257.aa	377	870
05cp20518orf9	1134	1585	3964593.aa	305	777

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05cp20518orf9	1134	1585	4687507.aa	305	808
09cp10502orf14	1221	1672	2111040.aa	100	506
09cp10713orf26	1226	1677	7031343.aa	988	864
11ce11603orf22	1235	1686	26306340.aa	212	655
14ce10720orf2	1301	1752	1181418.aa	884	407
14cp10119orf7	1311	1762	1370202.aa	37	427
14gp11820orf4	1326	1777	3953952.aa	968	774
16cp30109orf6	1341	1792	4490717.aa	975	797
29gp10119orf5	1354	1805	30603402.aa	237	688
hp1p11256orf7	1364	1815	4740887.aa	335	815
hp1p13868orf24	1366	1817	33397538.aa	260	718
hp1p14013orf4	1376	1827	663530.aa	370	859
hp3e11024orf16	1391	1842	20173437.aa	91	496
hp3e11024orf16	1391	1842	34573431.aa	276	738
hp3e11024orf6	1395	1846	4062813.aa	311	784
hp6p10723orf7	1445	1896	24406401.aa	173	602
03ee11215orf20	1079	1530	2150290.aa	102	510
07ge20415orf22	1186	1637	3958537.aa	304	775
01ce11618orf20	1010	1461	882827.aa	380	874
01ep10216orf6	1016	1467	23441078.aa	127	543
07ap80601orf5	1172	1623	917200.aa	993	878
04ge11713orf35	1098	1549	24256572.aa	925	594
03ap21820orf9	1076	1527	24415917.aa	181	610
07ce10203orf14	1174	1625	24395801.aa	171	600

D. OTHER SURFACE AND MEMBRANE PROTEINS**D.1. Proteins likely to contain a single membrane****spanning region**

02cp11822orf8	1060	1511	907827.aa	381	875
05ae20220orf51	1110	1561	29458178.aa	229	676
05ae20220orf6	1112	1563	4548792.aa	323	801
11ae10305orf4	1230	1681	6696887.aa	371	860
12ae11404orf8	1260	1711	35417942.aa	284	747
12ge20305orf35	1280	1731	22453166.aa	116	529
13ee11718orf2	1292	1743	1038312.aa	3	387
13ee12016orf19	1296	1747	10580417.aa	6	391
13ee12016orf19	1296	1747	21618785.aa	907	515
14ce21516orf3	1307	1758	24634750.aa	193	625
hp6p10723orf20	1442	1893	23831562.aa	145	568
hp6p10723orf5	1444	1895	14726542.aa	59	454
02ce10213orf1	1042	1493	4531568.aa	322	800
02ae11612orf36	1039	1490	2040717.aa	94	499
04ge11713orf41	1100	1551	3991067.aa	306	779
			10037799.aa	881	385

D.2. Proteins likely to contain two membrane spans

05cp11911orf15	1122	1573	26052137.aa	939	648
12ae10622orf16	1254	1705	25925.aa	205	643
12ae11404orf12	1256	1707	23438840.aa	123	537

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12ge10305orf10	1272	1723	21503772.aa	906	511
12ge10305orf10	1272	1723	24488537.aa	928	616
12ge10305orf21	1275	1726	489057.aa	346	829
14cp10119orf14	1309	1760	23473437.aa	129	546
14cp10119orf14	1309	1760	40339452.aa	307	780
14cp10923orf14	1313	1764	23515833.aa	133	553
27ze10351orf22	1347	1798	23486342.aa	131	548
27ze10351orf7	1352	1803	11924177.aa	886	410
29gp10119orf7	1356	1807	24413512.aa	179	608
hp5p15641orf5	1438	1889	21563752.aa	104	513
hp6p10723orf13	1441	1892	26351567.aa	213	656
01ce11618orf19	1009	1460	55843.aa	359	845
01xe21717orf40	1026	1477	23610905.aa	140	563
02ce10213orf23	1048	1499	23867207.aa	146	570
02cp20821orf8	1063	1514	4572168.aa	327	805
07ge20415orf39	1190	1641	5993958.aa	365	851
D.3. Proteins likely to contain 3 membrane spanning regions					
03ge10505orf14	1083	1534	1364378.aa	33	423
05ae20220orf88	1113	1564	4708337.aa	331	810
09cp10502orf16	1222	1673	24409577.aa	175	604
13ee12016orf18	1295	1746	25398250.aa	200	636
16ep10117orf7	1343	1794	36134661.aa	292	757
hp3e11024orf17	1392	1843	1206675.aa	23	412
hp6p10723orf43	1443	1894	4744128.aa	336	816
D.4. Proteins likely to contain 4 membrane spanning regions					
03xe11215orf5	1085	1536	3933437.aa	301	771
04ep71403orf12	1093	1544	12694087.aa	28	418
05ap11505orf10	1117	1568	26758437.aa	941	662
05cp11911orf13	1121	1572	21511555.aa	103	512
05cp11911orf13	1121	1572	29531590.aa	231	679
05cp20518orf61	1131	1582	24409641.aa	176	605
13ee10216orf5	1287	1738	12969218.aa	31	421
13ee10216orf5	1287	1738	23494043.aa	917	552
hp5p15641orf9	1440	1891	23945317.aa	151	576
09ae11601orf11	1209	1660	23867687.aa	922	571
D.5. Proteins likely to contain 5 membrane spanning regions					
16ep10117orf6	1342	1793			
hp2p10625orf14	1381	1832	33986087.aa	265	725
hp3e10349orf25	1390	1841	23631317.aa	142	565
hp3p10349orf32	1409	1860	33218912.aa	259	717
02ae11612orf14	1035	1486	23437502.aa	122	536
			25995917.aa	206	647
			11878127.aa	885	409
D.6. Proteins likely to contain 6 membrane spanning regions					
01cp11710orf34	1014	1465	2042312.aa	96	501
01cp11710orf34	1014	1465	5083577.aa	353	838
04ep10206orf22	1088	1539	13704718.aa	38	428

04ep10206orf22	1088	1539	20023400.aa	89	494
11ge10309orf18	1242	1693	17089217.aa	77	479
07cp21714orf14	1178	1629	32663212.aa	954	711
07cp21714orf14	1178	1629	3360130.aa	264	722
D.7. Proteins likely to contain 7 or more membrane spanning regions					
04ep10206orf23	1089	1540	25976418.aa	937	645
04ep10206orf23	1089	1540	2915903.aa	226	670
16ae10508orf3	1340	1791	35360843.aa	283	746
03ap21820orf13	1074	1525	197166.aa	88	493
03ap21820orf13	1074	1525	234391.aa	125	540
03ap21820orf13	1074	1525	24417212.aa	183	612
05ae20220orf31	1107	1558	24798427.aa	195	629
07gp11807orf49	1204	1655	19531291.aa	81	484
07gp11807orf49	1204	1655	19536375.aa	901	485
02ep30607orf31	1066	1517	19536458.aa	82	486
02ep30607orf31	1066	1517	13865928.aa	42	433

[In Table 1, "nt" represents nucleotide Seq. ID number and "aa" represents amino Seq. ID number]

Definitions

- 5 A purified or isolated polypeptide or a substantially pure preparation of a polypeptide are used interchangeably herein and, as used herein, mean a polypeptide that has been separated from other proteins, lipids, and nucleic acids with which it naturally occurs. Preferably, the polypeptide is also separated from substances, e.g., antibodies or gel matrix, e.g., polyacrylamide, which are used to purify it. Preferably, the polypeptide
 10 constitutes at least 10, 20, 50 70, 80 or 95% dry weight of the purified preparation. Preferably, the preparation contains: sufficient polypeptide to allow protein sequencing; at least 1, 10, or 100 µg of the polypeptide; at least 1, 10, or 100 mg of the polypeptide.

15 A purified preparation of cells refers to, in the case of plant or animal cells, an *in vitro* preparation of cells and not an entire intact plant or animal. In the case of cultured cells or microbial cells, it consists of a preparation of at least 10% and more preferably 50% of the subject cells.

- 20 A purified or isolated or a substantially pure nucleic acid, e.g., a substantially pure DNA, (are terms used interchangeably herein) is a nucleic acid which is one or both of the following: not immediately contiguous with both of the coding sequences with which it is immediately contiguous (i.e., one at the 5' end and one at the 3' end) in the naturally-
 occurring genome of the organism from which the nucleic acid is derived; or which is substantially free of a nucleic acid with which it occurs in the organism from which the nucleic acid is derived. The term includes, for example, a recombinant DNA which is incorporated into a vector, e.g., into an autonomously replicating plasmid or virus, or into
 25 the genomic DNA of a prokaryote or eukaryote, or which exists as a separate molecule (e.g., a cDNA or a genomic DNA fragment produced by PCR or restriction endonuclease treatment) independent of other DNA sequences. Substantially pure DNA also includes a

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recombinant DNA which is part of a hybrid gene encoding additional *H. pylori* DNA sequence.

A "contig" as used herein is a nucleic acid representing a continuous stretch of genomic sequence of an organism.

5 An "open reading frame", also referred to herein as ORF, is a region of nucleic acid which encodes a polypeptide. This region may represent a portion of a coding sequence or a total sequence and can be determined from a stop to stop codon or from a start to stop codon.

10 As used herein, a "coding sequence" is a nucleic acid which is transcribed into messenger RNA and/or translated into a polypeptide when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a translation start codon at the five prime terminus and a translation stop code at the three prime terminus. A coding sequence can include but is not limited to messenger RNA, synthetic DNA, and recombinant nucleic acid sequences.

15 A "complement" of a nucleic acid as used herein refers to an anti-parallel or antisense sequence that participates in Watson-Crick base-pairing with the original sequence.

20 A "gene product" is a protein or structural RNA which is specifically encoded by a gene.

25 As used herein, the term "probe" refers to a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of interest. Probes are often associated with or capable of associating with a label. A label is a chemical moiety capable of detection. Typical labels comprise dyes, radioisotopes, luminescent and chemiluminescent moieties, fluorophores, enzymes, precipitating agents, amplification sequences, and the like.

30 Similarly, a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of interest and immobilizes such molecule is referred herein as a "capture ligand". Capture ligands are typically associated with or capable of associating with a support such as nitro-cellulose, glass, nylon membranes, beads, particles and the like. The specificity of hybridization is dependent on conditions such as the base pair composition of the nucleotides, and the temperature and salt concentration of the reaction. These conditions are readily discernable to one of ordinary skill in the art using routine experimentation.

35 Homologous refers to the sequence similarity or sequence identity between two polypeptides or between two nucleic acid molecules. When a position in both of the two compared sequences is occupied by the same base or amino acid monomer subunit, e.g., if a position in each of two DNA molecules is occupied by adenine, then the molecules are homologous at that position. The percent of homology between two sequences is a function of the number of matching or homologous positions shared by the two sequences divided by the number of positions compared x 100. For example, if 6 of 10 of the positions in two sequences are matched or homologous then the two sequences are 60%

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homologous. By way of example, the DNA sequences ATTGCC and TATGGC share 50% homology. Generally, a comparison is made when two sequences are aligned to give maximum homology.

Nucleic acids are hybridizable to each other when at least one strand of a nucleic acid can anneal to the other nucleic acid under defined stringency conditions. Stringency of hybridization is determined by: (a) the temperature at which hybridization and/or washing is performed; and (b) the ionic strength and polarity of the hybridization and washing solutions. Hybridization requires that the two nucleic acids contain complementary sequences; depending on the stringency of hybridization, however, mismatches may be tolerated. Typically, hybridization of two sequences at high stringency (such as, for example, in a solution of 0.5X SSC, at 65° C) requires that the sequences be essentially completely homologous. Conditions of intermediate stringency (such as, for example, 2X SSC at 65 ° C) and low stringency (such as, for example 2X SSC at 55° C), require correspondingly less overall complementarity between the hybridizing sequences. (1X SSC is 0.15 M NaCl, 0.015 M Na citrate).

The terms peptides, proteins, and polypeptides are used interchangeably herein.

As used herein, the term "surface protein" refers to all surface accessible proteins, e.g. inner and outer membrane proteins, proteins adhering to the cell wall, and secreted proteins.

A polypeptide has *H. pylori* biological activity if it has one, two and preferably more of the following properties: (1) if when expressed in the course of an *H. pylori* infection, it can promote, or mediate the attachment of *H. pylori* to a cell; (2) it has an enzymatic activity, structural or regulatory function characteristic of an *H. pylori* protein; (3) or the gene which encodes it can rescue a lethal mutation in an *H. pylori* gene. A polypeptide has biological activity if it is an antagonist, agonist, or super-agonist of a polypeptide having one of the above-listed properties.

A biologically active fragment or analog is one having an *in vivo* or *in vitro* activity which is characteristic of the *H. pylori* polypeptides of the invention contained in the Sequence Listing, or of other naturally occurring *H. pylori* polypeptides, e.g., one or more of the biological activities described herein. Especially preferred are fragments which exist *in vivo*, e.g., fragments which arise from post transcriptional processing or which arise from translation of alternatively spliced RNA's. Fragments include those expressed in native or endogenous cells as well as those made in expression systems, e.g., in CHO cells. Because peptides such as *H. pylori* polypeptides often exhibit a range of physiological properties and because such properties may be attributable to different portions of the molecule, a useful *H. pylori* fragment or *H. pylori* analog is one which exhibits a biological activity in any biological assay for *H. pylori* activity. Most preferably the fragment or analog possesses 10%, preferably 40%, more preferably 60%, 70%, 80% or 90% or greater of the activity of *H. pylori*, in any *in vivo* or *in vitro* assay.

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Analogs can differ from naturally occurring *H. pylori* polypeptides in amino acid sequence or in ways that do not involve sequence, or both. Non-sequence modifications include changes in acetylation, methylation, phosphorylation, carboxylation, or glycosylation. Preferred analogs include *H. pylori* polypeptides (or biologically active fragments thereof) whose sequences differ from the wild-type sequence by one or more conservative amino acid substitutions or by one or more non-conservative amino acid substitutions, deletions, or insertions which do not substantially diminish the biological activity of the *H. pylori* polypeptide. Conservative substitutions typically include the substitution of one amino acid for another with similar characteristics, e.g., substitutions within the following groups: valine, glycine; glycine, alanine; valine, isoleucine, leucine; aspartic acid, glutamic acid; asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine. Other conservative substitutions can be made in view of the table below.

15

TABLE 2
CONSERVATIVE AMINO ACID REPLACEMENTS

For Amino Acid	Code	Replace with any of
Alanine	A	D-Ala, Gly, beta-Ala, L-Cys, D-Cys
Arginine	R	D-Arg, Lys, D-Lys, homo-Arg, D-homo-Arg, Met, Ile, D-Met, D-Ile, Orn, D-Orn
Asparagine	N	D-Asn, Asp, D-Asp, Glu, D-Glu, Gln, D-Gln
Aspartic Acid	D	D-Asp, D-Asn, Asn, Glu, D-Glu, Gln, D-Gln
Cysteine	C	D-Cys, S-Me-Cys, Met, D-Met, Thr, D-Thr
Glutamine	Q	D-Gln, Asn, D-Asn, Glu, D-Glu, Asp, D-Asp
Glutamic Acid	E	D-Glu, D-Asp, Asp, Asn, D-Asn, Gln, D-Gln
Glycine	G	Ala, D-Ala, Pro, D-Pro, β -Ala, Acp
Isoleucine	I	D-Ile, Val, D-Val, Leu, D-Leu, Met, D-Met
Leucine	L	D-Leu, Val, D-Val, Leu, D-Leu, Met, D-Met
Lysine	K	D-Lys, Arg, D-Arg, homo-Arg, D-homo-Arg, Met, D-Met, Ile, D-Ile, Orn, D-Orn
Methionine	M	D-Met, S-Me-Cys, Ile, D-Ile, Leu, D-Leu, Val, D-Val
Phenylalanine	F	D-Phe, Tyr, D-Thr, L-Dopa, His, D-His, Trp, D-Trp, Trans-3,4, or 5-phenylproline, cis-3,4, or 5-phenylproline

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Proline	P	D-Pro, L-L-thioazolidine-4-carboxylic acid, D- or L-oxazolidine-4-carboxylic acid
Serine	S	D-Ser, Thr, D-Thr, allo-Thr, Met, D-Met, Met(O), D-Met(O), L-Cys, D-Cys
Threonine	T	D-Thr, Ser, D-Ser, allo-Thr, Met, D-Met, Met(O), D-Met(O), Val, D-Val
Tyrosine	Y	D-Tyr, Phe, D-Phe, L-Dopa, His, D-His
Valine	V	D-Val, Leu, D-Leu, Ile, D-Ile, Met, D-Met

Other analogs within the invention are those with modifications which increase peptide stability; such analogs may contain, for example, one or more non-peptide bonds (which replace the peptide bonds) in the peptide sequence. Also included are: analogs that 5 include residues other than naturally occurring L-amino acids, e.g., D-amino acids or non-naturally occurring or synthetic amino acids, e.g., β or γ amino acids; and cyclic analogs.

As used herein, the term "fragment", as applied to an *H. pylori* analog, will ordinarily be at least about 20 residues, more typically at least about 40 residues, preferably at least about 60 residues in length. Fragments of *H. pylori* polypeptides can be generated 10 by methods known to those skilled in the art. The ability of a candidate fragment to exhibit a biological activity of *H. pylori* polypeptide can be assessed by methods known to those skilled in the art as described herein. Also included are *H. pylori* polypeptides containing residues that are not required for biological activity of the peptide or that result from alternative mRNA splicing or alternative protein processing events.

15 An "immunogenic component" as used herein is a moiety, such as an *H. pylori* polypeptide, analog or fragment thereof, that is capable of eliciting a humoral and/or cellular immune response in a host animal.

An "antigenic component" as used herein is a moiety, such as an *H. pylori* polypeptide, analog or fragment thereof, that is capable of binding to a specific antibody 20 with sufficiently high affinity to form a detectable antigen-antibody complex.

As used herein, the term "transgene" means a nucleic acid (encoding, e.g., one or more polypeptides), which is partly or entirely heterologous, i.e., foreign, to the transgenic animal or cell into which it is introduced, or, is homologous to an endogenous gene of the transgenic animal or cell into which it is introduced, but which is designed to be inserted, or 25 is inserted, into the cell's genome in such a way as to alter the genome of the cell into which it is inserted (e.g., it is inserted at a location which differs from that of the natural gene or its insertion results in a knockout). A transgene can include one or more transcriptional regulatory sequences and any other nucleic acid, such as introns, that may be necessary for optimal expression of the selected nucleic acid, all operably linked to the selected nucleic 30 acid, and may include an enhancer sequence.

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As used herein, the term "transgenic cell" refers to a cell containing a transgene.

- As used herein, a "transgenic animal" is any animal in which one or more, and preferably essentially all, of the cells of the animal includes a transgene. The transgene can be introduced into the cell, directly or indirectly by introduction into a precursor of the cell,
- 5 by way of deliberate genetic manipulation, such as by a process of transformation of competent cells or by microinjection or by infection with a recombinant virus. This molecule may be integrated within a chromosome, or it may be extrachromosomally replicating DNA.

The term "antibody" as used herein is intended to include fragments thereof which
10 are specifically reactive with *H. pylori* polypeptides.

- As used herein, the term "cell-specific promoter" means a DNA sequence that serves as a promoter, i.e., regulates expression of a selected DNA sequence operably linked to the promoter, and which effects expression of the selected DNA sequence in specific cells of a tissue. The term also covers so-called "leaky" promoters, which
15 regulate expression of a selected DNA primarily in one tissue, but cause expression in other tissues as well.

Misexpression, as used herein, refers to a non-wild type pattern of gene expression. It includes: expression at non-wild type levels, i.e., over or under expression; a pattern of expression that differs from wild type in terms of the time or stage at which the gene is
20 expressed, e.g., increased or decreased expression (as compared with wild type) at a predetermined developmental period or stage; a pattern of expression that differs from wild type in terms of decreased expression (as compared with wild type) in a predetermined cell type or tissue type; a pattern of expression that differs from wild type in terms of the splicing size, amino acid sequence, post-transitional modification, or biological activity of
25 the expressed polypeptide; a pattern of expression that differs from wild type in terms of the effect of an environmental stimulus or extracellular stimulus on expression of the gene, e.g., a pattern of increased or decreased expression (as compared with wild type) in the presence of an increase or decrease in the strength of the stimulus.

As used herein, "host cells" and other such terms denoting microorganisms or
30 higher eukaryotic cell lines cultured as unicellular entities refers to cells which can become or have been used as recipients for a recombinant vector or other transfer DNA, and include the progeny of the original cell which has been transfected. It is understood by individuals skilled in the art that the progeny of a single parental cell may not necessarily be completely identical in genomic or total DNA compliment to the original parent, due to
35 accident or deliberate mutation.

As used herein, the term "control sequence" refers to a nucleic acid having a base sequence which is recognized by the host organism to effect the expression of encoded sequences to which they are ligated. The nature of such control sequences differs depending upon the host organism; in prokaryotes, such control sequences generally include a

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promoter, ribosomal binding site, terminators, and in some cases operators; in eukaryotes, generally such control sequences include promoters, terminators and in some instances, enhancers. The term control sequence is intended to include at a minimum, all components whose presence is necessary for expression, and may also include additional components
5 whose presence is advantageous, for example, leader sequences.

As used herein, the term "operably linked" refers to sequences joined or ligated to function in their intended manner. For example, a control sequence is operably linked to coding sequence by ligation in such a way that expression of the coding sequence is achieved under conditions compatible with the control sequence and host cell.

10 The metabolism of a substance, as used herein, means any aspect of the, expression, function, action, or regulation of the substance. The metabolism of a substance includes modifications, e.g., covalent or non-covalent modifications of the substance. The metabolism of a substance includes modifications, e.g., covalent or non-covalent modification, the substance induces in other substances. The metabolism of a substance
15 also includes changes in the distribution of the substance. The metabolism of a substance includes changes the substance induces in the distribution of other substances.

A "sample" as used herein refers to a biological sample, such as, for example, tissue or fluid isolated from an individual (including without limitation plasma, serum, cerebrospinal fluid, lymph, tears, saliva and tissue sections) or from *in vitro* cell culture constituents, as well as samples from the environment.

The practice of the invention will employ, unless otherwise indicated, conventional techniques of chemistry, molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. See e.g., Sambrook, Fritsch, and Maniatis, *Molecular Cloning; Laboratory Manual* 2nd ed. (1989); *DNA Cloning*, Volumes I and II (D.N. Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed. 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds. 1984); the series, *Methods in Enzymology* (Academic Press, Inc.), particularly Vol. 154 and Vol. 155 (Wu and Grossman, eds.) and *PCR-A Practical Approach* (McPherson, Quirke, and Taylor, eds., 1991).

30

I. Isolation of Nucleic Acids of *H. pylori* and Uses Therefor

H. pylori Genomic Sequence

This invention provides nucleotide sequences of the genome of *H. pylori* which thus
35 comprises a DNA sequence library of *H. pylori* genomic DNA. The detailed description that follows provides nucleotide sequences of *H. pylori*, and also describes how the sequences were obtained and how ORFs and protein-coding sequences were identified. Also described are methods of using the disclosed *H. pylori* sequences in methods including diagnostic and therapeutic applications. Furthermore, the library can be used as a

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database for identification and comparison of medically important sequences in this and other strains of *H. pylori*.

To determine the genomic sequence of *H. pylori*, DNA was isolated from a strain of *H. pylori* (ATCC # 55679) and mechanically sheared by nebulization to a median size of 2 kb. Following size fractionation by gel electrophoresis, the fragments were blunt-ended, ligated to adapter oligonucleotides, and cloned into each of 20 different pMPX vectors (Rice et al., abstracts of Meeting of Genome Mapping and Sequencing, Cold Spring Harbor, NY, 5/11-5/15, 1994, p. 225) to construct a series of "shotgun" subclone libraries.

DNA sequencing was achieved using multiplex sequencing procedures essentially as disclosed in Church et al., 1988, *Science* 240:185; U.S. Patents No. 4,942,124 and 5,149,625). DNA was extracted from pooled cultures and subjected to chemical or enzymatic sequencing. Sequencing reactions were resolved by electrophoresis, and the products were transferred and covalently bound to nylon membranes. Finally, the membranes were sequentially hybridized with a series of labelled oligonucleotides complimentary to "tag" sequences present in the different shotgun cloning vectors. In this manner, a large number of sequences could be obtained from a single set of sequencing reactions. The cloning and sequencing procedures are described in more detail in the Exemplification.

Individual sequence reads obtained in this manner were assembled using the FALCON™ program (Church et al., 1994, *Automated DNA Sequencing and Analysis*, J.C. Venter, ed., Academic Press) and PHRAP (P. Green, Abstracts of DOE Human Genome Program Contractor-Grantee Workshop V, Jan. 1996, p.157). The average contig length was about 3-4 kb.

A variety of approaches are used to order the contigs so as to obtain a continuous sequence representing the entire *H. pylori* genome. Synthetic oligonucleotides are designed that are complementary to sequences at the end of each contig. These oligonucleotides may be hybridized to libaries of *H. pylori* genomic DNA in, for example, lambda phage vectors or plasmid vectors to identify clones that contain sequences corresponding to the junctional regions between individual contigs. Such clones are then used to isolate template DNA and the same oligonucleotides are used as primers in polymerase chain reaction (PCR) to amplify junctional fragments, the nucleotide sequence of which is then determined.

The *H. pylori* sequences were analyzed for the presence of open reading frames (ORFs) comprising at least 180 nucleotides. As a result of the analysis of ORFs based on stop-to-stop codon reads, it should be understood that these ORFs may not correspond to the ORF of a naturally-occurring *H. pylori* polypeptide. These ORFs may contain start codons which indicate the initiation of protein synthesis of a naturally-occurring *H. pylori* polypeptide. Such start codons within the ORFs provided herein can be identified by those of ordinary skill in the relevant art, and the resulting ORF and the encoded *H. pylori* polypeptide is within the scope of this invention. For example, within the ORFs a codon

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such as AUG or GUG (encoding methionine or valine) which is part of the initiation signal for protein synthesis can be identified and the ORF modified to correspond to a naturally-occurring *H. pylori* polypeptide. The predicted coding regions were defined by evaluating the coding potential of such sequences with the program GENEMARK™ (Borodovsky and 5 McIninch, 1993, *Comp. Chem.* 17:123).

Other *H. pylori* Nucleic Acids

The nucleic acids of this invention may be obtained directly from the DNA of the above referenced *H. pylori* strain by using the polymerase chain reaction (PCR). See "PCR, 10 *A Practical Approach*" (McPherson, Quirke, and Taylor, eds., IRL Press, Oxford, UK, 1991) for details about the PCR. High fidelity PCR can be used to ensure a faithful DNA copy prior to expression. In addition, the authenticity of amplified products can be checked by conventional sequencing methods. Clones carrying the desired sequences described in 15 this invention may also be obtained by screening the libraries by means of the PCR or by hybridization of synthetic oligonucleotide probes to filter lifts of the library colonies or plaques as known in the art (see, e.g., Sambrook et al., *Molecular Cloning, A Laboratory Manual* 2nd edition, 1989, Cold Spring Harbor Press, NY).

It is also possible to obtain nucleic acids encoding *H. pylori* polypeptides from a cDNA library in accordance with protocols herein described. A cDNA encoding an *H. 20 pylori* polypeptide can be obtained by isolating total mRNA from an appropriate strain. Double stranded cDNAs can then be prepared from the total mRNA. Subsequently, the cDNAs can be inserted into a suitable plasmid or viral (e.g., bacteriophage) vector using any one of a number of known techniques. Genes encoding *H. pylori* polypeptides can also be cloned using established polymerase chain reaction techniques in accordance with the 25 nucleotide sequence information provided by the invention. The nucleic acids of the invention can be DNA or RNA. Preferred nucleic acids of the invention are contained in the Sequence Listing.

The nucleic acids of the invention can also be chemically synthesized using standard techniques. Various methods of chemically synthesizing polydeoxynucleotides 30 are known, including solid-phase synthesis which, like peptide synthesis, has been fully automated in commercially available DNA synthesizers (See e.g., Itakura et al. U.S. Patent No. 4,598,049; Caruthers et al. U.S. Patent No. 4,458,066; and Itakura U.S. Patent Nos. 4,401,796 and 4,373,071, incorporated by reference herein).

Nucleic acids isolated or synthesized in accordance with features of the present 35 invention are useful, by way of example, without limitation, as probes, primers, capture ligands, antisense genes and for developing expression systems for the synthesis of proteins and peptides corresponding to such sequences. As probes, primers, capture ligands and antisense agents, the nucleic acid normally consists of all or part (approximately twenty or more nucleotides for specificity as well as the ability to form stable hybridization products)

of the nucleic acids of the invention contained in the Sequence Listing. These uses are described in further detail below.

Probes

5 A nucleic acid isolated or synthesized in accordance with the sequence of the invention contained in the Sequence Listing can be used as a probe to specifically detect *H. pylori*. With the sequence information set forth in the present application, sequences of twenty or more nucleotides are identified which provide the desired inclusivity and exclusivity with respect to *H. pylori*, and extraneous nucleic acids likely to be encountered
10 during hybridization conditions. More preferably, the sequence will comprise at least twenty to thirty nucleotides to convey stability to the hybridization product formed between the probe and the intended target molecules.

Sequences larger than 1000 nucleotides in length are difficult to synthesize but can be generated by recombinant DNA techniques. Individuals skilled in the art will readily
15 recognize that the nucleic acids, for use as probes, can be provided with a label to facilitate detection of a hybridization product.

Nucleic acid isolated and synthesized in accordance with the sequence of the invention contained in the Sequence Listing can also be useful as probes to detect homologous regions (especially homologous genes) of other *Helicobacter* species using
20 appropriate stringency hybridization conditions as described herein.

Capture Ligand

For use as a capture ligand, the nucleic acid selected in the manner described above with respect to probes, can be readily associated with a support. The manner in which nucleic acid is associated with supports is well known. Nucleic acid having twenty or more
25 nucleotides in a sequence of the invention contained in the Sequence Listing have utility to separate *H. pylori* nucleic acid from the nucleic acid of each other and other organisms. Nucleic acid having twenty or more nucleotides in a sequence of the invention contained in the Sequence Listing can also have utility to separate other *Helicobacter* species from each other and from other organisms. Preferably, the sequence will comprise at least twenty
30 nucleotides to convey stability to the hybridization product formed between the probe and the intended target molecules. Sequences larger than 1000 nucleotides in length are difficult to synthesize but can be generated by recombinant DNA techniques.

Primers

Nucleic acid isolated or synthesized in accordance with the sequences described
35 herein have utility as primers for the amplification of *H. pylori* nucleic acid. These nucleic acids may also have utility as primers for the amplification of nucleic acids in other *Helicobacter* species. With respect to polymerase chain reaction (PCR) techniques, nucleic acid sequences of \geq 10-15 nucleotides of the invention contained in the Sequence Listing have utility in conjunction with suitable enzymes and reagents to create copies of *H. pylori*.

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nucleic acid. More preferably, the sequence will comprise twenty or more nucleotides to convey stability to the hybridization product formed between the primer and the intended target molecules. Binding conditions of primers greater than 100 nucleotides are more difficult to control to obtain specificity. High fidelity PCR can be used to ensure a faithful
5 DNA copy prior to expression. In addition, amplified products can be checked by conventional sequencing methods.

The copies can be used in diagnostic assays to detect specific sequences, including genes from *H. pylori* and/or other *Helicobacter* species. The copies can also be incorporated into cloning and expression vectors to generate polypeptides corresponding to
10 the nucleic acid synthesized by PCR, as is described in greater detail herein.

Antisense

Nucleic acid or nucleic acid-hybridizing derivatives isolated or synthesized in accordance with the sequences described herein have utility as antisense agents to prevent the expression of *H. pylori* genes. These sequences also have utility as antisense agents to
15 prevent expression of genes of other *Helicobacter* species.

In one embodiment, nucleic acid or derivatives corresponding to *H. pylori* nucleic acids is loaded into a suitable carrier such as a liposome or bacteriophage for introduction into bacterial cells. For example, a nucleic acid having twenty or more nucleotides is capable of binding to bacteria nucleic acid or bacteria messenger RNA. Preferably, the
20 antisense nucleic acid is comprised of 20 or more nucleotides to provide necessary stability of a hybridization product of non-naturally occurring nucleic acid and bacterial nucleic acid and/or bacterial messenger RNA. Nucleic acid having a sequence greater than 1000 nucleotides in length is difficult to synthesize but can be generated by recombinant DNA techniques. Methods for loading antisense nucleic acid in liposomes is known in the art as
25 exemplified by U.S. Patent 4,241,046 issued December 23, 1980 to Papahadjopoulos et al.

II. Expression of *H. pylori* Nucleic Acids

Nucleic acid isolated or synthesized in accordance with the sequences described herein have utility to generate polypeptides. The nucleic acid of the invention exemplified
30 in the Sequence Listing or fragments of said nucleic acid encoding active portions of *H. pylori* polypeptides can be cloned into suitable vectors or used to isolate nucleic acid. The isolated nucleic acid is combined with suitable DNA linkers and cloned into a suitable vector.

The function of a specific gene or operon can be ascertained by expression in a
35 bacterial strain under conditions where the activity of the gene product(s) specified by the gene or operon in question can be specifically measured. Alternatively, a gene product may be produced in large quantities in an expressing strain for use as an antigen, an industrial reagent, for structural studies, etc. This expression can be accomplished in a mutant strain which lacks the activity of the gene to be tested, or in a strain that does not produce the

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- same gene product(s). This includes, but is not limited to other *Helicobacter* strains, or other bacterial strains such as *E. coli*, *Nocardia*, *Corynebacterium*, *Campylobacter*, and *Streptomyces* species. In some cases the expression host will utilize the natural *Helicobacter* promoter whereas in others, it will be necessary to drive the gene with a 5 promoter sequence derived from the expressing organism (e.g., an *E. coli* beta-galactosidase promoter for expression in *E. coli*).

To express a gene product using the natural *H. pylori* promoter, a procedure such as the following can be used. A restriction fragment containing the gene of interest, together with its associated natural promoter element and regulatory sequences (identified using the 10 DNA sequence data) is cloned into an appropriate recombinant plasmid containing an origin of replication that functions in the host organism and an appropriate selectable marker. This can be accomplished by a number of procedures known to those skilled in the art. It is most preferably done by cutting the plasmid and the fragment to be cloned with the same restriction enzyme to produce compatible ends that can be ligated to join the two 15 pieces together. The recombinant plasmid is introduced into the host organism by, for example, electroporation and cells containing the recombinant plasmid are identified by selection for the marker on the plasmid. Expression of the desired gene product is detected using an assay specific for that gene product.

In the case of a gene that requires a different promoter, the body of the gene (coding 20 sequence) is specifically excised and cloned into an appropriate expression plasmid. This subcloning can be done by several methods, but is most easily accomplished by PCR amplification of a specific fragment and ligation into an expression plasmid after treating the PCR product with a restriction enzyme or exonuclease to create suitable ends for cloning.

25 A suitable host cell for expression of a gene can be any prokaryotic or eucaryotic cell. For example, an *H. pylori* polypeptide can be expressed in bacterial cells such as *E. coli*, insect cells (baculovirus), yeast, or mammalian cells such as Chinese hamster ovary cell (CHO). Other suitable host cells are known to those skilled in the art.

30 Expression in eucaryotic cells such as mammalian, yeast, or insect cells can lead to partial or complete glycosylation and/or formation of relevant inter- or intra-chain disulfide bonds of a recombinant peptide product. Examples of vectors for expression in yeast *S. cerevisiae* include pYEpSec1 (Baldari, et al., (1987) *Embo J.* 6:229-234), pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz et al., (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Baculovirus vectors available 35 for expression of proteins in cultured insect cells (SF 9 cells) include the pAc series (Smith et al., (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow, V.A., and Summers, M.D., (1989) *Virology* 170:31-39). Generally, COS cells (Gluzman, Y., (1981) *Cell* 23:175-182) are used in conjunction with such vectors as pCDM 8 (Aruffo, A. and Seed, B., (1987) *Proc. Natl. Acad. Sci. USA* 84:8573-8577) for transient

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amplification/expression in mammalian cells, while CHO (dhfr⁻ Chinese Hamster Ovary) cells are used with vectors such as pMT2PC (Kaufman et al. (1987), *EMBO J.* 6:187-195) for stable amplification/expression in mammalian cells. Vector DNA can be introduced into mammalian cells via conventional techniques such as calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, or electroporation. Suitable methods for transforming host cells can be found in Sambrook et al. (Molecular Cloning: A Laboratory Manual, 2nd Edition, Cold Spring Harbor Laboratory press (1989)), and other laboratory textbooks.

Expression in prokaryotes is most often carried out in *E. coli* with either fusion or non-fusion inducible expression vectors. Fusion vectors usually add a number of NH₂ terminal amino acids to the expressed target gene. These NH₂ terminal amino acids often are referred to as a reporter group. Such reporter groups usually serve two purposes: 1) to increase the solubility of the target recombinant protein; and 2) to aid in the purification of the target recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the reporter group and the target recombinant protein to enable separation of the target recombinant protein from the reporter group subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Amrad Corp., Melbourne, Australia), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase, maltose E binding protein, or protein A, respectively, to the target recombinant protein. A preferred reporter group is poly(His), which may be fused to the amino or carboxy terminus of the protein and which renders the recombinant fusion protein easily purifiable by metal chelate chromatography.

Inducible non-fusion expression vectors include pTrc (Amann et al., (1988) *Gene* 69:301-315) and pET11d (Studier et al., Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, California (1990) 60-89). While target gene expression relies on host RNA polymerase transcription from the hybrid trp-lac fusion promoter in pTrc, expression of target genes inserted into pET11d relies on transcription from the T7 gn10-lac 0 fusion promoter mediated by coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 under the transcriptional control of the lacUV 5 promoter.

For example, a host cell transfected with a nucleic acid vector directing expression of a nucleotide sequence encoding an *H. pylori* polypeptide can be cultured under appropriate conditions to allow expression of the polypeptide to occur. The polypeptide may be secreted and isolated from a mixture of cells and medium containing the peptide. Alternatively, the polypeptide may be retained cytoplasmically and the cells harvested, lysed and the protein isolated. A cell culture includes host cells, media and other

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byproducts. Suitable media for cell culture are well known in the art. Polypeptides of the invention can be isolated from cell culture medium, host cells, or both using techniques known in the art for purifying proteins including ion-exchange chromatography, gel filtration chromatography, ultrafiltration, electrophoresis, and immunoaffinity purification
5 with antibodies specific for such polypeptides. Additionally, in many situations, polypeptides can be produced by chemical cleavage of a native protein (e.g., tryptic digestion) and the cleavage products can then be purified by standard techniques.

In the case of membrane bound proteins, these can be isolated from a host cell by contacting a membrane-associated protein fraction with a detergent forming a solubilized
10 complex, where the membrane-associated protein is no longer entirely embedded in the membrane fraction and is solubilized at least to an extent which allows it to be chromatographically isolated from the membrane fraction. Several different criteria are used for choosing a detergent suitable for solubilizing these complexes. For example, one property considered is the ability of the detergent to solubilize the *H. pylori* protein within
15 the membrane fraction at minimal denaturation of the membrane-associated protein allowing for the activity or functionality of the membrane-associated protein to return upon reconstitution of the protein. Another property considered when selecting the detergent is the critical micelle concentration (CMC) of the detergent in that the detergent of choice preferably has a high CMC value allowing for ease of removal after reconstitution. A third
20 property considered when selecting a detergent is the hydrophobicity of the detergent. Typically, membrane-associated proteins are very hydrophobic and therefore detergents which are also hydrophobic, e.g., the triton series, would be useful for solubilizing the hydrophobic proteins. Another property important to a detergent can be the capability of the detergent to remove the *H. pylori* protein with minimal protein-protein interaction
25 facilitating further purification. A fifth property of the detergent which should be considered is the charge of the detergent. For example, if it is desired to use ion exchange resins in the purification process then preferably detergent should be an uncharged detergent. Chromatographic techniques which can be used in the final purification step are known in the art and include hydrophobic interaction, lectin affinity, ion exchange, dye
30 affinity and immunoaffinity.

One strategy to maximize recombinant *H. pylori* peptide expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, California (1990) 119-128). Another
35 strategy would be to alter the nucleic acid encoding an *H. pylori* peptide to be inserted into an expression vector so that the individual codons for each amino acid would be those preferentially utilized in highly expressed *E. coli* proteins (Wada et al., (1992) *Nuc. Acids Res.* 20:2111-2118). Such alteration of nucleic acids of the invention can be carried out by standard DNA synthesis techniques.

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The nucleic acids of the invention can also be chemically synthesized using standard techniques. Various methods of chemically synthesizing polydeoxynucleotides are known, including solid-phase synthesis which, like peptide synthesis, has been fully automated in commercially available DNA synthesizers (See, e.g., Itakura et al. U.S. Patent No. 4,598,049; Caruthers et al. U.S. Patent No. 4,458,066; and Itakura U.S. Patent Nos. 4,401,796 and 4,373,071, incorporated by reference herein).

III. *H. pylori* Polypeptides

- This invention encompasses isolated *H. pylori* polypeptides encoded by the disclosed *H. pylori* genomic sequences, including the polypeptides of the invention contained in the Sequence Listing. Polypeptides of the invention are preferably at least 5 amino acid residues in length. Using the DNA sequence information provided herein, the amino acid sequences of the polypeptides encompassed by the invention can be deduced using methods well-known in the art. It will be understood that the sequence of an entire nucleic acid encoding an *H. pylori* polypeptide can be isolated and identified based on an ORF that encodes only a fragment of the cognate protein-coding region. This can be achieved, for example, by using the isolated nucleic acid encoding the ORF, or fragments thereof, to prime a polymerase chain reaction with genomic *H. pylori* DNA as template; this is followed by sequencing the amplified product.
- The polypeptides of the invention can be isolated from wild-type or mutant *H. pylori* cells or from heterologous organisms or cells (including, but not limited to, bacteria, yeast, insect, plant and mammalian cells) into which an *H. pylori* nucleic acid has been introduced and expressed. In addition, the polypeptides can be part of recombinant fusion proteins.
- H. pylori* polypeptides of the invention can be chemically synthesized using commercially automated procedures such as those referenced herein.

Many of the polypeptides of the invention are related to one another. Some of these relationships are described in Table 3 below. Most polypeptides described in Table 3 are over 90% identical to one another as noted in the last two columns; some are between 70% and 90% identical to one another; and very few share between 60% and 70% identity with each other. The polypeptides represented by the sequence identification numbers in the third column of Table 3 result from translations carried out from stop codon to stop codon in the genomic nucleotide sequence of the invention, while those in the first column result from translations carried out from the first methionine or valine codon following the prior stop codon and proceeding to the final stop codon in the nucleotide sequence. In some cases, the nucleotide sequence encoding the related polypeptides is slightly different, resulting in some differences in amino acid residues of the related polypeptides. In many cases, the related polypeptides differ significantly in length, with one polypeptide containing amino acid residues in addition to those in common between the two

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polypeptides. In all cases, the relationships described in Table 3 are highly significant, and the nucleotide sequences encoding these related polypeptides are also very similar to one another. For example, the nucleotide probes derived from the coding sequence of the polypeptides in column one can be used in PCR or hybridization experiments to identify 5 clones carrying the nucleotide sequence encoding the polypeptides of column three.

The relationships between the polypeptides shown in Table 3 can be classified in five broad categories as follows. First, for many polypeptides (designated "A" in the last column of the Table 3), the polypeptide denoted in column one is identical to the polypeptide denoted in column three except for an occasional addition of a few putative 10 amino acid residues at the N-terminus which result from the fact that the polypeptides of column three were derived by translating from stop codon to stop codon instead of from a predicted start codon (i.e., Met or Val) to a stop codon as was done for the polypeptides in column one.

Second, for most polypeptides (designated "B" in the last column of the Table 3), 15 the polypeptide of column one is at least 95% identical to the polypeptide of column three except that the polypeptide in column three is longer (at either or both ends) by one or more amino acid residues which do not result from the difference between reading from stop to stop instead of from start to stop.

Third, for some polypeptides (designated "C" in the last column of Table 3), the 20 converse is true, the polypeptide of column one is at least 95% identical to the polypeptide of column three except that the polypeptide in column three is shorter (at either or both ends).

Fourth, for some polypeptides (designated "D" in the last column of Table 3), the 25 polypeptide of column one shares a high level of amino acid identity (i.e., at least 95%) with the polypeptide of column three in the region in which they overlap, but shares little or no identity (i.e., less than 95%) at one or both ends. The level of identity of the polypeptides in columns one and three in categories "B", "C" and "D" is highly significant. For example, a typical *H. pylori* gene product will exhibit amino acid sequence identities of between 92% to 100% among strains of *H. pylori* isolated from human patients (see Table 30 10 below).

Finally, a fifth class of polypeptides in column one (designated "E" in the last column of Table 3) are closely related but differ significantly (i.e., less than 95% identical) from the polypeptide of column three. These polypeptides are likely "paralogs," members of related gene families in *H. pylori*.

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TABLE 3

SeqID #	Length (aa)	SeqID #	Length (aa)	% Identity: Overlap Length	Category
384	509	1779	593	100.0 : 504 aa	B
386	133	1713	205	99.2 : 127 aa	B
387	158	1743	340	98.7 : 155 aa	B
388	112	1489	330	100.0 : 105 aa	B
389	650	1643	369	95.4 : 65 aa	D
390	62	1598	327	90.2 : 61 aa	E
391	619	1747	991	99.3 : 608 aa	B
392	110	1570	183	93.1 : 101 aa	E
393	68	1811	85	97.1 : 68 aa	B
394	446	1884	594	99.5 : 433 aa	B
395	84	1503	347	100.0 : 84 aa	B
396	40	1504	519	88.2 : 34 aa	E
397	300	1531	273	98.9 : 267 aa	C
398	214	1795	197	99.0 : 192 aa	C
399	137	1639	199	96.4 : 137 aa	B
400	272	1725	285	99.3 : 271 aa	B
401	287	1470	455	98.9 : 277 aa	D
402	106	1596	302	99.1 : 106 aa	B
403	157	1654	197	99.3 : 150 aa	B
404	278	1552	362	100.0 : 277 aa	B
405	120	1858	529	100.0 : 116 aa	B
406	226	1562	297	100.0 : 216 aa	B
407	62	1752	157	77.6 : 58 aa	E
408	50	1663	74	97.9 : 47 aa	B
410	188	1803	351	87.1 : 155 aa	E
411	130	1685	497	100.0 : 129 aa	B
412	183	1843	185	100.0 : 183 aa	A
413	194	1874	508	97.6 : 169 aa	D
414	235	1518	246	100.0 : 235 aa	B
415	88	1538	676	97.5 : 80 aa	B
416	109	1871	335	99.1 : 109 aa	B
417	107	1782	593	94.4 : 90 aa	E
418	136	1544	441	100.0 : 135 aa	B
419	54	1513	175	97.0 : 33 aa	E
420	125	1642	539	96.7 : 122 aa	B
421	249	1738	346	99.6 : 249 aa	B
422	86	1715	128	97.5 : 79 aa	B
423	128	1534	149	100.0 : 128 aa	B
424	93	1875	178	100.0 : 93 aa	B
425	88	1804	105	97.7 : 88 aa	B
426	128	1524	116	62.4 : 117 aa	E
427	108	1762	109	100.0 : 108 aa	A
428	118	1539	276	100.0 : 118 aa	B
429	54	1754	113	89.6 : 48 aa	E
430	288	1483	377	95.5 : 286 aa	B
431	303	1785	248	98.2 : 170 aa	D
431	303	1784	148	96.4 : 138 aa	D
432	192	1478	408	99.5 : 192 aa	B
433	168	1517	426	99.3 : 151 aa	D

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434	153	1679	403	100.0 : 153 aa	B
435	162	1806	173	98.1 : 161 aa	B
436	59	1834	80	37.5 : 24 aa	E
437	222	1533	288	100.0 : 221 aa	B
438	53	1737	260	93.5 : 31 aa	E
439	109	1683	121	100.0 : 109 aa	B
440	73	1773	280	100.0 : 73 aa	B
441	237	1685	497	96.0 : 198 aa	D
442	92	1521	646	100.0 : 84 aa	D
443	97	1774	327	100.0 : 96 aa	B
444	280	1556	284	100.0 : 280 aa	A
445	187	1604	253	95.5 : 155 aa	D
446	58	1510	198	96.4 : 55 aa	B
447	85	1496	155	100.0 : 85 aa	B
448	90	1724	90	100.0 : 90 aa	A
449	105	1788	141	98.0 : 100 aa	D
450	172	1495	239	100.0 : 172 aa	B
451	212	1456	139	81.7 : 126 aa	E
452	182	1702	192	97.0 : 166 aa	D
453	224	1658	228	100.0 : 224 aa	A
454	131	1895	159	100.0 : 131 aa	B
455	73	1787	370	100.0 : 54 aa	D
456	92	1587	295	96.6 : 87 aa	B
457	205	1735	310	100.0 : 195 aa	B
458	41	1479	144	97.6 : 41 aa	B
459	219	1584	297	100.0 : 219 aa	B
460	188	1546	375	89.3 : 187 aa	E
461	231	1780	438	97.3 : 225 aa	B
462	63	1645	71	100.0 : 63 aa	B
463	183	1664	242	97.8 : 182 aa	B
464	117	1586	234	99.1 : 113 aa	B
465	153	1773	280	98.0 : 153 aa	B
466	43	1610	308	100.0 : 43 aa	B
467	240	1636	255	97.0 : 237 aa	B
468	209	1868	240	96.6 : 206 aa	B
469	95	1628	321	98.5 : 65 aa	D
470	229	1595	375	96.5 : 228 aa	B
471	92	1713	205	90.1 : 71 aa	E
472	96	1492	352	95.4 : 87 aa	B
473	1178	1748	1183	100.0 : 1178 aa	A
474	163	1822	113	92.7 : 109 aa	E
474	163	1820	88	93.1 : 58 aa	E
475	466	1840	467	100.0 : 466 aa	A
476	60	1500	90	97.0 : 33 aa	D
477	249	1854	254	100.0 : 248 aa	B
478	44	1772	528	100.0 : 44 aa	B
479	421	1693	421	99.8 : 421 aa	A
480	167	1555	340	98.1 : 162 aa	B
481	89	1888	236	100.0 : 89 aa	B
482	237	1873	461	97.5 : 236 aa	B
483	471	1594	428	99.3 : 301 aa	C
484	123	1655	366	87.9 : 107 aa	E
485	127	1655	366	99.2 : 127 aa	B
486	259	1517	259	100.0 : 259 aa	A
487	17	1481	101	93.3 : 15 aa	E
488	77	1704	246	100.0 : 77 aa	B

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489	180	1554	180	100.0 : 180 aa	A
490	213	1638	577	92.3 : 209 aa	E
491	148	1452	157	100.0 : 148 aa	B
492	281	1519	849	99.6 : 281 aa	B
493	144	1525	377	94.9 : 118 aa	D
494	73	1539	276	95.8 : 71 aa	B
495	311	1670	446	99.0 : 311 aa	B
496	115	1842	384	99.1 : 114 aa	B
497	200	1600	459	100.0 : 200 aa	B
498	264	1828	458	100.0 : 264 aa	B
499	339	1490	362	99.7 : 339 aa	B
500	146	1449	430	94.4 : 142 aa	E
501	60	1465	240	98.3 : 58 aa	B
502	351	1458	532	98.6 : 346 aa	B
503	233	1666	296	94.3 : 230 aa	E
504	32	1513	175	100.0 : 32 aa	B
505	171	1462	452	91.8 : 171 aa	B
506	33	1672	121	100.0 : 24 aa	D
507	100	1650	192	80.0 : 90 aa	E
508	79	1772	528	80.8 : 78 aa	E
509	70	1662	88	96.2 : 53 aa	D
510	130	1530	131	100.0 : 130 aa	A
511	53	1723	163	91.8 : 49 aa	E
512	79	1572	189	98.5 : 65 aa	D
513	102	1889	114	99.0 : 100 aa	B
514	15	1516	407	100.0 : 12 aa	B
515	378	1747	991	97.9 : 377 aa	B
516	1027	1692	2440	100.0 : 1027 aa	B
517	155	1831	182	89.6 : 154 aa	E
518	62	1552	362	74.5 : 47 aa	E
519	237	1557	241	100.0 : 237 aa	A
520	83	1627	424	100.0 : 83 aa	B
522	64	1680	227	98.4 : 63 aa	B
523	228	1532	241	100.0 : 228 aa	B
524	273	1710	189	97.2 : 180 aa	C
524	273	1712	115	100.0 : 99 aa	C
525	15	1612	65	100.0 : 15 aa	B
526	115	1733	112	94.6 : 111 aa	C
527	67	1755	156	100.0 : 62 aa	D
528	323	1635	336	100.0 : 322 aa	B
529	10	1731	101	50.0 : 10 aa	B
530	12	1455	284	100.0 : 12 aa	B
531	79	1528	101	94.9 : 79 aa	B
532	95	1887	279	100.0 : 95 aa	B
533	154	1591	168	100.0 : 152 aa	B
534	68	1501	283	100.0 : 67 aa	B
535	313	1519	849	95.5 : 313 aa	B
536	319	1486	325	100.0 : 319 aa	A
537	118	1707	154	90.9 : 110 aa	E
538	89	1674	161	88.2 : 76 aa	E
539	92	1838	100	100.0 : 92 aa	A
540	138	1525	377	86.9 : 137 aa	B
541	277	1661	394	96.0 : 273 aa	D
542	254	1567	392	98.0 : 254 aa	B
543	185	1467	594	99.5 : 185 aa	B
544	37	1886	326	100.0 : 37 aa	B

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545	94	1772	528	89.1 : 92 aa	E
546	182	1760	366	100.0 : 182 aa	B
547	247	1776	150	100.0 : 146 aa	C
547	247	1775	88	100.0 : 87 aa	C
548	422	1798	426	100.0 : 422 aa	A
549	61	1620	78	96.7 : 60 aa	B
550	54	1566	309	37.8 : 45 aa	E
551	298	1751	518	98.0 : 297 aa	B
552	91	1738	346	95.5 : 88 aa	D
553	111	1764	130	100.0 : 111 aa	B
554	137	1626	93	100.0 : 84 aa	D
555	124	1717	114	89.2 : 111 aa	E
556	86	1597	432	89.7 : 78 aa	E
557	87	1457	97	100.0 : 86 aa	B
558	108	1750	154	99.1 : 108 aa	B
559	142	1619	211	97.9 : 141 aa	B
560	231	1580	315	99.6 : 231 aa	B
561	186	1446	275	88.3 : 180 aa	E
562	183	1515	198	100.0 : 183 aa	B
563	154	1477	188	100.0 : 154 aa	B
564	288	1767	303	100.0 : 288 aa	B
565	420	1841	424	100.0 : 420 aa	A
566	72	1450	486	98.5 : 67 aa	D
567	205	1799	270	99.5 : 199 aa	D
568	328	1893	338	100.0 : 328 aa	B
569	140	1855	614	84.8 : 125 aa	E
570	76	1499	184	98.1 : 53 aa	D
571	194	1660	201	100.0 : 193 aa	B
572	140	1583	163	96.9 : 130 aa	D
573	308	1676	316	100.0 : 308 aa	B
574	339	1667	468	99.1 : 335 aa	B
575	207	1688	208	98.1 : 207 aa	A
576	251	1891	267	100.0 : 251 aa	B
577	69	1745	109	96.7 : 61 aa	D
578	112	1519	849	99.1 : 112 aa	B
579	152	1649	543	98.7 : 152 aa	B
580	130	1853	220	98.3 : 120 aa	D
581	113	1614	134	100.0 : 113 aa	B
582	174	1569	209	100.0 : 174 aa	B
583	35	1752	157	34.4 : 32 aa	E
584	308	1728	316	100.0 : 307 aa	B
585	702	1857	797	99.9 : 702 aa	B
586	293	1633	664	96.2 : 293 aa	B
587	52	1542	429	100.0 : 52 aa	B
588	182	1504	519	100.0 : 182 aa	B
589	251	1622	262	99.6 : 251 aa	B
590	40	1632	61	97.5 : 40 aa	B
591	122	1691	717	99.1 : 113 aa	D
592	113	1768	121	100.0 : 113 aa	B
593	437	1520	448	100.0 : 437 aa	A
594	146	1549	200	93.2 : 146 aa	E
595	128	1494	131	99.2 : 127 aa	B
596	95	1667	468	100.0 : 93 aa	B
597	102	1447	149	100.0 : 91 aa	D
598	127	1879	138	100.0 : 127 aa	B
599	502	1881	928	99.2 : 500 aa	B

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600	42	1625	91	100.0 : 42 aa	B
601	341	1454	381	99.7 : 341 aa	B
602	465	1694	442	98.2 : 433 aa	D
602	465	1896	259	99.6 : 238 aa	D
603	193	1484	229	99.4 : 170 aa	D
604	141	1673	130	97.6 : 126 aa	D
605	159	1582	358	83.3 : 156 aa	E
606	376	1565	382	100.0 : 376 aa	B
607	352	1862	363	99.1 : 352 aa	B
608	88	1807	144	98.7 : 77 aa	D
609	86	1553	181	72.0 : 82 aa	E
610	76	1527	77	100.0 : 76 aa	A
611	98	1732	118	98.9 : 95 aa	B
612	162	1525	377	91.3 : 161 aa	E
613	58	1547	152	98.3 : 58 aa	B
614	66	1470	455	85.2 : 61 aa	E
615	117	1844	982	95.5 : 111 aa	D
616	83	1723	163	96.3 : 82 aa	B
617	77	1763	275	89.6 : 77 aa	E
618	176	1696	149	93.6 : 125 aa	E
618	176	1698	231	92.3 : 65 aa	E
619	144	1498	577	96.0 : 124 aa	D
620	90	1516	407	98.9 : 90 aa	B
621	268	1571	275	100.0 : 268 aa	B
622	171	1753	206	99.4 : 171 aa	B
623	102	1559	256	100.0 : 84 aa	D
624	117	1819	640	94.2 : 104 aa	E
625	237	1758	842	99.6 : 233 aa	B
626	199	1464	200	100.0 : 198 aa	C
627	225	1611	347	97.7 : 221 aa	B
627	225	1608	97	97.8 : 91 aa	C
628	86	1772	528	90.4 : 83 aa	E
629	496	1558	539	100.0 : 496 aa	B
630	142	1778	332	99.1 : 116 aa	D
631	153	1709	111	76.9 : 108 aa	E
631	153	1708	76	60.9 : 46 aa	E
633	93	1848	106	100.0 : 93 aa	B
634	177	1603	531	98.9 : 175 aa	B
635	88	1812	93	100.0 : 88 aa	A
636	115	1746	122	100.0 : 115 aa	B
637	261	1850	304	98.5 : 260 aa	B
638	191	1691	717	99.5 : 185 aa	B
639	351	1697	373	99.7 : 351 aa	B
640	351	1601	355	100.0 : 342 aa	D
641	146	1592	320	96.6 : 145 aa	B
642	190	1796	376	100.0 : 190 aa	B
643	489	1705	957	99.4 : 468 aa	D
644	249	1706	249	100.0 : 248 aa	A
645	120	1540	269	100.0 : 104 aa	D
646	109	1550	350	100.0 : 108 aa	B
648	158	1573	237	95.5 : 155 aa	D
649	312	1721	312	100.0 : 312 aa	A
650	56	1839	242	98.1 : 52 aa	D
651	199	1813	261	99.5 : 196 aa	B
652	82	1756	99	96.3 : 81 aa	D
653	89	1475	227	100.0 : 89 aa	B

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654	111	1535	119	98.2 : 111 aa	B
655	65	1686	276	98.3 : 59 aa	D
656	268	1892	272	100.0 : 268 aa	A
657	100	1597	432	100.0 : 84 aa	D
658	80	1640	276	97.2 : 72 aa	D
659	205	1824	217	100.0 : 205 aa	B
660	124	1471	67	98.4 : 64 aa	D
660	124	1472	186	96.7 : 60 aa	D
661	93	1618	95	98.9 : 93 aa	B
662	80	1568	170	98.7 : 79 aa	B
663	214	1749	224	100.0 : 214 aa	B
664	78	1668	214	97.3 : 75 aa	D
665	177	1844	982	78.6 : 173 aa	E
666	258	1578	275	94.1 : 254 aa	E
667	75	1742	360	100.0 : 75 aa	B
668	421	1699	421	99.5 : 421 aa	A
669	81	1542	429	100.0 : 81 aa	B
670	112	1540	269	76.1 : 113 aa	E
671	326	1689	246	92.8 : 208 aa	E
672	272	1727	279	100.0 : 271 aa	A
673	78	1661	394	100.0 : 78 aa	B
674	400	1736	419	100.0 : 400 aa	B
675	91	1522	273	95.5 : 88 aa	D
676	126	1561	131	100.0 : 126 aa	A
677	195	1577	301	76.5 : 196 aa	E
678	72	1814	90	98.6 : 72 aa	B
679	111	1572	189	100.0 : 111 aa	B
680	142	1847	207	92.6 : 135 aa	E
681	63	1516	407	96.4 : 56 aa	D
682	310	1700	446	99.3 : 301 aa	B
683	169	1744	219	100.0 : 169 aa	B
684	85	1611	347	88.1 : 84 aa	E
685	77	1829	251	97.3 : 75 aa	D
686	197	1634	425	99.0 : 194 aa	D
687	142	1722	197	100.0 : 136 aa	D
688	86	1805	87	100.0 : 86 aa	A
689	121	1759	356	97.5 : 118 aa	B
690	59	1789	77	84.6 : 52 aa	E
691	142	1675	420	97.1 : 140 aa	B
692	80	1722	197	83.3 : 60 aa	E
693	180	1659	187	100.0 : 179 aa	B
694	75	1529	159	100.0 : 75 aa	B
695	99	1849	119	100.0 : 99 aa	B
696	209	1701	430	99.5 : 205 aa	B
697	75	1616	196	100.0 : 75 aa	B
698	121	1678	460	100.0 : 121 aa	B
699	102	1579	139	99.0 : 100 aa	B
700	131	1595	375	99.2 : 131 aa	B
701	441	1488	444	96.9 : 426 aa	D
702	127	1774	327	99.1 : 116 aa	D
703	287	1765	327	93.9 : 279 aa	E
704	46	1581	111	95.2 : 21 aa	D
705	115	1647	117	100.0 : 115 aa	A
706	86	1463	111	100.0 : 86 aa	B
707	44	1588	68	100.0 : 44 aa	B
708	560	1589	1413	98.8 : 560 aa	B

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709	125	1607	443	95.8 : 118 aa	D
710	96	1469	540	100.0 : 73 aa	D
711	81	1629	244	96.3 : 80 aa	D
712	141	1671	375	100.0 : 125 aa	D
713	51	1867	193	96.1 : 51 aa	B
714	233	1833	240	99.5 : 218 aa	D
715	266	1644	271	100.0 : 265 aa	B
716	158	1883	226	94.7 : 150 aa	E
717	191	1860	240	100.0 : 189 aa	B
718	243	1817	256	99.6 : 243 aa	B
719	236	1617	667	98.3 : 236 aa	B
720	175	1523	592	97.1 : 172 aa	B
721	226	1770	340	92.7 : 218 aa	E
722	79	1629	244	100.0 : 74 aa	D
723	65	1506	229	100.0 : 49 aa	D
724	138	1675	426	93.2 : 132 aa	E
725	210	1832	215	100.0 : 210 aa	A
726	296	1821	223	100.0 : 190 aa	D
726	296	1819	640	99.1 : 106 aa	D
727	94	1706	249	97.8 : 91 aa	D
728	83	1593	171	100.0 : 83 aa	B
729	203	1448	268	100.0 : 202 aa	B
730	220	1656	242	100.0 : 220 aa	B
731	116	1818	196	100.0 : 115 aa	B
732	248	1474	248	100.0 : 248 aa	A
733	150	1459	347	100.0 : 118 aa	D
734	228	1545	302	96.9 : 227 aa	B
735	187	1597	432	100.0 : 172 aa	D
736	198	1761	354	100.0 : 198 aa	B
737	208	1780	438	93.8 : 208 aa	E
738	201	1842	384	100.0 : 193 aa	D
739	127	1669	405	21.6 : 74 aa	E
740	79	1615	280	97.3 : 75 aa	D
741	49	1878	443	91.3 : 46 aa	E
742	412	1877	425	97.8 : 412 aa	B
743	89	1482	111	100.0 : 89 aa	B
744	192	1502	222	98.4 : 189 aa	B
745	109	1797	304	96.3 : 109 aa	B
746	116	1791	359	94.8 : 116 aa	B
747	163	1711	321	100.0 : 163 aa	B
748	40	1483	377	100.0 : 40 aa	B
749	45	1770	340	95.2 : 42 aa	D
750	118	1867	193	92.2 : 116 aa	E
751	200	1491	211	100.0 : 200 aa	B
752	79	1890	80	100.0 : 79 aa	A
753	98	1837	268	98.7 : 79 aa	D
754	146	1653	413	100.0 : 141 aa	B
755	206	1638	577	93.7 : 206 aa	B
756	97	1526	89	100.0 : 66 aa	D
757	197	1794	198	100.0 : 197 aa	A
758	149	1872	94	97.5 : 80 aa	D
759	68	1882	291	100.0 : 68 aa	B
760	135	1631	162	99.3 : 134 aa	B
761	93	1884	594	100.0 : 69 aa	D
762	73	1883	226	100.0 : 73 aa	B
763	268	1859	430	95.4 : 263 aa	B

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764	274	1537	277	100.0 : 273 aa	B
765	134	1714	136	99.2 : 133 aa	A
766	72	1810	74	95.8 : 71 aa	A
767	147	1802	285	100.0 : 147 aa	B
768	144	1541	241	100.0 : 144 aa	B
769	47	1684	75	100.0 : 47 aa	B
770	129	1505	183	90.2 : 122 aa	E
771	242	1536	235	99.1 : 232 aa	C
772	97	1851	129	99.0 : 97 aa	B
773	143	1826	259	96.5 : 143 aa	B
774	218	1777	383	99.5 : 217 aa	B
775	84	1637	143	100.0 : 84 aa	B
776	76	1774	327	95.9 : 73 aa	D
777	155	1585	263	79.7 : 133 aa	E
778	192	1480	299	91.5 : 189 aa	E
779	171	1551	186	99.4 : 171 aa	B
780	141	1760	366	99.2 : 129 aa	D
781	70	1741	95	100.0 : 70 aa	B
782	153	1687	223	98.0 : 153 aa	B
783	183	1869	184	100.0 : 183 aa	A
784	67	1846	231	100.0 : 67 aa	B
785	254	1730	256	100.0 : 253 aa	B
786	173	1466	251	100.0 : 166 aa	D
787	259	1808	322	100.0 : 238 aa	D
788	294	1786	131	93.7 : 126 aa	E
788	294	1630	163	94.0 : 116 aa	E
789	194	1655	366	99.2 : 122 aa	D
789	194	1646	75	100.0 : 72 aa	C
790	132	1790	273	100.0 : 132 aa	B
791	213	1575	216	98.1 : 213 aa	A
792	47	1605	86	100.0 : 47 aa	B
793	143	1864	342	93.0 : 143 aa	E
794	69	1766	93	100.0 : 69 aa	B
795	144	1504	519	95.7 : 138 aa	D
796	190	1590	193	100.0 : 190 aa	A
797	84	1792	215	83.5 : 79 aa	E
798	135	1613	138	100.0 : 135 aa	A
799	255	1885	424	99.6 : 253 aa	B
800	243	1493	205	87.1 : 140 aa	E
800	243	1497	131	100.0 : 126 aa	C
801	252	1563	255	100.0 : 252 aa	A
802	165	1720	91	100.0 : 88 aa	C
802	165	1718	99	92.7 : 82 aa	E
803	171	1602	297	85.5 : 159 aa	E
804	62	1485	165	100.0 : 61 aa	B
805	199	1514	219	100.0 : 199 aa	B
806	131	1880	391	86.2 : 130 aa	E
807	101	1719	257	95.0 : 100 aa	B
808	80	1585	263	98.8 : 80 aa	B
809	447	1781	344	99.7 : 331 aa	D
809	447	1783	118	98.3 : 117 aa	C
810	218	1564	250	100.0 : 218 aa	B
811	192	1478	408	99.5 : 192 aa	B
812	341	1729	354	100.0 : 340 aa	B
813	201	1523	592	100.0 : 158 aa	D
814	130	1769	306	92.3 : 130 aa	E

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815	144	1835	548	78.4 : 116 aa	E
815	144	1815	377	84.3 : 121 aa	E
816	309	1894	310	100.0 : 309 aa	A
817	164	1823	156	96.7 : 153 aa	D
818	54	1703	87	100.0 : 53 aa	B
819	202	1716	215	99.5 : 202 aa	B
820	169	1870	115	100.0 : 110 aa	D
821	186	1451	254	100.0 : 186 aa	B
822	72	1609	180	96.6 : 58 aa	D
823	122	1633	664	94.9 : 118 aa	D
824	13	1695	70	100.0 : 13 aa	B
824	13	1567	392	100.0 : 13 aa	B
825	99	1771	144	100.0 : 86 aa	D
826	71	1512	154	98.6 : 71 aa	B
827	150	1456	139	93.7 : 127 aa	E
828	255	1651	155	100.0 : 155 aa	C
828	255	1648	109	98.0 : 102 aa	D
829	106	1726	147	99.1 : 106 aa	B
830	527	1509	567	99.8 : 524 aa	B
831	124	1740	214	99.2 : 123 aa	B
832	110	1690	400	98.2 : 110 aa	B
833	326	1856	325	100.0 : 325 aa	C
834	253	1543	191	96.7 : 184 aa	D
835	597	1876	638	100.0 : 594 aa	B
836	156	1621	345	99.4 : 154 aa	B
837	157	1624	253	97.4 : 155 aa	B
838	191	1465	241	96.8 : 190 aa	B
839	90	1548	231	92.9 : 85 aa	E
840	277	1682	298	99.6 : 277 aa	B
841	58	1508	270	98.1 : 54 aa	D
842	139	1734	139	88.4 : 129 aa	E
843	279	1476	276	100.0 : 269 aa	C
844	36	1852	83	94.4 : 36 aa	B
845	129	1460	196	100.0 : 129 aa	B
846	127	1473	172	100.0 : 105 aa	D
847	276	1657	319	100.0 : 276 aa	B
848	126	1801	187	98.4 : 126 aa	B
849	242	1669	405	97.0 : 236 aa	D
850	151	1816	217	100.0 : 151 aa	B
851	154	1641	194	100.0 : 154 aa	B
852	496	1665	327	97.5 : 314 aa	C
853	179	1606	272	97.2 : 179 aa	B
855	160	1487	198	96.9 : 160 aa	B
856	94	1836	420	100.0 : 93 aa	B
857	146	1845	371	99.3 : 146 aa	B
858	205	1507	366	98.5 : 202 aa	B
859	173	1827	198	100.0 : 149 aa	D
860	193	1681	294	100.0 : 175 aa	D
861	104	1865	253	100.0 : 104 aa	B
862	355	1599	358	100.0 : 355 aa	B
863	93	1825	236	97.8 : 92 aa	B
864	82	1677	315	97.5 : 81 aa	B
865	234	1861	249	99.1 : 233 aa	B
866	239	1652	405	99.2 : 238 aa	B
867	86	1468	201	77.4 : 84 aa	E
868	289	1574	395	94.4 : 284 aa	E

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869	436	1863	662	100.0 : 436 aa	B
870	114	1560	121	100.0 : 114 aa	B
871	173	1757	362	98.8 : 173 aa	B
872	116	1866	145	98.1 : 105 aa	D
873	127	1797	304	63.9 : 83 aa	E
873	127	1799	270	89.7 : 58 aa	E
873	127	1800	62	97.4 : 38 aa	D
873	127	1801	187	82.0 : 50 aa	E
874	150	1461	179	100.0 : 150 aa	B
875	209	1511	339	98.9 : 188 aa	D
876	234	1739	615	99.6 : 230 aa	B
877	395	1830	879	99.7 : 379 aa	D
878	103	1623	413	97.0 : 99 aa	D
879	265	1809	566	89.8 : 265 aa	B
880	364	1576	442	98.6 : 346 aa	D

IV. Identification of Nucleic Acids Encoding Vaccine Components and Targets for Agents Effective Against *H. pylori*

The disclosed *H. pylori* genome sequence includes segments that direct the synthesis of ribonucleic acids and polypeptides, as well as origins of replication, promoters, other types of regulatory sequences, and intergenic nucleic acids. The invention encompasses nucleic acids encoding immunogenic components of vaccines and targets for agents effective against *H. pylori*. Identification of said immunogenic components involved in the determination of the function of the disclosed sequences, which can be achieved using a variety of approaches. Non-limiting examples of these approaches are described briefly below.

Homology to known sequences: Computer-assisted comparison of the disclosed *H. pylori* sequences with previously reported sequences present in publicly available databases is useful for identifying functional *H. pylori* nucleic acid and polypeptide sequences. It will be understood that protein-coding sequences, for example, may be compared as a whole, and that a high degree of sequence homology between two proteins (such as, for example, >80-90%) at the amino acid level indicates that the two proteins also possess some degree of functional homology, such as, for example, among enzymes involved in metabolism, DNA synthesis, or cell wall synthesis, and proteins involved in transport, cell division, etc. In addition, many structural features of particular protein classes have been identified and correlate with specific consensus sequences, such as, for example, binding domains for nucleotides, DNA, metal ions, and other small molecules; sites for covalent modifications such as phosphorylation, acylation, and the like; sites of protein:protein interactions, etc. These consensus sequences may be quite short and thus may represent only a fraction of the entire protein-coding sequence. Identification of such a feature in an *H. pylori* sequence is therefore useful in determining the function of the encoded protein and identifying useful targets of antibacterial drugs.

Of particular relevance to the present invention are structural features that are common to secretory, transmembrane, and surface proteins, including secretion signal

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peptides and hydrophobic transmembrane domains. *H. pylori* proteins identified as containing putative signal sequences and/or transmembrane domains are useful as immunogenic components of vaccines.

5 Identification of essential genes: Nucleic acids that encode proteins essential for growth or viability of *H. pylori* are preferred drug targets. *H. pylori* genes can be tested for their biological relevance to the organism by examining the effect of deleting and/or disrupting the genes, i.e., by so-called gene "knockout", using techniques known to those skilled in the relevant art. In this manner, essential genes may be identified.

10 Strain-specific sequences: Because of the evolutionary relationship between different *H. pylori* strains, it is believed that the presently disclosed *H. pylori* sequences are useful for identifying, and/or discriminating between, previously known and new *H. pylori* strains. It is believed that other *H. pylori* strains will exhibit at least 70% sequence homology with the presently disclosed sequence. Systematic and routine analyses of DNA sequences derived from samples containing *H. pylori* strains, and comparison with the present sequence allows for the identification of sequences that can be used to discriminate between strains, as well as those that are common to all *H. pylori* strains. In one embodiment, the invention provides nucleic acids, including probes, and peptide and polypeptide sequences that discriminate between different strains of *H. pylori*. Strain-specific components can also be identified functionally by their ability to elicit or react with 15 antibodies that selectively recognize one or more *H. pylori* strains.

20 In another embodiment, the invention provides nucleic acids, including probes, and peptide and polypeptide sequences that are common to all *H. pylori* strains but are *not* found in other bacterial species.

25 Specific Example: Determination Of Candidate Protein Antigens For Antibody And Vaccine Development

The selection of candidate protein antigens for vaccine development can be derived from the nucleic acids encoding *H. pylori* polypeptides. First, the ORF's can be analyzed for homology to other known exported or membrane proteins and analyzed using the 30 discriminant analysis described by Klein, et al. (Klein, P., Kanehsia, M., and DeLisi, C. (1985) *Biochimica et Biophysica Acta* 815, 468-476) for predicting exported and membrane proteins.

35 Homology searches can be performed using the BLAST algorithm contained in the Wisconsin Sequence Analysis Package (Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711) to compare each predicted ORF amino acid sequence with all sequences found in the current GenBank, SWISS-PROT and PIR databases. BLAST searches for local alignments between the ORF and the databank sequences and reports a probability score which indicates the probability of finding this sequence by chance in the database. ORF's with significant homology (e.g. probabilities

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lower than 1×10^{-6} that the homology is only due to random chance) to membrane or exported proteins represent protein antigens for vaccine development. Possible functions can be provided to *H. pylori* genes based on sequence homology to genes cloned in other organisms.

- 5 Discriminant analysis (Klein, et al. supra) can be used to examine the ORF amino acid sequences. This algorithm uses the intrinsic information contained in the ORF amino acid sequence and compares it to information derived from the properties of known membrane and exported proteins. This comparison predicts which proteins will be exported, membrane associated or cytoplasmic. ORF amino acid sequences identified as
 10 exported or membrane associated by this algorithm are likely protein antigens for vaccine development.

Infrequently it is not possible to distinguish between multiple possible nucleotides at a given position in the nucleic acid sequence. In those cases the ambiguities are denoted by an extended alphabet as follows:

- 15 These are the official IUPAC-IUB single-letter base codes

Code	Base Description
G	Guanine
A	Adenine
T	Thymine
C	Cytosine
R	Purine (A or G)
Y	Pyrimidine (C or T or U)
M	Amino (A or C)
K	Ketone (G or T)
S	Strong interaction (C or G)
W	Weak interaction (A or T)
H	Not-G (A or C or T)
B	Not-A (C or G or T)
V	Not-T (not-U) (A or C or G)
D	Not-C (A or G or T)
N	Any (A or C or G or T)

- 20 The amino acid translations of this invention account for the ambiguity in the nucleic acid sequence by translating the ambiguous codon as the letter "X". In all cases, the permissible amino acid residues at a position are clear from an examination of the nucleic acid sequence based on the standard genetic code.

V. Production of Fragments and Analogs of *H. pylori* Nucleic Acids and Polypeptides

Based on the discovery of the *H. pylori* gene products of the invention provided in the Sequence Listing, one skilled in the art can alter the disclosed structure (of *H. pylori* genes), e.g., by producing fragments or analogs, and test the newly produced structures for activity. Examples of techniques known to those skilled in the relevant art which allow the production and testing of fragments and analogs are discussed below. These, or analogous methods can be used to make and screen libraries of polypeptides, e.g., libraries of random peptides or libraries of fragments or analogs of cellular proteins for the ability to bind *H. pylori* polypeptides. Such screens are useful for the identification of inhibitors of *H. pylori*.

10

Generation of Fragments

Fragments of a protein can be produced in several ways, e.g., recombinantly, by proteolytic digestion, or by chemical synthesis. Internal or terminal fragments of a polypeptide can be generated by removing one or more nucleotides from one end (for a terminal fragment) or both ends (for an internal fragment) of a nucleic acid which encodes the polypeptide. Expression of the mutagenized DNA produces polypeptide fragments. Digestion with "end-nibbling" endonucleases can thus generate DNA's which encode an array of fragments. DNA's which encode fragments of a protein can also be generated by random shearing, restriction digestion or a combination of the above-discussed methods.

20 Fragments can also be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase F-Moc or t-Boc chemistry. For example, peptides of the present invention may be arbitrarily divided into fragments of desired length with no overlap of the fragments, or divided into overlapping fragments of a desired length.

25

Alteration of Nucleic Acids and Polypeptides: Random Methods

Amino acid sequence variants of a protein can be prepared by random mutagenesis of DNA which encodes a protein or a particular domain or region of a protein. Useful methods include PCR mutagenesis and saturation mutagenesis. A library of random amino acid sequence variants can also be generated by the synthesis of a set of degenerate oligonucleotide sequences. (Methods for screening proteins in a library of variants are elsewhere herein).

(A) PCR Mutagenesis

In PCR mutagenesis, reduced Taq polymerase fidelity is used to introduce random mutations into a cloned fragment of DNA (Leung et al., 1989, *Technique* 1:11-15). The DNA region to be mutagenized is amplified using the polymerase chain reaction (PCR) under conditions that reduce the fidelity of DNA synthesis by Taq DNA polymerase, e.g., by using a dGTP/dATP ratio of five and adding Mn²⁺ to the PCR reaction. The pool of amplified DNA fragments are inserted into appropriate cloning vectors to provide random mutant libraries.

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(B) Saturation Mutagenesis

Saturation mutagenesis allows for the rapid introduction of a large number of single base substitutions into cloned DNA fragments (Mayers et al., 1985, *Science* 229:242). This technique includes generation of mutations, e.g., by chemical treatment or irradiation of 5 single-stranded DNA *in vitro*, and synthesis of a complimentary DNA strand. The mutation frequency can be modulated by modulating the severity of the treatment, and essentially all possible base substitutions can be obtained. Because this procedure does not involve a genetic selection for mutant fragments both neutral substitutions, as well as those that alter function, are obtained. The distribution of point mutations is not biased toward 10 conserved sequence elements.

(C) Degenerate Oligonucleotides

A library of homologs can also be generated from a set of degenerate oligonucleotide sequences. Chemical synthesis of a degenerate sequences can be carried out in an automatic DNA synthesizer, and the synthetic genes then ligated into an 15 appropriate expression vector. The synthesis of degenerate oligonucleotides is known in the art (see for example, Narang, SA (1983) *Tetrahedron* 39:3; Itakura et al. (1981) *Recombinant DNA, Proc 3rd Cleveland Sympos. Macromolecules*, ed. AG Walton, Amsterdam: Elsevier pp273-289; Itakura et al. (1984) *Annu. Rev. Biochem.* 53:323; Itakura et al. (1984) *Science* 198:1056; Ike et al. (1983) *Nucleic Acid Res.* 11:477. Such techniques 20 have been employed in the directed evolution of other proteins (see, for example, Scott et al. (1990) *Science* 249:386-390; Roberts et al. (1992) *PNAS* 89:2429-2433; Devlin et al. (1990) *Science* 249: 404-406; Cwirla et al. (1990) *PNAS* 87: 6378-6382; as well as U.S. Patents Nos. 5,223,409, 5,198,346, and 5,096,815).

25 Alteration of Nucleic Acids and Polypeptides: Methods for Directed Mutagenesis

Non-random or directed, mutagenesis techniques can be used to provide specific sequences or mutations in specific regions. These techniques can be used to create variants which include, e.g., deletions, insertions, or substitutions, of residues of the known amino acid sequence of a protein. The sites for mutation can be modified individually or in series, 30 e.g., by (1) substituting first with conserved amino acids and then with more radical choices depending upon results achieved, (2) deleting the target residue, or (3) inserting residues of the same or a different class adjacent to the located site, or combinations of options 1-3.

(A) Alanine Scanning Mutagenesis

Alanine scanning mutagenesis is a useful method for identification of certain 35 residues or regions of the desired protein that are preferred locations or domains for mutagenesis, Cunningham and Wells (*Science* 244:1081-1085, 1989). In alanine scanning, a residue or group of target residues are identified (e.g., charged residues such as Arg, Asp, His, Lys, and Glu) and replaced by a neutral or negatively charged amino acid (most preferably alanine or polyalanine). Replacement of an amino acid can affect the interaction

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of the amino acids with the surrounding aqueous environment in or outside the cell. Those domains demonstrating functional sensitivity to the substitutions are then refined by introducing further or other variants at or for the sites of substitution. Thus, while the site for introducing an amino acid sequence variation is predetermined, the nature of the 5 mutation per se need not be predetermined. For example, to optimize the performance of a mutation at a given site, alanine scanning or random mutagenesis may be conducted at the target codon or region and the expressed desired protein subunit variants are screened for the optimal combination of desired activity.

(B) Oligonucleotide-Mediated Mutagenesis

10 Oligonucleotide-mediated mutagenesis is a useful method for preparing substitution, deletion, and insertion variants of DNA, see, e.g., Adelman et al., (*DNA* 2:183, 1983). Briefly, the desired DNA is altered by hybridizing an oligonucleotide encoding a mutation to a DNA template, where the template is the single-stranded form of a plasmid or bacteriophage containing the unaltered or native DNA sequence of the desired protein.

15 After hybridization, a DNA polymerase is used to synthesize an entire second complementary strand of the template that will thus incorporate the oligonucleotide primer, and will code for the selected alteration in the desired protein DNA. Generally, oligonucleotides of at least 25 nucleotides in length are used. An optimal oligonucleotide will have 12 to 15 nucleotides that are completely complementary to the template on either 20 side of the nucleotide(s) coding for the mutation. This ensures that the oligonucleotide will hybridize properly to the single-stranded DNA template molecule. The oligonucleotides are readily synthesized using techniques known in the art such as that described by Crea et al. (*Proc. Natl. Acad. Sci. USA*, 75: 5765[1978]).

(C) Cassette Mutagenesis

25 Another method for preparing variants, cassette mutagenesis, is based on the technique described by Wells et al. (*Gene*, 34:315[1985]). The starting material is a plasmid (or other vector) which includes the protein subunit DNA to be mutated. The codon(s) in the protein subunit DNA to be mutated are identified. There must be a unique restriction endonuclease site on each side of the identified mutation site(s). If no such 30 restriction sites exist, they may be generated using the above-described oligonucleotide-mediated mutagenesis method to introduce them at appropriate locations in the desired protein subunit DNA. After the restriction sites have been introduced into the plasmid, the plasmid is cut at these sites to linearize it. A double-stranded oligonucleotide encoding the sequence of the DNA between the restriction sites but containing the desired mutation(s) is 35 synthesized using standard procedures. The two strands are synthesized separately and then hybridized together using standard techniques. This double-stranded oligonucleotide is referred to as the cassette. This cassette is designed to have 3' and 5' ends that are comparable with the ends of the linearized plasmid, such that it can be directly ligated to

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the plasmid. This plasmid now contains the mutated desired protein subunit DNA sequence.

(D) Combinatorial Mutagenesis

Combinatorial mutagenesis can also be used to generate mutants (Ladner et al., WO 5 88/06630). In this method, the amino acid sequences for a group of homologs or other related proteins are aligned, preferably to promote the highest homology possible. All of the amino acids which appear at a given position of the aligned sequences can be selected to create a degenerate set of combinatorial sequences. The variegated library of variants is generated by combinatorial mutagenesis at the nucleic acid level, and is encoded by a 10 variegated gene library. For example, a mixture of synthetic oligonucleotides can be enzymatically ligated into gene sequences such that the degenerate set of potential sequences are expressible as individual peptides, or alternatively, as a set of larger fusion proteins containing the set of degenerate sequences.

15 Other Modifications of *H. pylori* Nucleic Acids and Polypeptides

It is possible to modify the structure of an *H. pylori* polypeptide for such purposes as increasing solubility, enhancing stability (e.g., shelf life *ex vivo* and resistance to proteolytic degradation *in vivo*). A modified *H. pylori* protein or peptide can be produced in which the amino acid sequence has been altered, such as by amino acid substitution, 20 deletion, or addition as described herein.

An *H. pylori* peptide can also be modified by substitution of cysteine residues preferably with alanine, serine, threonine, leucine or glutamic acid residues to minimize dimerization via disulfide linkages. In addition, amino acid side chains of fragments of the protein of the invention can be chemically modified. Another modification is cyclization of 25 the peptide.

In order to enhance stability and/or reactivity, an *H. pylori* polypeptide can be modified to incorporate one or more polymorphisms in the amino acid sequence of the protein resulting from any natural allelic variation. Additionally, D-amino acids, non-natural amino acids, or non-amino acid analogs can be substituted or added to produce a 30 modified protein within the scope of this invention. Furthermore, an *H. pylori* polypeptide can be modified using polyethylene glycol (PEG) according to the method of A. Sehon and co-workers (Wie et al., *supra*) to produce a protein conjugated with PEG. In addition, PEG can be added during chemical synthesis of the protein. Other modifications of *H. pylori* proteins include reduction/alkylation (Tarr, *Methods of Protein Microcharacterization*, J. E. 35 Silver ed., Humana Press, Clifton NJ 155-194 (1986)); acylation (Tarr, *supra*); chemical coupling to an appropriate carrier (Mishell and Shiigi, eds, *Selected Methods in Cellular Immunology*, WH Freeman, San Francisco, CA (1980), U.S. Patent 4,939,239; or mild formalin treatment (Marsh, (1971) *Int. Arch. of Allergy and Appl. Immunol.*, 41: 199 - 215).

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To facilitate purification and potentially increase solubility of an *H. pylori* protein or peptide, it is possible to add an amino acid fusion moiety to the peptide backbone. For example, hexa-histidine can be added to the protein for purification by immobilized metal ion affinity chromatography (Hochuli, E. et al., (1988) *BioTechnology*, 6: 1321 - 1325). In 5 addition, to facilitate isolation of peptides free of irrelevant sequences, specific endoprotease cleavage sites can be introduced between the sequences of the fusion moiety and the peptide.

To potentially aid proper antigen processing of epitopes within an *H. pylori* polypeptide, canonical protease sensitive sites can be engineered between regions, each 10 comprising at least one epitope via recombinant or synthetic methods. For example, charged amino acid pairs, such as KK or RR, can be introduced between regions within a protein or fragment during recombinant construction thereof. The resulting peptide can be rendered sensitive to cleavage by cathepsin and/or other trypsin-like enzymes which would generate portions of the protein containing one or more epitopes. In addition, such charged 15 amino acid residues can result in an increase in the solubility of the peptide.

Primary Methods for Screening Polypeptides and Analogs

Various techniques are known in the art for screening generated mutant gene products. Techniques for screening large gene libraries often include cloning the gene 20 library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the genes under conditions in which detection of a desired activity, e.g., in this case, binding to *H. pylori* polypeptide or an interacting protein, facilitates relatively easy isolation of the vector encoding the gene whose product was detected. Each of the techniques described below is amenable to high through-put analysis 25 for screening large numbers of sequences created, e.g., by random mutagenesis techniques.

(A) Two Hybrid Systems

Two hybrid assays such as the system described above (as with the other screening methods described herein), can be used to identify polypeptides, e.g., fragments or analogs of a naturally-occurring *H. pylori* polypeptide, e.g., of cellular proteins, or of randomly 30 generated polypeptides which bind to an *H. pylori* protein. (The *H. pylori* domain is used as the bait protein and the library of variants are expressed as fish fusion proteins.) In an analogous fashion, a two hybrid assay (as with the other screening methods described herein), can be used to find polypeptides which bind a *H. pylori* polypeptide.

(B) Display Libraries

In one approach to screening assays, the candidate peptides are displayed on the 35 surface of a cell or viral particle, and the ability of particular cells or viral particles to bind an appropriate receptor protein via the displayed product is detected in a "panning assay". For example, the gene library can be cloned into the gene for a surface membrane protein of a bacterial cell, and the resulting fusion protein detected by panning (Ladner et al., WO

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88/06630; Fuchs et al. (1991) *Bio/Technology* 9:1370-1371; and Goward et al. (1992) *TIBS* 18:136-140). In a similar fashion, a detectably labeled ligand can be used to score for potentially functional peptide homologs. Fluorescently labeled ligands, e.g., receptors, can be used to detect homologs which retain ligand-binding activity. The use of fluorescently 5 labeled ligands, allows cells to be visually inspected and separated under a fluorescence microscope, or, where the morphology of the cell permits, to be separated by a fluorescence-activated cell sorter.

A gene library can be expressed as a fusion protein on the surface of a viral particle. For instance, in the filamentous phage system, foreign peptide sequences can be expressed 10 on the surface of infectious phage, thereby conferring two significant benefits. First, since these phage can be applied to affinity matrices at concentrations well over 10^{13} phage per milliliter, a large number of phage can be screened at one time. Second, since each infectious phage displays a gene product on its surface, if a particular phage is recovered from an affinity matrix in low yield, the phage can be amplified by another round of 15 infection. The group of almost identical *E. coli* filamentous phages M13, fd., and f1 are most often used in phage display libraries. Either of the phage gIII or gVIII coat proteins can be used to generate fusion proteins without disrupting the ultimate packaging of the viral particle. Foreign epitopes can be expressed at the NH₂-terminal end of pIII and phage bearing such epitopes recovered from a large excess of phage lacking this epitope (Ladner 20 et al. PCT publication WO 90/02909; Garrard et al., PCT publication WO 92/09690; Marks et al. (1992) *J. Biol. Chem.* 267:16007-16010; Griffiths et al. (1993) *EMBO J* 12:725-734; Clackson et al. (1991) *Nature* 352:624-628; and Barbas et al. (1992) *PNAS* 89:4457-4461).

A common approach uses the maltose receptor of *E. coli* (the outer membrane protein, LamB) as a peptide fusion partner (Charbit et al. (1986) *EMBO J* 5, 3029-3037). 25 Oligonucleotides have been inserted into plasmids encoding the LamB gene to produce peptides fused into one of the extracellular loops of the protein. These peptides are available for binding to ligands, e.g., to antibodies, and can elicit an immune response when the cells are administered to animals. Other cell surface proteins, e.g., OmpA (Schorr et al. (1991) *Vaccines* 91, pp. 387-392), PhoE (Agterberg, et al. (1990) *Gene* 88, 37-45), and 30 PAL (Fuchs et al. (1991) *Bio/Tech* 9, 1369-1372), as well as large bacterial surface structures have served as vehicles for peptide display. Peptides can be fused to pilin, a protein which polymerizes to form the pilus-a conduit for interbacterial exchange of genetic information (Thiry et al. (1989) *Appl. Environ. Microbiol.* 55, 984-993). Because of its role in interacting with other cells, the pilus provides a useful support for the presentation 35 of peptides to the extracellular environment. Another large surface structure used for peptide display is the bacterial motive organ, the flagellum. Fusion of peptides to the subunit protein flagellin offers a dense array of many peptide copies on the host cells (Kuwajima et al. (1988) *Bio/Tech.* 6, 1080-1083). Surface proteins of other bacterial species have also served as peptide fusion partners. Examples include the *Staphylococcus*

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protein A and the outer membrane IgA protease of *Neisseria* (Hansson et al. (1992) *J. Bacteriol.* 174, 4239-4245 and Klauser et al. (1990) *EMBO J.* 9, 1991-1999).

In the filamentous phage systems and the LamB system described above, the physical link between the peptide and its encoding DNA occurs by the containment of the DNA within a particle (cell or phage) that carries the peptide on its surface. Capturing the peptide captures the particle and the DNA within. An alternative scheme uses the DNA-binding protein LacI to form a link between peptide and DNA (Cull et al. (1992) *PNAS USA* 89:1865-1869). This system uses a plasmid containing the LacI gene with an oligonucleotide cloning site at its 3'-end. Under the controlled induction by arabinose, a LacI-peptide fusion protein is produced. This fusion retains the natural ability of LacI to bind to a short DNA sequence known as LacO operator (LacO). By installing two copies of LacO on the expression plasmid, the LacI-peptide fusion binds tightly to the plasmid that encoded it. Because the plasmids in each cell contain only a single oligonucleotide sequence and each cell expresses only a single peptide sequence, the peptides become specifically and stably associated with the DNA sequence that directed its synthesis. The cells of the library are gently lysed and the peptide-DNA complexes are exposed to a matrix of immobilized receptor to recover the complexes containing active peptides. The associated plasmid DNA is then reintroduced into cells for amplification and DNA sequencing to determine the identity of the peptide ligands. As a demonstration of the practical utility of the method, a large random library of dodecapeptides was made and selected on a monoclonal antibody raised against the opioid peptide dynorphin B. A cohort of peptides was recovered, all related by a consensus sequence corresponding to a six-residue portion of dynorphin B. (Cull et al. (1992) *Proc. Natl. Acad. Sci. U.S.A.* 89:1869)

This scheme, sometimes referred to as peptides-on-plasmids, differs in two important ways from the phage display methods. First, the peptides are attached to the C-terminus of the fusion protein, resulting in the display of the library members as peptides having free carboxy termini. Both of the filamentous phage coat proteins, pIII and pVIII, are anchored to the phage through their C-termini, and the guest peptides are placed into the outward-extending N-terminal domains. In some designs, the phage-displayed peptides are presented right at the amino terminus of the fusion protein. (Cwirla, et al. (1990) *Proc. Natl. Acad. Sci. U.S.A.* 87, 6378-6382) A second difference is the set of biological biases affecting the population of peptides actually present in the libraries. The LacI fusion molecules are confined to the cytoplasm of the host cells. The phage coat fusions are exposed briefly to the cytoplasm during translation but are rapidly secreted through the inner membrane into the periplasmic compartment, remaining anchored in the membrane by their C-terminal hydrophobic domains, with the N-termini, containing the peptides, protruding into the periplasm while awaiting assembly into phage particles. The peptides in the LacI and phage libraries may differ significantly as a result of their exposure to different proteolytic activities. The phage coat proteins require transport across the inner

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membrane and signal peptidase processing as a prelude to incorporation into phage. Certain peptides exert a deleterious effect on these processes and are underrepresented in the libraries (Gallop et al. (1994) *J. Med. Chem.* 37(9):1233-1251). These particular biases are not a factor in the LacI display system.

- 5 The number of small peptides available in recombinant random libraries is enormous. Libraries of 10^7 - 10^9 independent clones are routinely prepared. Libraries as large as 10^{11} recombinants have been created, but this size approaches the practical limit for clone libraries. This limitation in library size occurs at the step of transforming the DNA containing randomized segments into the host bacterial cells. To circumvent this
- 10 limitation, an *in vitro* system based on the display of nascent peptides in polysome complexes has recently been developed. This display library method has the potential of producing libraries 3-6 orders of magnitude larger than the currently available phage/phagemid or plasmid libraries. Furthermore, the construction of the libraries, expression of the peptides, and screening, is done in an entirely cell-free format.
- 15 In one application of this method (Gallop et al. (1994) *J. Med. Chem.* 37(9):1233-1251), a molecular DNA library encoding 10^{12} decapeptides was constructed and the library expressed in an *E. coli* S30 *in vitro* coupled transcription/translation system. Conditions were chosen to stall the ribosomes on the mRNA, causing the accumulation of a substantial proportion of the RNA in polysomes and yielding complexes containing nascent
- 20 peptides still linked to their encoding RNA. The polysomes are sufficiently robust to be affinity purified on immobilized receptors in much the same way as the more conventional recombinant peptide display libraries are screened. RNA from the bound complexes is recovered, converted to cDNA, and amplified by PCR to produce a template for the next round of synthesis and screening. The polysome display method can be coupled to the
- 25 phage display system. Following several rounds of screening, cDNA from the enriched pool of polysomes was cloned into a phagemid vector. This vector serves as both a peptide expression vector, displaying peptides fused to the coat proteins, and as a DNA sequencing vector for peptide identification. By expressing the polysome-derived peptides on phage, one can either continue the affinity selection procedure in this format or assay the peptides
- 30 on individual clones for binding activity in a phage ELISA, or for binding specificity in a completion phage ELISA (Barret, et al. (1992) *Anal. Biochem.* 204,357-364). To identify the sequences of the active peptides one sequences the DNA produced by the phagemid host.

35 Secondary Screening of Polypeptides and Analogs

The high through-put assays described above can be followed by secondary screens in order to identify further biological activities which will, e.g., allow one skilled in the art to differentiate agonists from antagonists. The type of a secondary screen used will depend on the desired activity that needs to be tested. For example, an assay can be developed in

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which the ability to inhibit an interaction between a protein of interest and its respective ligand can be used to identify antagonists from a group of peptide fragments isolated through one of the primary screens described above.

Therefore, methods for generating fragments and analogs and testing them for activity are known in the art. Once the core sequence of interest is identified, it is routine for one skilled in the art to obtain analogs and fragments.

Peptide Mimetics of *H. pylori* Polypeptides

The invention also provides for reduction of the protein binding domains of the subject *H. pylori* polypeptides to generate mimetics, e.g. peptide or non-peptide agents. The peptide mimetics are able to disrupt binding of a polypeptide to its counter ligand, e.g., in the case of an *H. pylori* polypeptide binding to a naturally occurring ligand. The critical residues of a subject *H. pylori* polypeptide which are involved in molecular recognition of a polypeptide can be determined and used to generate *H. pylori*-derived peptidomimetics which competitively or noncompetitively inhibit binding of the *H. pylori* polypeptide with an interacting polypeptide (see, for example, European patent applications EP-412,762A and EP-B31,080A).

For example, scanning mutagenesis can be used to map the amino acid residues of a particular *H. pylori* polypeptide involved in binding an interacting polypeptide, peptidomimetic compounds (e.g. diazepine or isoquinoline derivatives) can be generated which mimic those residues in binding to an interacting polypeptide, and which therefore can inhibit binding of an *H. pylori* polypeptide to an interacting polypeptide and thereby interfere with the function of *H. pylori* polypeptide. For instance, non-hydrolyzable peptide analogs of such residues can be generated using benzodiazepine (e.g., see Freidinger et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), azepine (e.g., see Huffman et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), substituted gamma lactam rings (Garvey et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), keto-methylene pseudopeptides (Ewenson et al. (1986) *J Med Chem* 29:295; and Ewenson et al. in *Peptides: Structure and Function* (Proceedings of the 9th American Peptide Symposium) Pierce Chemical Co. Rockland, IL, 1985), β-turn dipeptide cores (Nagai et al. (1985) *Tetrahedron Lett* 26:647; and Sato et al. (1986) *J Chem Soc Perkin Trans* 1:1231), and β-aminoalcohols (Gordon et al. (1985) *Biochem Biophys Res Commun* 126:419; and Dann et al. (1986) *Biochem Biophys Res Commun* 134:71).

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VI. Vaccine Formulations for *H. pylori* Nucleic Acids and Polypeptides

This invention also features vaccine compositions for protection against infection by *H. pylori* or for treatment of *H. pylori* infection, a gram-negative spiral microaerophilic bacterium. In one embodiment, the vaccine compositions contain one or more immunogenic components such as a surface protein from *H. pylori*, or portion thereof, and a pharmaceutically acceptable carrier. Nucleic acids within the scope of the invention are exemplified by the nucleic acids of the invention contained in the Sequence Listing which encode *H. pylori* surface proteins. For example, the preferred nucleic acid for a vaccine composition of the invention is isolated from the group of nucleic acids which encode cell envelope proteins as outlined in Table 1. More specifically, the amino acids of SEQ ID NO:812, SEQ ID NO:820, SEQ ID NO:880, SEQ ID NO:658, SEQ ID NO:865, SEQ ID NO:1729, SEQ ID NO:1861, or fragments thereof, can be used alone or in combination for the formulation of vaccine compositions of the invention, as well as, their corresponding nucleic acids of SEQ ID NO:977, SEQ ID NO:978, SEQ ID NO:994, SEQ ID NO:215, SEQ ID NO:989, SEQ ID NO:1278, and SEQ ID NO:1410. However, any nucleic acid encoding an immunogenic *H. pylori* protein, or portion thereof, which is capable of expression in a cell, can be used in the present invention. These vaccines have therapeutic and prophylactic utilities.

One aspect of the invention provides a vaccine composition for protection against infection by *H. pylori* which contains at least one immunogenic fragment of an *H. pylori* protein and a pharmaceutically acceptable carrier. Preferred fragments include peptides of at least about 10 amino acid residues in length, preferably about 10-20 amino acid residues in length, and more preferably about 12-16 amino acid residues in length.

Immunogenic components of the invention can be obtained, for example, by screening polypeptides recombinantly produced from the corresponding fragment of the nucleic acid encoding the full-length *H. pylori* protein. In addition, fragments can be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry.

In one embodiment, immunogenic components are identified by the ability of the peptide to stimulate T cells. Peptides which stimulate T cells, as determined by, for example, T cell proliferation or cytokine secretion are defined herein as comprising at least one T cell epitope. T cell epitopes are believed to be involved in initiation and perpetuation of the immune response to the protein allergen which is responsible for the clinical symptoms of allergy. These T cell epitopes are thought to trigger early events at the level of the T helper cell by binding to an appropriate HLA molecule on the surface of an antigen presenting cell, thereby stimulating the T cell subpopulation with the relevant T cell receptor for the epitope. These events lead to T cell proliferation, lymphokine secretion, local inflammatory reactions, recruitment of additional immune cells to the site of antigen/T cell interaction, and activation of the B cell cascade, leading to the production of

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antibodies. A T cell epitope is the basic element, or smallest unit of recognition by a T cell receptor, where the epitope comprises amino acids essential to receptor recognition (e.g., approximately 6 or 7 amino acid residues). Amino acid sequences which mimic those of the T cell epitopes are within the scope of this invention.

5 Screening immunogenic components can be accomplished using one or more of several different assays. For example, *in vitro*, peptide T cell stimulatory activity is assayed by contacting a peptide known or suspected of being immunogenic with an antigen presenting cell which presents appropriate MHC molecules in a T cell culture. Presentation of an immunogenic *H. pylori* peptide in association with appropriate MHC molecules to T 10 cells in conjunction with the necessary costimulation has the effect of transmitting a signal to the T cell that induces the production of increased levels of cytokines, particularly of interleukin-2 and interleukin-4. The culture supernatant can be obtained and assayed for interleukin-2 or other known cytokines. For example, any one of several conventional assays for interleukin-2 can be employed, such as the assay described in *Proc. Natl. Acad. Sci USA*, 86: 1333 (1989) the pertinent portions of which are incorporated herein by reference. A kit for an assay for the production of interferon is also available from Genzyme Corporation (Cambridge, MA).

20 Alternatively, a common assay for T cell proliferation entails measuring tritiated thymidine incorporation. The proliferation of T cells can be measured *in vitro* by determining the amount of ³H-labeled thymidine incorporated into the replicating DNA of cultured cells. Therefore, the rate of DNA synthesis and, in turn, the rate of cell division can be quantified.

25 Vaccine compositions of the invention containing immunogenic components (e.g., *H. pylori* polypeptide or fragment thereof or nucleic acid encoding an *H. pylori* polypeptide or fragment thereof) preferably include a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier that does not cause an allergic reaction or other untoward effect in patients to whom it is administered. Suitable pharmaceutically acceptable carriers include, for example, one or more of water, saline, phosphate buffered saline, dextrose, glycerol, ethanol and the like, as well as combinations thereof. Pharmaceutically acceptable carriers may further comprise minor amounts of auxiliary substances such as wetting or emulsifying agents, preservatives or buffers, which enhance the shelf life or effectiveness of the antibody. For vaccines of the invention containing *H. pylori* polypeptides, the polypeptide is coadministered with a suitable adjuvant.

30 It will be apparent to those of skill in the art that the therapeutically effective amount of DNA or protein of this invention will depend, *inter alia*, upon the administration schedule, the unit dose of antibody administered, whether the protein or DNA is administered in combination with other therapeutic agents, the immune status and health of the patient, and the therapeutic activity of the particular protein or DNA.

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- Vaccine compositions are conventionally administered parenterally, e.g., by injection, either subcutaneously or intramuscularly. Methods for intramuscular immunization are described by Wolff et al. (1990) *Science* 247: 1465-1468 and by Sedegah et al. (1994) *Immunology* 91: 9866-9870. Other modes of administration include oral and
- 5 pulmonary formulations, suppositories, and transdermal applications. Oral immunization is preferred over parenteral methods for inducing protection against infection by *H. pylori*. Czinn et. al. (1993) *Vaccine* 11: 637-642. Oral formulations include such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, and the like.
- 10 The vaccine compositions of the invention can include an adjuvant, including, but not limited to aluminum hydroxide; N-acetyl-muramyl--L-threonyl-D-isoglutamine (thr-MDP); N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine (CGP 11637, referred to as nor-MDP); N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (CGP 19835A, referred to as MTP-PE);
- 15 RIBI, which contains three components from bacteria; monophosphoryl lipid A; trehalose dimycolate; cell wall skeleton (MPL + TDM + CWS) in a 2% squalene/Tween 80 emulsion; and cholera toxin. Others which may be used are non-toxic derivatives of cholera toxin, including its B subunit, and/or conjugates or genetically engineered fusions of the *H. pylori* polypeptide with cholera toxin or its B subunit, procholeragenoid, fungal
- 20 polysaccharides, including schizophyllan, muramyl dipeptide, muramyl dipeptide derivatives, phorbol esters, labile toxin of *E. coli*, non-*H. pylori* bacterial lysates, block polymers or saponins.

Other suitable delivery methods include biodegradable microcapsules or immuno-stimulating complexes (ISCOMs), cochleates, or liposomes, genetically engineered attenuated live vectors such as viruses or bacteria, and recombinant (chimeric) virus-like particles, e.g., bluetongue. The amount of adjuvant employed will depend on the type of adjuvant used. For example, when the mucosal adjuvant is cholera toxin, it is suitably used in an amount of 5 µg to 50 µg, for example 10 µg to 35 µg. When used in the form of microcapsules, the amount used will depend on the amount employed in the matrix of the microcapsule to achieve the desired dosage. The determination of this amount is within the skill of a person of ordinary skill in the art.

Carrier systems in humans may include enteric release capsules protecting the antigen from the acidic environment of the stomach, and including *H. pylori* polypeptide in an insoluble form as fusion proteins. Suitable carriers for the vaccines of the invention are enteric coated capsules and polylactide-glycolide microspheres. Suitable diluents are 0.2 N NaHCO₃ and/or saline.

Vaccines of the invention can be administered as a primary prophylactic agent in adults or in children, as a secondary prevention, after successful eradication of *H. pylori* in an infected host, or as a therapeutic agent in the aim to induce an immune response in a

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susceptible host to prevent infection by *H. pylori*. The vaccines of the invention are administered in amounts readily determined by persons of ordinary skill in the art. Thus, for adults a suitable dosage will be in the range of 10 µg to 10 g, preferably 10 µg to 100 mg, for example 50 µg to 50 mg. A suitable dosage for adults will also be in the range of 5 µg to 500 mg. Similar dosage ranges will be applicable for children. Those skilled in the art will recognize that the optimal dose may be more or less depending upon the patient's body weight, disease, the route of administration, and other factors. Those skilled in the art will also recognize that appropriate dosage levels can be obtained based on results with known oral vaccines such as, for example, a vaccine based on an *E. coli* lysate (6 mg dose daily up to total of 540 mg) and with an enterotoxigenic *E. coli* purified antigen (4 doses of 1 mg) (Schulman et al., *J. Urol.* 150:917-921 (1993); Boedecker et al., *American Gastroenterological Assoc.* 999:A-222 (1993)). The number of doses will depend upon the disease, the formulation, and efficacy data from clinical trials. Without intending any limitation as to the course of treatment, the treatment can be administered over 3 to 8 doses for a primary immunization schedule over 1 month (Boedeker, *American Gastroenterological Assoc.* 888:A-222 (1993)).

In a preferred embodiment, a vaccine composition of the invention can be based on a killed whole *E. coli* preparation with an immunogenic fragment of an *H. pylori* protein of the invention expressed on its surface or it can be based on an *E. coli* lysate, wherein the killed *E. coli* acts as a carrier or an adjuvant.

It will be apparent to those skilled in the art that some of the vaccine compositions of the invention are useful only for preventing *H. pylori* infection, some are useful only for treating *H. pylori* infection, and some are useful for both preventing and treating *H. pylori* infection. In a preferred embodiment, the vaccine composition of the invention provides protection against *H. pylori* infection by stimulating humoral and/or cell-mediated immunity against *H. pylori*. It should be understood that amelioration of any of the symptoms of *H. pylori* infection is a desirable clinical goal, including a lessening of the dosage of medication used to treat *H. pylori*-caused disease, or an increase in the production of antibodies in the serum or mucous of patients.

30

VII. Antibodies Reactive With *H. pylori* Polypeptides

The invention also includes antibodies specifically reactive with the subject *H. pylori* polypeptide. Anti-protein/anti-peptide antisera or monoclonal antibodies can be made by standard protocols (See, for example, *Antibodies: A Laboratory Manual* ed. by Harlow and Lane (Cold Spring Harbor Press: 1988)). A mammal such as a mouse, a hamster or rabbit can be immunized with an immunogenic form of the peptide. Techniques for conferring immunogenicity on a protein or peptide include conjugation to carriers or other techniques well known in the art. An immunogenic portion of the subject *H. pylori* polypeptide can be administered in the presence of adjuvant. The progress of immunization

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can be monitored by detection of antibody titers in plasma or serum. Standard ELISA or other immunoassays can be used with the immunogen as antigen to assess the levels of antibodies.

In a preferred embodiment, the subject antibodies are immunospecific for antigenic determinants of the *H. pylori* polypeptides of the invention, e.g. antigenic determinants of a polypeptide of the invention contained in the Sequence Listing, or a closely related human or non-human mammalian homolog (e.g., 90% homologous, more preferably at least 95% homologous). In yet a further preferred embodiment of the invention, the anti-*H. pylori* antibodies do not substantially cross react (i.e., react specifically) with a protein which is for example, less than 80% percent homologous to a sequence of the invention contained in the Sequence Listing. By "not substantially cross react", it is meant that the antibody has a binding affinity for a non-homologous protein which is less than 10 percent, more preferably less than 5 percent, and even more preferably less than 1 percent, of the binding affinity for a protein of the invention contained in the Sequence Listing. In a most preferred embodiment, there is no crossreactivity between bacterial and mammalian antigens.

The term antibody as used herein is intended to include fragments thereof which are also specifically reactive with *H. pylori* polypeptides. Antibodies can be fragmented using conventional techniques and the fragments screened for utility in the same manner as described above for whole antibodies. For example, F(ab')₂ fragments can be generated by treating antibody with pepsin. The resulting F(ab')₂ fragment can be treated to reduce disulfide bridges to produce Fab' fragments. The antibody of the invention is further intended to include bispecific and chimeric molecules having an anti-*H. pylori* portion.

Both monoclonal and polyclonal antibodies (Ab) directed against *H. pylori* polypeptides or *H. pylori* polypeptide variants, and antibody fragments such as Fab' and F(ab')₂, can be used to block the action of *H. pylori* polypeptide and allow the study of the role of a particular *H. pylori* polypeptide of the invention in aberrant or unwanted intracellular signaling, as well as the normal cellular function of the *H. pylori* and by microinjection of anti-*H. pylori* polypeptide antibodies of the present invention.

Antibodies which specifically bind *H. pylori* epitopes can also be used in immunohistochemical staining of tissue samples in order to evaluate the abundance and pattern of expression of *H. pylori* antigens. Anti *H. pylori* polypeptide antibodies can be used diagnostically in immuno-precipitation and immuno-blotting to detect and evaluate *H. pylori* levels in tissue or bodily fluid as part of a clinical testing procedure. Likewise, the ability to monitor *H. pylori* polypeptide levels in an individual can allow determination of the efficacy of a given treatment regimen for an individual afflicted with such a disorder. The level of an *H. pylori* polypeptide can be measured in cells found in bodily fluid, such as in urine samples or can be measured in tissue, such as produced by gastric biopsy. Diagnostic assays using anti-*H. pylori* antibodies can include, for example, immunoassays

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designed to aid in early diagnosis of *H. pylori* infections. The present invention can also be used as a method of detecting antibodies contained in samples from individuals infected by this bacterium using specific *H. pylori* antigens.

Another application of anti-*H. pylori* polypeptide antibodies of the invention is in the immunological screening of cDNA libraries constructed in expression vectors such as λgt11, λgt18-23, λZAP, and λORF8. Messenger libraries of this type, having coding sequences inserted in the correct reading frame and orientation, can produce fusion proteins. For instance, λgt11 will produce fusion proteins whose amino termini consist of β-galactosidase amino acid sequences and whose carboxy termini consist of a foreign polypeptide. Antigenic epitopes of a subject *H. pylori* polypeptide can then be detected with antibodies, as, for example, reacting nitrocellulose filters lifted from infected plates with anti-*H. pylori* polypeptide antibodies. Phage, scored by this assay, can then be isolated from the infected plate. Thus, the presence of *H. pylori* gene homologs can be detected and cloned from other species, and alternate isoforms (including splicing variants) can be detected and cloned.

VIII. Kits Containing Nucleic Acids, Polypeptides or Antibodies of the Invention

The nucleic acid, polypeptides and antibodies of the invention can be combined with other reagents and articles to form kits. Kits for diagnostic purposes typically comprise the nucleic acid, polypeptides or antibodies in vials or other suitable vessels. Kits typically comprise other reagents for performing hybridization reactions, polymerase chain reactions (PCR), or for reconstitution of lyophilized components, such as aqueous media, salts, buffers, and the like. Kits may also comprise reagents for sample processing such as detergents, chaotropic salts and the like. Kits may also comprise immobilization means such as particles, supports, wells, dipsticks and the like. Kits may also comprise labeling means such as dyes, developing reagents, radioisotopes, fluorescent agents, luminescent or chemiluminescent agents, enzymes, intercalating agents and the like. With the nucleic acid and amino acid sequence information provided herein, individuals skilled in art can readily assemble kits to serve their particular purpose. Kits further can include instructions for use.

30

IX. Drug Screening Assays Using *H. pylori* Polypeptides

By making available purified and recombinant *H. pylori* polypeptides, the present invention provides assays which can be used to screen for drugs which are either agonists or antagonists of the normal cellular function, in this case, of the subject *H. pylori* polypeptides, or of their role in intracellular signaling. Such inhibitors or potentiators may be useful as new therapeutic agents to combat *H. pylori* infections in humans. A variety of assay formats will suffice and, in light of the present inventions, will be comprehended by the skilled artisan.

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In many drug screening programs which test libraries of compounds and natural extracts, high throughput assays are desirable in order to maximize the number of compounds surveyed in a given period of time. Assays which are performed in cell-free systems, such as may be derived with purified or semi-purified proteins, are often preferred
5 as "primary" screens in that they can be generated to permit rapid development and relatively easy detection of an alteration in a molecular target which is mediated by a test compound. Moreover, the effects of cellular toxicity and/or bioavailability of the test compound can be generally ignored in the *in vitro* system, the assay instead being focused primarily on the effect of the drug on the molecular target as may be manifest in an
10 alteration of binding affinity with other proteins or change in enzymatic properties of the molecular target. Accordingly, in an exemplary screening assay of the present invention, the compound of interest is contacted with an isolated and purified *H. pylori* polypeptide.

Screening assays can be constructed *in vitro* with a purified *H. pylori* polypeptide or fragment thereof, such as an *H. pylori* polypeptide having enzymatic activity, such that the
15 activity of the polypeptide produces a detectable reaction product. The efficacy of the compound can be assessed by generating dose response curves from data obtained using various concentrations of the test compound. Moreover, a control assay can also be performed to provide a baseline for comparison. Suitable products include those with distinctive absorption, fluorescence, or chemi-luminescence properties, for example,
20 because detection may be easily automated. A variety of synthetic or naturally occurring compounds can be tested in the assay to identify those which inhibit or potentiate the activity of the *H. pylori* polypeptide. Some of these active compounds may directly, or with chemical alterations to promote membrane permeability or solubility, also inhibit or potentiate the same activity (e.g., enzymatic activity) in whole, live *H. pylori* cells.
25

EXEMPLIFICATION

I. Cloning and Sequencing of *H. pylori* DNA

H. pylori chromosomal DNA was isolated according to a basic DNA protocol
30 outlined in Schleif R.F. and Wensink P.C., *Practical Methods in Molecular Biology*, p.98, Springer-Verlag, NY., 1981, with minor modifications. Briefly, cells were pelleted, resuspended in TE (10 mM Tris, 1 mM EDTA, pH 7.6) and GES lysis buffer (5.1 M guanidium thiocyanate, 0.1 M EDTA, pH 8.0, 0.5% N-laurylsarcosine) was added. Suspension was chilled and ammonium acetate (NH₄Ac) was added to final concentration
35 of 2.0 M. DNA was extracted, first with chloroform, then with phenol-chloroform, and reextracted with chloroform. DNA was precipitated with isopropanol, washed twice with 70% EtOH, dried and resuspended in TE.

Following isolation whole genomic *H. pylori* DNA was nebulized (Bodenteich et al., *Automated DNA Sequencing and Analysis* (J.C. Venter, ed.), Academic Press, 1994) to

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a median size of 2000 bp. After nebulization, the DNA was concentrated and separated on a standard 1% agarose gel. Several fractions, corresponding to approximate sizes 900-1300 bp, 1300-1700 bp, 1700-2200 bp, 2200-2700 bp, were excised from the gel and purified by the GeneClean procedure (Bio101, Inc.).

5 The purified DNA fragments were then blunt-ended using T4 DNA polymerase. The healed DNA was then ligated to unique BstXI-linker adapters (5' TCTAGACCACCTGC and 5' GTGGTCTAGA in 100-1000 fold molar excess). These linkers are complimentary to the BstXI-cut pMPX vectors, while the overhang is not self-complimentary. Therefore, the linkers will not concatemerize nor will the cut-vector
10 religate itself easily. The linker-adopted inserts were separated from the unincorporated linkers on a 1% agarose gel and purified using GeneClean. The linker-adopted inserts were then ligated to each of the 20 pMPX vectors to construct a series of "shotgun" subclone libraries. The vectors contain an out-of-frame lacZ gene at the cloning site which becomes in-frame in the event that an adapter-dimer is cloned, allowing these to be avoided by their
15 blue-color.

All subsequent steps were based on the multiplex DNA sequencing protocols outlined in Church G.M. and Kieffer-Higgins S., *Science* 240:185-188, 1988. Only major modifications to the protocols are highlighted. Briefly, each of the 20 vectors was then transformed into DH5 α competent cells (Gibco/BRL, DH5 α transformation protocol). The
20 libraries were assessed by plating onto antibiotic plates containing ampicillin, methicillin and IPTG/Xgal. The plates were incubated overnight at 37°C. Successful transformants were then used for plating of clones and pooling into the multiplex pools. The clones were picked and pooled into 40 ml growth medium cultures. The cultures were grown overnight at 37°C. DNA was purified using the Qiagen Midi-prep kits and Tip-100 columns
25 (Qiagen, Inc.). In this manner, 100 μ g of DNA was obtained per pool. Fifteen 96-well plates of DNA were generated to obtain a 5-10 fold sequence redundancy assuming 250-300 base average read-lengths.

These purified DNA samples were then sequenced using the multiplex DNA sequencing based on chemical degradation methods (Church G.M. and Kieffer-Higgins S.,
30 *Science* 240:185-188, 1988) or by Sequithrem (Epicenter Technologies) dideoxy sequencing protocols. The sequencing reactions were electrophoresed and transferred onto nylon membranes by direct transfer electrophoresis from 40 cm gels (Richterich P. and Church G.M., *Methods in Enzymology* 218:187-222, 1993) or by electroblotting (Church,
supra). 24 samples were run per gel. 45 successful membranes were produced by chemical sequencing and 8 were produced by dideoxy sequencing. The DNA was covalently bound
35 to the membranes by exposure to ultraviolet light, and hybridized with labeled oligonucleotides complimentary to tag sequences on the vectors (Church, *supra*). The membranes were washed to rinse off non-specifically bound probe, and exposed to X-ray film to visualize individual sequence ladders. After autoradiography, the hybridized probe

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was removed by incubation at 65° C, and the hybridization cycle repeated with another tag sequence until the membrane had been probed 38 times for chemical sequencing membranes and 10 times for the dideoxy sequencing membranes. Thus, each gel produced a large number of films, each containing new sequencing information. Whenever a new
5 blot was processed, it was initially probed for an internal standard sequence added to each of the pools.

Digital images of the films were generated using a laser-scanning densitometer (Molecular Dynamics, Sunnyvale, CA). The digitized images were processed on computer workstations (VaxStation 4000's) using the program REPLICA™ (Church et al.,
10 *Automated DNA Sequencing and Analysis* (J.C. Venter, ed.), Academic Press, 1994). Image processing included lane straightening, contrast adjustment to smooth out intensity differences, and resolution enhancement by iterative gaussian deconvolution. The sequences were then automatically picked in REPLICA™ and displayed for interactive proofreading before being stored in a project database. The proofreading was accomplished
15 by a quick visual scan of the film image followed by mouse clicks on the bands of the displayed image to modify the base calls. Many of the sequence errors could be detected and corrected because multiple sequence reads covering the same portion of the genomic DNA provide adequate sequence redundancy for editing. Each sequence automatically received an identification number (corresponding to microtiter plate, probe information,
20 and lane set number). This number serves as a permanent identifier of the sequence so it is always possible to identify the original of any particular sequence without recourse to a specialized database.

Routine assembly of *H. pylori* sequences was done using the program FALCON (Church, Church et al., *Automated DNA Sequencing and Analysis* (J.C. Venter, ed.),
25 Academic Press, 1994). This program has proven to be fast and reliable for most sequences. The assembled contigs were displayed using a modified version of GelAssemble, developed by the Genetics Computer Group (GCG) (Devereux et al., *Nucleic Acid Res.* 12:387-95, 1984) that interacts with REPLICA™. This provided for an integrated editor that allows multiple sequence gel images to be instantaneously called up
30 from the REPLICA™ database and displayed to allow rapid scanning of contigs and proofreading of gel traces where discrepancies occurred between different sequence reads in the assembly.

II. Identification, cloning and expression of recombinant *H. pylori* DNA sequences

To facilitate the cloning, expression and purification of membrane and secreted proteins from *H. pylori* a powerful gene expression system, the pET System (Novagen), for cloning and expression of recombinant proteins in *E. coli*, was selected. Also, a DNA sequence encoding a peptide tag, the His-Tag, was fused to the 3' end of DNA sequences of interest in order to facilitate purification of the recombinant protein products. The 3' end
35

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was selected for fusion in order to avoid alteration of any 5' terminal signal sequence. The exception to the above was ppiB, a gene cloned for use as a control in the expression studies. In this study, the sequence for *H. pylori* ppiB contains a DNA sequence encoding a His-Tag fused to the 5' end of the full length gene, because the protein product of this gene does not contain a signal sequence and is expressed as a cytosolic protein.

PCR Amplification and cloning of DNA sequences containing ORF's for membrane and secreted proteins from the J99 Strain of Helicobacter pylori.

Sequences chosen (from the list of the DNA sequences of the invention) for cloning from the J99 strain of *H. pylori* were prepared for amplification cloning by polymerase chain reaction (PCR). Synthetic oligonucleotide primers (Table 4) specific for the 5' and 3' ends of open reading frames (ORFs) were designed and purchased (GibcoBRL Life Technologies, Gaithersburg, MD, USA). All forward primers (specific for the 5' end of the sequence) were designed to include an NcoI cloning site at the extreme 5' terminus, except for HpSeq. 4821082 (SEQ ID NO: 820) where NdeI was used. These primers were designed to permit initiation of protein translation at a methionine residue followed by a valine residue and the coding sequence for the remainder of the native *H. pylori* DNA sequence. An exception is *H. pylori* sequence 4821082 (SEQ ID NO: 820) where the initiator methionine is immediately followed by the remainder of the native *H. pylori* DNA sequence. All reverse primers (specific for the 3' end of any *H. pylori* ORF) included a EcoRI site at the extreme 5' terminus to permit cloning of each *H. pylori* sequence into the reading frame of the pET-28b. The pET-28b vector provides sequence encoding an additional 20 carboxy-terminal amino acids (only 19 amino acids in HpSeq. 26380318 (SEQ ID NO: 658) and HpSeq. 14640637 (SEQ ID NO: 447)) including six histidine residues (at the extreme C-terminus), which comprise the His-Tag. An exception to the above, as noted earlier, is the vector construction for the ppiB gene. A synthetic oligonucleotide primer specific for the 5' end of ppiB gene encoded a BamHI site at its extreme 5' terminus and the primer for the 3' end of the ppiB gene encoded a XhoI site at its extreme 5' terminus.

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TABLE 4
Oligonucleotide primers used for PCR amplification of *H. pylori* DNA sequences

Outer membrane Proteins	Forward primer 5' to 3'	Reverse Primer 5' to 3'
16225006 (SEQ ID NO: 465)	5'-TATACCATGGTGGG CGCTAA-3' (SEQ ID NO:1897)	5'-ATGAATTGGAGTAAG GATTTTG-3' (SEQ ID NO:1898)
26054702 (SEQ ID NO: 649)	5'-TTAACCATGGTGAAA AGCGATA-3' (SEQ ID NO:1899)	5'-TAGAATTCCGCATAAC GATCAATC-3' (SEQ ID NO:1900)
7116626 (SEQ ID NO: 865)	5'-ATATCCATGGTGAGT TTGATGA-3' (SEQ ID NO:1901)	5'-ATGAATTCAATTTC TATTGCCA-3' (SEQ ID NO:1902)
29479681 (SEQ ID NO: 677)	5'-AATTCCATGGTGGGG GCTATG-3' (SEQ ID NO:1903)	5'-ATGAATTCTCGATAG CCAAAATC-3' (SEQ ID NO:1904)
14640637 (SEQ ID NO: 447)	5'-AATTCCATGGTGCAT AACTTCCATT-3' (SEQ ID NO:1905)	5'-AAGAATTCTCTAGCA TCCAAATGGA-3' (SEQ ID NO:1906)
Periplasmic/ Secreted Proteins		
30100332 (SEQ ID NO: 685)	5'-ATTCCATGGTCATG TCTCATATT-3' (SEQ ID NO:1907)	5'-ATGAATTCCATCTTT TATTCCAC-3' (SEQ ID NO:1908)
4721061 (SEQ ID NO: 812)	5'-AACCATGGTGATT TAAGCATTGAAAG-3' (SEQ ID NO:1909)	5'-AAGAATTCCACTCA AAATTTTTAACAG-3' (SEQ ID NO:1910)
Other Surface Proteins		
4821082 (SEQ ID NO: 820)	5'-GATCATCCATATGTT ATCTCTAAT-3' (SEQ ID NO:1911)	5'-TGAATTCAACCATT TAACCCTG-3' (SEQ ID NO:1912)
978477 (SEQ ID NO: 880)	5'-TATACCATGGTGAA ATTTCCTTTA-3' (SEQ ID NO:1913)	5'-AGAATTCAATTGCG TCTTGAAAAG-3' (SEQ ID NO:1914)
Inner Membrane Protein		
26380318 (SEQ ID NO: 658)	5'-TATACCATGGTGAT GGACAAACTC-3' (SEQ ID NO:1915)	5'-ATGAATTCCCACTT GGGCGATA-3' (SEQ ID NO:1916)
Cytoplasmic Protein		
ppi	5'-TTATGGATCCAAAC CAATTAAGGACT-3' (SEQ ID NO:1917)	5'-TATCTCGAGTTATA GAGAAGGGC-3' (SEQ ID NO:1918)

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Genomic DNA prepared from the J99 strain of *H. pylori* (ATCC #55679) was used as the source of template DNA for PCR amplification reactions (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). To amplify a DNA sequence containing an *H. pylori* ORF, genomic DNA (50 nanograms) was

- 5 introduced into a reaction vial containing 2 mM MgCl₂, 1 micromolar synthetic oligonucleotide primers (forward and reverse primers) complementary to and flanking a defined *H. pylori* ORF, 0.2 mM of each deoxynucleotide triphosphate; dATP, dGTP, dCTP, dTTP and 2.5 units of heat stable DNA polymerase (AmpliTaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA) in a final volume of 100 microliters. The following
10 thermal cycling conditions were used to obtain amplified DNA products for each ORF using a Perkin Elmer Cetus/ GeneAmp PCR System 9600 thermal cycler:

- Sequences 26054702 (SEQ ID NO: 649), 7116626 (SEQ ID NO: 865), 29479681 (SEQ ID NO: 677), 30100332 (SEQ ID NO: 685), 4821082 (SEQ ID NO: 820) and 978477 (SEQ ID NO: 880);
15 Denaturation at 94°C for 2 min,
2 cycles at 94°C for 15 sec, 30°C for 15 sec and 72°C for 1.5 min
23 cycles at 94°C for 15 sec, 55°C for 15 sec and 72°C for 1.5 min
Reactions were concluded at 72°C for 6 minutes.
20 Sequence 16225006 (SEQ ID NO: 465);
Denaturation at 94°C for 2 min,
25 cycles at 95°C for 15 sec, 55°C for 15 sec and 72°C for 1.5 min
Reaction was concluded at 72°C for 6 minutes.
25 Sequence 4721061 (SEQ ID NO: 812);
Denaturation at 94°C for 2 min.
2 cycles at 94°C for 15 sec, 36°C for 15 sec and 72°C for 1.5 min
23 cycles at 94°C for 15 sec, 60°C for 15 sec and 72°C for 1.5 min
30 Reactions were concluded at 72°C for 6 minutes.

- Sequence 26380318 (SEQ ID NO: 658);
Denaturation at 94°C for 2 min.
2 cycles at 94°C for 15 sec, 38°C for 15 sec and 72°C for 1.5 min
35 23 cycles at 94°C for 15 sec, 62°C for 15 sec and 72°C for 1.5 min
Reactions were concluded at 72°C for 6 minutes.

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Sequence 14640637 (SEQ ID NO: 447);

Denaturation at 94°C for 2 min,

2 cycles at 94°C for 15 sec, 33°C for 15 sec and 72°C for 1.5 min

30 cycles at 94°C for 15 sec, 55°C for 15 sec and 72°C for 1.5 min

5 Reactions were concluded at 72°C for 6 minutes.

Conditions for amplification of *H. pylori* ppiB;

Denaturation at 94°C for 2 min,

2 cycles at 94°C for 15 sec, 32°C for 15 sec and 72°C for 1.5 min

10 25 cycles at 94°C for 15 sec, 56°C for 15 sec and 72°C for 1.5 min

Reactions were concluded at 72°C for 6 minutes

Upon completion of thermal cycling reactions, each sample of amplified DNA was washed and purified using the Qiaquick Spin PCR purification kit (Qiagen, Gaithersburg, MD, USA). All amplified DNA samples were subjected to digestion with the restriction endonucleases, NcoI and EcoRI (New England BioLabs, Beverly, MA, USA), or in the case of HpSeq. 4821082 (SEQ ID NO: 820), with NdeI and EcoRI (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). DNA samples were then subjected to electrophoresis on 1.0 % NuSeive (FMC BioProducts, Rockland, ME USA) agarose gels. DNA was visualized by exposure to ethidium bromide and long wave uv irradiation. DNA contained in slices isolated from the agarose gel was purified using the Bio 101 GeneClean Kit protocol (Bio 101 Vista, CA, USA)

Cloning of H. pylori DNA sequences into the pET-28b prokaryotic expression vector.

The pET-28b vector was prepared for cloning by digestion with NcoI and EcoRI, or 25 in the case of *H. pylori* sequence 4821082 (SEQ ID NO: 820) with NdeI and EcoRI (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). In the case of cloning ppiB, the pET-28a vector, which encodes a His-Tag that can be fused to the 5' end of an inserted gene, was used and the cloning site prepared for cloning with the ppiB gene by digestion with BamHI and XhoI restriction endonucleases.

30 Following digestion, DNA inserts were cloned (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994) into the previously digested pET-28b expression vector, except for the amplified insert for ppiB, which was cloned into the pET-28a expression vector. Products of the ligation reaction were then used to transform the BL21 strain of *E. coli* (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994) as described below.

Transformation of competent bacteria with recombinant plasmids

Competent bacteria, *E. coli* strain BL21 or *E. coli* strain BL21(DE3), were transformed with recombinant pET expression plasmids carrying the cloned *H. pylori*

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sequences according to standard methods (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). Briefly, 1 microliter of ligation reaction was mixed with 50 microliters of electrocompetent cells and subjected to a high voltage pulse, after which, samples were incubated in 0.45 milliliters SOC medium (0.5% yeast extract, 5 2.0 % tryptone, 10 mM NaCl, 2.5 mM KCl, 10 mM MgCl₂, 10 mM MgSO₄ and 20, mM glucose) at 37°C with shaking for 1 hour. Samples were then spread on LB agar plates containing 25 microgram/ml kanamycin sulfate for growth overnight. Transformed colonies of BL21 were then picked and analyzed to evaluate cloned inserts as described below.

10

Identification of recombinant pET expression plasmids carrying H. pylori sequences

Individual BL21 clones transformed with recombinant pET-28b-H.pylori ORFs were analyzed by PCR amplification of the cloned inserts using the same forward and reverse primers, specific for each *H. pylori* sequence, that were used in the original PCR 15 amplification cloning reactions. Successful amplification verified the integration of the *H. pylori* sequences in the expression vector (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994).

20

Isolation and Preparation of plasmid DNA from BL21 transformants

Individual clones of recombinant pET-28b vectors carrying properly cloned *H. pylori* ORFs were picked and incubated in 5 mls of LB broth plus 25 microgram/ml kanamycin sulfate overnight. The following day plasmid DNA was isolated and purified 25 using the Qiagen plasmid purification protocol (Qiagen Inc., Chatsworth, CA, USA).

25

Expression of recombinant H. pylori sequences in E. coli

The pET vector can be propagated in any *E. coli* K-12 strain e.g. HMS174, HB101, JM109, DH5, etc. for the purpose of cloning or plasmid preparation. Hosts for expression include *E. coli* strains containing a chromosomal copy of the gene for T7 RNA polymerase. These hosts are lysogens of bacteriophage DE3, a lambda derivative that carries the lacI 30 gene, the lacUV5 promoter and the gene for T7 RNA polymerase. T7 RNA polymerase is induced by addition of isopropyl-B-D-thiogalactoside (IPTG), and the T7 RNA polymerase transcribes any target plasmid, such as pET-28b, carrying a T7 promoter and a gene of interest. Strains used include: BL21(DE3) (Studier, F.W., Rosenberg, A.H., Dunn, J.J., and Dubendorff, J.W. (1990) Meth. Enzymol. 185, 60-89).

35

To express recombinant *H. pylori* sequences, 50 nanograms of plasmid DNA isolated as described above was used to transform competent BL21(DE3) bacteria as described above (provided by Novagen as part of the pET expression system kit). The lacZ gene (beta-galactosidase) was expressed in the pET-System as described for the *H. pylori* recombinant constructions. Transformed cells were cultured in SOC medium for 1 hour,

and the culture was then plated on LB plates containing 25 micrograms/ml kanamycin sulfate. The following day, bacterial colonies were pooled and grown in LB medium containing kanamycin sulfate (25 micrograms/ml) to an optical density at 600 nm of 0.5 to 1.0 O.D. units, at which point, 1 millimolar IPTG was added to the culture for 3 hours to induce gene expression of the *H. pylori* recombinant DNA constructions .

After induction of gene expression with IPTG, bacteria were pelleted by centrifugation in a Sorvall RC-3B centrifuge at 3500 x g for 15 minutes at 4°C. Pellets were resuspended in 50 milliliters of cold 10 mM Tris-HCl, pH 8.0, 0.1 M NaCl and 0.1 mM EDTA (STE buffer). Cells were then centrifuged at 2000 x g for 20 min at 4°C. Wet pellets were weighed and frozen at -80°C until ready for protein purification.

III. Purification of recombinant proteins from *E. coli*

Analytical Methods

The concentrations of purified protein preparations were quantified spectrophotometrically using absorbance coefficients calculated from amino acid content (Perkins, S.J. 1986 Eur. J. Biochem. 157, 169-180). Protein concentrations were also measured by the method of Bradford, M.M. (1976) Anal. Biochem. 72, 248-254, and Lowry, O.H., Rosebrough, N., Farr, A.L. & Randall, R.J. (1951) J. Biol. Chem. 193, pages 265-275, using bovine serum albumin as a standard.

SDS-polyacrylamide gels (12% or 4.0 to 25 % acrylamide gradient gels) were purchased from BioRad (Hercules, CA, USA), and stained with Coomassie blue. Molecular weight markers included rabbit skeletal muscle myosin (200 kDa), *E. coli* (-galactosidase (116 kDa), rabbit muscle phosphorylase B (97.4 kDa), bovine serum albumin (66.2 kDa), ovalbumin (45 kDa), bovine carbonic anhydrase (31 kDa), soybean trypsin inhibitor (21.5 kDa), egg white lysozyme (14.4 kDa) and bovine aprotinin (6.5 kDa).

1. Purification of soluble proteins

All steps were carried out at 4°C. Frozen cells were thawed, resuspended in 5 volumes of lysis buffer (20 mM Tris, pH 7.9, 0.5 M NaCl, 5 mM imidazole with 10% glycerol, 0.1 % 2-mercaptoethanol, 200 µg/ ml lysozyme, 1 mM phenylmethylsulfonyl fluoride (PMSF), and 10 ug/ml each of leupeptin, aprotinin, pepstatin, L-1-chloro-3-[4-tosylamido]-7-amino-2-heptanone (TLCK), L-1-chloro-3-[4-tosylamido]-4-phenyl-2-butanone (TPCK), and soybean trypsin inhibitor, and ruptured by several passages through a small volume microfluidizer (Model M-110S, Microfluidics International Corporation, Newton, MA). The resultant homogenate was made 0.1 % Brij 35, and centrifuged at 100,000 x g for 1 hour to yield a clear supernatant (crude extract).

Following filtration through a 0.8 µm Supor filter (Gelman Sciences, FRG) the crude extract was loaded directly onto a Ni²⁺- nitrilotriacetate-agarose (NTA) with a 5 milliliter bed volume (Hochuli, E.. Dbeli, H., and Schacheer, A. (1987) J. Chromatography

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411, 177-184) pre-equilibrated in lysis buffer containing 10 % glycerol, 0.1 % Brij 35 and 1 mM PMSF. The column was washed with 250 ml (50 bed volumes) of lysis buffer containing 10 % glycerol, 0.1 % Brij 35, and was eluted with sequential steps of lysis buffer containing 10 % glycerol, 0.05 % Brij 35, 1 mM PMSF, and 20, 100, 200, and 500 5 mM imidazole in succession. Fractions were monitored by absorbance at OD₂₈₀ nm, and peak fractions were analyzed by SDS-PAGE. Fractions containing the recombinant protein eluted at 100 mM imidazole.

10 *Recombinant protein 14640637 (SEQ ID NO: 447) and proteins, beta-galactosidase (lacZ) and peptidyl-prolyl cis-trans isomerase (ppiB)*

Fractions containing the recombinant proteins from the Ni²⁺-NTA-agarose columns were pooled and then concentrated to approximately 5 ml by centrifugal filtration (Centriprep-10, Amicon, MA), and loaded directly onto a 180-ml column (1.6 X 91 cm) of Sephadryl S-100 HR gel filtration medium equilibrated in Buffer A (10 mM Hepes, pH 7.5, 15 150 mM NaCl, 0.1 mM EGTA) and run in Buffer A at 18 ml/h. Fractions containing the recombinant protein were identified by absorbance at 280 nm and analyzed by SDS-PAGE. Fractions were pooled and concentrated by centrifugal filtration.

15 *Recombinant protein 7116626 (SEQ ID NO: 865)*

20 Fractions containing the recombinant protein from the Ni²⁺-NTA-agarose column were pooled and dialyzed overnight against 1 liter of dialysis buffer (10 mM MOPS, pH 6.5, 50 mM NaCl, 0.1 mM EGTA, 0.02% Brij 35 and 1 mM PMSF). In the morning, a fine white precipitate was removed by centrifugation and the resulting supernatant was loaded onto an 8 ml (8 x 75 mm) MonoS high performance liquid chromatography column 25 (Pharmacia Biotechnology, Inc., Piscataway, NJ, USA) equilibrated in buffer B (10 mM MOPS, pH 6.5, 0.1 mM EGTA) containing 50 mM NaCl. The column was washed with 10 bed volumes of buffer B containing 50 mM NaCl, and developed with a 50-ml linear gradient of increasing NaCl (50 to 500 mM). Recombinant protein 7116626 (SEQ ID NO: 865) eluted as a sharp peak at 300 mM NaCl.

30

2. Purification of insoluble proteins from inclusion bodies

The following steps were carried out at 4°C. Cell pellets were resuspended in lysis buffer with 10% glycerol 200 µg/ ml lysozyme, 5 mM EDTA, 1mM PMSF and 0.1 % - mercaptoethanol. After passage through the cell disrupter, the resulting homogenate was 35 made 0.2 % deoxycholate, stirred 10 minutes, then centrifuged at 20,000 x g, for 30 min. The pellets were washed with lysis buffer containing 10 % glycerol, 10 mM EDTA, 1% Triton X-100, 1 mM PMSF and 0.1% -mercaptoethanol, followed by several washes with lysis buffer containing 1 M urea, 1 mM PMSF and 0.1 % 2-mercaptoethanol. The resulting

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white pellet was composed primarily of inclusion bodies, free of unbroken cells and membranous materials..

5 *Recombinant proteins 26054702 (SEQ ID NO: 649), 16225006 (SEQ ID NO: 465),
30100332 (SEQ ID NO: 685), 4721061 (SEQ ID NO: 812)*

The following steps were carried out at room temperature. Purified inclusion bodies
were dissolved in 20 ml 8.0 M urea in lysis buffer with 1 mM PMSF and 0.1 % 2-
mercaptoethanol, and incubated at room temperature for 1 hour. Materials that did not
dissolve were removed by centrifugation. The clear supernatant was filtered, then loaded
10 onto a Ni²⁺ -NTA agarose column pre-equilibrated in 8.0 M urea in Lysis Buffer. The
column was washed with 250 ml (50 bed volumes) of lysis buffer containing 8 M urea, 1.0
mM PMSF and 0.1 % 2-mercaptoethanol, and developed with sequential steps of lysis
buffer containing 8M urea, 1 mM PMSF, 0.1 % 2-mercaptoethanol and 20, 100, 200, and
500 mM imidazole in succession. Fractions were monitored by absorbance at OD₂₈₀ nm,
15 and peak fractions were analyzed by SDS-PAGE. Fractions containing the recombinant
protein eluted at 100 mM imidazole.

20 *Recombinant proteins 29479681 (SEQ ID NO: 677), 978477 (SEQ ID NO: 880), 26380318
(SEQ ID NO: 658)*

20 The pellet containing the inclusion bodies was solubilized in buffer B containing 8
M urea, 1 mM PMSF and 0.1 % 2-mercaptoethanol, and incubated for 1 hour at room
temperature. Insoluble materials were removed by centrifugation at 20,000 x g for 30 min,
and the cleared supernatant was loaded onto a 15 ml (1.6 x 7.5 cm) SP-Sepharose column
pre-equilibrated in buffer B, 6 M urea, 1 mM PMSF, 0.1 % 2-mercaptoethanol. After
25 washing the column with 10 bed volumes, the column was developed with a linear gradient
from 0 to 500 mM NaCl.

Dialysis and concentration of protein samples

30 Urea was removed slowly from the protein samples by dialysis against Tris-
buffered saline (TBS; 10 mM Tris pH 8.0, 150 mM NaCl) containing 0.5 % deoxycholate
(DOC) with sequential reduction in urea concentration as follows; 6M, 4M, 3M, 2M, 1M,
0.5 M and finally TBS without any urea. Each dialysis step was conducted for a minimum
of 4 hours at room temperature.

35 After dialysis, samples were concentrated by pressure filtration using Amicon
stirred-cells. Protein concentrations were measured using the methods of Perkins (1986
Eur. J. Biochem. 157, 169-180), Bradford ((1976) Anal. Biochem. 72, 248-254) and Lowry
((1951) J. Biol. Chem. 193, pages 265-275).

The recombinant proteins purified by the methods described above are summarized
in Table 5 below.

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TABLE 5

J99 Sequence Identifier	Homolog Identified by Blast	Gene symbol of Homolog	Bacterial cell fraction used to purify recombinant proteins	Method of purification	Relative MW on SDS-PAGE gel	Final concentration of purified protein	Composition of buffer
Outer Membrane Proteins							
16225006 (SEQ ID NO: 465)	P28635	YEAC	Inclusion bodies	His-Tag	18 kDa	5 mg/ml	B
26054702 (SEQ ID NO: 649)	P15929	fgh	Inclusion bodies	His-Tag	37 kDa	1.18 mg/ml	B
					----	as dry pellet	
7116626 (SEQ ID NO: 865)	P26093	e(P4)	Soluble fraction	His-Tag	29 kDa	0.8 mg/ml	A
						1.85 mg/ml	C
29479681 (SEQ ID NO: 677)	P13036	feeA	Inclusions bodies	SP-Sephadex	23 kDa	2.36 mg/ml	B
						0.5 mg/ml	B
14640637 (SEQ ID NO: 447)	P16665	TPF1	Soluble fraction	His-Tag	17 kDa	2.4 mg/ml	A
					gel filtration S100 HR		

TABLE 5 (continued)

Periplasmic/Secreted Protein		dppA	Inclusion bodies	His-Tag	11 kDa	2.88 mg/ml	B
3010032 (SEQ ID NO: 685)	P23847						
4721061 (SEQ ID NO: 812)	P36175	GCP	Inclusion bodies	His-Tag	38 kDa	2.8 mg/ml	B
Other Surface Proteins							
4821082 (SEQ ID NO: 820)	P08089	M protein	Inclusion bodies	His-Tag	20 kDa	1.16 mg/ml	B
978477 (SEQ ID NO: 880)	L28919	FBB54	Inclusion bodies	SP-Sephadose	44 kDa	2.56 mg/ml	B
Inner Membrane Proteins							
26380318 (SEQ ID NO: 658)	P15933	fIC	Inclusion bodies	SP-Sephadose	11 kDa	0.3 mg/ml	B
Control Proteins with His-Tag							
P00722	lacZ	Soluble fraction	His-Tag	116 kDa	10 mg/ml	A	
			gel filtration S200 HR				
		ppiB	Soluble fraction	His-Tag	21 kDa	4.4 mg/ml	A
				gel filtration S100 HR			
Buffer compositions:							
A=10 mM Hepes pH 7.5, 150 mM NaCl, 0.1 mM EGTA							
B= 10 mM Tris pH 8.0, 150 mM NaCl, 0.5% DOC							
C= 10 mM MOPS pH 6.5, 300 mM NaCl, 0.1 EGTA							

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IV. Analysis of *H. pylori* proteins as Vaccine candidates

To investigate the immunomodulatory effect of *H. pylori* proteins, a mouse/*H. pylori* model was used. This model mimics the human *H. pylori* infection in many respects. The focus is on the effect of oral immunization in *H. pylori* infected animals in 5 order to test the concept of therapeutic oral immunotherapy.

Animals

Female SPF BALB/c mice were purchased from Bomholt Breeding center (Denmark). They were kept in ordinary makrolon cages with free supply of water and food. 10 The animals were 4-6 weeks old at arrival.

Infection

After a minimum of one week of acclimatization, the animals were infected with a type 2 strain (VacA negative) of *H. pylori* (strain 244, originally isolated from an ulcer 15 patient). In our hands, this strain has earlier proven to be a good colonizer of the mouse stomach. The bacteria were grown overnight in Brucella broth supplemented with 10 % fetal calf serum, at 37°C in a microaerophilic atmosphere (10% CO₂, 5%O₂). The animals were given an oral dose of omeprazole (400 µmol/kg) and 3-5 h after this an oral 20 inoculation of *H. pylori* in broth (approximately 10⁸ cfu/animal). Positive take of the infection was checked in some animals 2-3 weeks after the inoculation.

Antigens

Recombinant *H. pylori* antigens were chosen based on their association with externally exposed *H. pylori* cell membrane. These antigens were selected from the 25 following groups: (1.) Outer Membrane Proteins; (2.) Periplastic/Secreted proteins; (3.) Outer Surface proteins; and (4.) Inner Membrane proteins. All recombinant proteins were constructed with a hexa-HIS tag for purification reasons and the non-*Helicobacter pylori* control protein (β -galactosidase from *E. coli*; LacZ), was constructed in the same way.

All antigens were given in a soluble form, i.e. dissolved in either a HEPES buffer or 30 in a buffer containing 0.5% Deoxycholate (DOC).

The antigens are listed in Table 6 below.

Table 6

Helicobacter pylori proteins

35 **Outer membrane Proteins**
SEQ ID NO:447
SEQ ID NO:677
SEQ ID NO:865
40 SEQ ID NO:812
SEQ ID NO:465

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Periplastic/Secreted proteins
SEQ ID NO:685

5 **Other cell envelope proteins**

SEQ ID NO:820

SEQ ID NO:880

10 **Flagella-associated proteins**
 SEQ ID NO:658

Control proteins

β-galactosidase (LacZ)

15 *Immunizations*

Ten animals in each group were immunized 4 times over a 34 day period (day 1, 15, 25 and 35). Purified antigens in solution or suspension were given at a dose of 100 µg/mouse. As an adjuvant, the animals were also given 10 µg/mouse of Cholera toxin (CT) with each immunization. Omeprazole (400 µmol/kg) was given orally to the animals 3-5 h prior to immunization as a way of protecting the antigens from acid degradation. Infected control animals received HEPES buffer + CT or DOC buffer + CT. Animals were sacrificed 2-4 weeks after final immunization. A general outline of the study is shown in Table 7 below.

25 Table 7

Study outline, therapeutic immunization:

Mice were all infected with *H. pylori* strain Ah244 at day 30. Proteins are listed by their SeqID #'s.

	<u>Substance</u>	<u>Mouse strain</u> <u>n=10</u>	<u>Dose/mouse</u>	<u>Dates for dosing</u>
	1. Controls, PBS	Balb/c	0,3 ml	0, 14, 24, 34
	2. Cholera toxin, 10 µg	Balb/c	0,3 ml	0, 14, 24, 34
35	3. Protein 447, 100 µg + CT 10 µg	Balb/c	0,3 ml	0, 14, 24, 34
	4. Protein 465, 100 µg + CT 10 µg	Balb/c	0,3 ml	0, 14, 24, 34
	5. Protein 649, 100 µg + CT 10 µg	Balb/c	0,3 ml	0, 14, 24, 34
	6. Protein 658, 100 µg + CT 10 µg	Balb/c	0,3 ml	0, 14, 24, 34
	7. Protein 677, 100 µg + CT 10 µg	Balb/c	0,3 ml	0, 14, 24, 34
40	8. Protein 685, 100 µg + CT 10 µg	Balb/c	0,3 ml	0, 14, 24, 34
	9. Protein 812, 100 µg + CT 10 µg	Balb/c	0,3 ml	0, 14, 24, 34
	10. Protein 820, 100 µg + CT 10 µg	Balb/c	0,3 ml	0, 14, 24, 34
	11. Protein 880, 100 µg + CT 10 µg	Balb/c	0,3 ml	0, 14, 24, 34
	12. Protein 865, 100 µg + CT 10 µg	Balb/c	0,3 ml	0, 14, 24, 34

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Analysis of infection

- Mucosal infection: The mice were sacrificed by CO₂ and cervical dislocation. The abdomen was opened and the stomach removed. After cutting the stomach along the greater curvature, it was rinsed in saline. The mucosa from the antrum and corpus of an 5 area of 25mm² was scraped separately with a surgical scalpel. The mucosa scraping was suspended in Brucella broth and plated onto Blood Skirrow selective plates. The plates were incubated under microaerophilic conditions for 3-5 days and the number of colonies was counted. The identity of *H. pylori* was ascertained by urease and catalase test and by direct microscopy or Gram staining.
- 10 The urease test was performed essentially as follows. The reagent, Urea Agar Base Concentrate, was purchased from DIFCO Laboratories, Detroit, MI (Catalog # 0284-61-3). Urea agar base concentrate was diluted 1:10 with water. 1 ml of if the diluted concentrate was mixed with 100-200 µl of actively growing *H. pylori* cells. Color change to magenta indicated that cells were urease positive.
- 15 The catalase test was performed essentially as follows. The reagent, N,N,N',N'-Tetramethyl-p-Phenylenediamine, was purchased from Sigma, St. Louis, MO (Catalog # T3134). A solution of the reagent (1% w/v in water) was prepared. *H. pylori* cells were swabbed onto Whatman filter paper and overlaid with the 1% solution. Color change to dark blue indicated that the cells were catalase positive.
- 20 Serum antibodies: From all mice serum was prepared from blood drawn by heart puncture. Serum antibodies were identified by regular ELISA techniques, where the specific antigens of *Helicobacter pylori* were plated.
- 25 Mucosal antibodies: Gentle scrapings of a defined part of the corpus and of 4 cm of duodenum were performed in 50% of the mice in order to detect the presence of antibodies in the mucous. The antibody titers were determined by regular ELISA technique as for serum antibodies.
- 30 Statistical analysis: Wilcoxon-Mann-Whitney sign rank test was used for determination of significant effects of the antigens on *Helicobacter pylori* colonization. P<0.05 was considered significant. Because the antrum is the major colonization site for *Helicobacter* most emphasis was put upon changes in the antral colonization.

Results

- Antibodies in sera: All antigens tested given together with CT gave rise to a measurable specific titer in serum. The highest responses were seen with SEQ ID NOs:865, 812, 658, 447, and 820 (see Figure 1).

Antibodies in mucus: In the mucus scrapings, specific antibodies against all antigens tested were seen. By far the strongest response was seen with SEQ ID NOs:685, followed by 447, 865, and 658 (see Figure 2).

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Therapeutic immunization effects:

All control animals (BALB/c mice) were well colonized with *H. pylori* (strain AH244) in both antrum and corpus of the stomach. Of the antigens tested 3 proteins (SEQ ID NOS: 812, 820, and 447) gave a good and significant reduction and/or eradication of the *H. pylori* infection. The degree of colonization of the antrum was lower following immunization with SEQ ID NOS: 880, 658, and 865 compared to control. The effect of SEQ ID NOS: 465, 677, and 685 did not differ from control. The control protein lacZ, i.e. the non-*H. pylori* protein, had no eradication effect and in fact had higher *Helicobacter* colonization compared to the HEPES + CT control. All data are shown in Figures 3 and 4 for proteins dissolved in HEPES and DOC respectively. Data is shown as geometric mean values. n=8-10 Wilcoxon-Mann-Whitney sign rank test * = p<0.05; x/10 = number of mice showing eradication of *H. pylori* over the total number of mice examined.

The data presented indicate that all of the *H. pylori* associated proteins included in this study, when used as oral immunogens in conjunction with the oral adjuvant CT, resulted in stimulation of an immune response as measured by specific serum and mucosal antibodies. A majority of the proteins led to a reduction, and in some cases complete clearance of the colonization of *H. pylori* in this animal model. It should be noted that the reduction or clearance was due to heterologous protection rather than homologous protection (the polypeptides were based on the *H. pylori* J99 strain sequence and used in the therapeutic immunization studies against a different (AH244) challenge strain), indicating the vaccine potential against a wide variety of *H. pylori* strains.

The highest colonization in the antrum was seen in animals treated with the non-*Helicobacter* protein LacZ, indicating that the effects seen with the *Helicobacter pylori* antigens were specific.

Taken together these data strongly support the use of these *H. pylori* proteins in a pharmaceutical formulation for the use in humans to treat and/or prevent *H. pylori* infections.

V. Sequence Variance Analysis of genes in *Helicobacter pylori* strains

Four genes were cloned and sequenced from several strains of *H. pylori* to compare the DNA and deduced amino acid sequences. This information was used to determine the sequence variation between the *H. pylori* strain, J99, and other *H. pylori* strains isolated from human patients.

35 Preparation of Chromosomal DNA.

Cultures of *H. pylori* strains (as listed in Table 10) were grown in BLBB (1% Tryptone, 1% Peptamin 0.1% Glucose, 0.2% Yeast Extract 0.5% Sodium Chloride, 5% Fetal Bovine Serum) to an OD₆₀₀ of 0.2. Cells were centrifuged in a Sorvall RC-3B at 3500 x g at 4°C for 15 minutes and the pellet resuspended in 0.95 mls of 10 mM Tris-HCl,

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0.1 mM EDTA (TE). Lysozyme was added to a final concentration of 1mg/ml along with, SDS to 1% and RNase A + T1 to 0.5mg/ml and 5 units/ml respectively, and incubated at 37°C for one hour. Proteinase K was then added to a final concentration of 0.4mg/ml and the sample was incubated at 55 C for more than one hour. NaCl was added to the sample 5 to a concentration of 0.65 M, mixed carefully, and 0.15 ml of 10% CTAB in 0.7M NaCL (final is 1% CTAB/70mM NaCL) was added followed by incubation at 65°C for 20 minutes. At this point, the samples were extracted with chloroform:isoamyl alcohol, extracted with phenol, and extracted again with chloroform:isoamyl alcohol. DNA was precipitated with either EtOH (1.5 x volumes) or isopropanol (0.6 x volumes) at -70°C for 10 minutes, washed in 70% EtOH and resuspended in TE.

PCR Amplification and cloning.

Genomic DNA prepared from twelve strains of *Helicobacter pylori* was used as the source of template DNA for PCR amplification reactions (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). To amplify a DNA sequence containing an *H. pylori* ORF, genomic DNA (10 nanograms) was introduced into a reaction vial containing 2 mM MgCl₂, 1 micromolar synthetic oligonucleotide primers (forward and reverse primers, see Table 8) complementary to and flanking a defined *H. pylori* ORF, 0.2 mM of each deoxynucleotide triphosphate; dATP, dGTP, dCTP, dTTP and 15 0.5 units of heat stable DNA polymerase (AmpliTaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA) in a final volume of 20 microliters in duplicate reactions.

Table 8
Oligonucleotide primers used for PCR amplification of *H. pylori* DNA sequences.

25

Outer membrane Proteins	Forward primer 5' to 3'	Reverse Primer 5' to 3'
SEQ ID NO:649 (for strains AH4, AH15, AH61, 5294, 5640, AH18, and AH244)	5'-TTAACCATGGTGAAAAGC GATA-3' (SEQ ID NO:1919)	5'-TAGAATTCGCCTCTAAACT TTAG-3' (SEQ ID NO:1920)
SEQ ID NO:649 (for strains AH5, 5155, 7958, AH24, and J99)	5'-TTAACCATGGTGAAAAGC GATA-3' (SEQ ID NO:1921)	5'-TAGAATTCGCATAACGATCA ATC-3' (SEQ ID NO:1922)
SEQ ID NO:865	5'-ATATCCATGGTGAGTTGATGA TGA-3' (SEQ ID NO:1923)	5'-ATGAATTCAATTTTTATTGATGCCA-3' (SEQ ID NO:1924)
SEQ ID NO:677	5'-AATTCCATGGCTATCCAAA TCCG-3' (SEQ ID NO:1925)	5'-ATGAATTGCCAAATCGTAGTATT-3' (SEQ ID NO:1926)
SEQ ID NO:764	5'-GATACCATGGAATTATGAAAAG-3' (SEQ ID NO:1927)	5'-TGAATTGAAAAAGTGTAGTTATAC-3' (SEQ ID NO:1928)

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The following thermal cycling conditions were used to obtain amplified DNA products for each ORF using a Perkin Elmer Cetus/ GeneAmp PCR System 9600 thermal cycler:

- 5 Sequences (by SEQ ID NO:) 865 and 764;
Denaturation at 94°C for 2 min,
2 cycles at 94°C for 15 sec, 30°C for 15 sec and 72°C for 1.5 min
23 cycles at 94°C for 15 sec, 55°C for 15 sec and 72°C for 1.5 min
Reactions were concluded at 72°C for 6 minutes.
- 10 Sequence (by SEQ ID NO:) 649 for strains AH5, 5155, 7958, AH24, and J99;
Denaturation at 94°C for 2 min,
2 cycles at 94°C for 15 sec, 30°C for 15 sec and 72°C for 1.5 min
25 cycles at 94°C for 15 sec, 55°C for 15 sec and 72°C for 1.5 min
- 15 Reaction was concluded at 72°C for 6 minutes.
- Sequences (by SEQ ID NO:) 677 and 649 for strains AH4, AH15, AH61, 5294, 5640, AH18, and Hp244 ;
Denaturation at 94°C for 2 min,
- 20 2 cycles at 94°C for 15 sec, 30°C for 20 sec and 72°C for 2 min
25 cycles at 94°C for 15 sec, 55°C for 20 sec and 72°C for 2 min
Reactions were concluded at 72°C for 8 minutes.

Upon completion of thermal cycling reactions, each pair of samples were combined
25 and used directly for cloning into the pCR cloning vector as described below.

Cloning of H. pylori DNA sequences into the pCR TA cloning vector.

All amplified inserts were cloned into the pCR 2.1 (pCRII in the case of *H. pylori* sequence 865) vector by the method described in the Original TA cloning kit (Invitrogen, San Diego, CA). Products of the ligation reaction were then used to transform the TOP10F' (INVaF' in the case of *H. pylori* sequence 865) strain of *E. coli* as described below.

Transformation of competent bacteria with recombinant plasmids

Competent bacteria, *E. coli* strain TOP10F' or *E. coli* strain INVaF' were transformed with recombinant pCR expression plasmids carrying the cloned *H. pylori* sequences according to standard methods (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). Briefly, 2 microliters of 0.5 micromolar BME was added to each vial of 50 microliters of competent cells.

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- Subsequently, 2 microliters of ligation reaction was mixed with the competent cells and incubated on ice for 30 minutes. The cells and ligation mixture were then subjected to a "heat shock" at 42°C for 30 seconds, and were subsequently placed on ice for an additional 2 minutes, after which, samples were incubated in 0.45 milliliters SOC medium (0.5% yeast extract, 2.0 % tryptone, 10 mM NaCl, 2.5 mM KCl, 10 mM MgCl₂, 10 mM MgSO₄ and 20, mM glucose) at 37°C with shaking for 1 hour. Samples were then spread on LB agar plates containing 25 microgram/ml kanamycin sulfate or 100 micrograms/ml ampicillin for growth overnight. Transformed colonies of TOP10F' or INVaF' were then picked and analyzed to evaluate cloned inserts as described below.
- 5 10 *Identification of recombinant PCR plasmids carrying H. pylori sequences*
- Individual TOP10F' or INVaF' clones transformed with recombinant pCR-H.pylori ORFs were analyzed by PCR amplification of the cloned inserts using the same forward and reverse primers, specific for each *H. pylori* sequence, that were used in the original PCR amplification cloning reactions. Successful amplification verified the integration of 15 the *H. pylori* sequences in the cloning vector (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994).
- Individual clones of recombinant pCR vectors carrying properly cloned *H. pylori* ORFs were picked for sequence analysis. Sequence analysis was performed on ABI Sequencers using standard protocols (Perkin Elmer) using vector-specific primers (as found 20 in PCRII or pCR2.1, Invitrogen, San Diego, CA) and sequencing primers specific to the ORF as listed in Table 9 below.

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Table 9Oligonucleotide primers used for sequencing of *H. pylori* DNA sequences.

Outer membrane Proteins	Forward primers 5' to 3'	Reverse Primers 5' to 3'
SEQ ID NO:649	5'-CCCTTCATTAGAAATCG-3' (SEQ ID NO:1929) 5'-ATTCAACCAATTCAATGCG-3' (SEQ ID NO:1930) 5'-GCCCTTTGATTGAAGCT-3' (SEQ ID NO:1931) 5'-TCGCTCCAAGATACCAAGA AGT-3' (SEQ ID NO:1932) 5'-CTTGAATTAGGGCAAAGA TCG-3' (SEQ ID NO:1933) 5'-ATGCCTTTACCCAAAGA AGT-3' (SEQ ID NO:1934) 5'-ATAACGCCACTCCTTATT GGT-3' (SEQ ID NO:1935)	5'-CTTGGGTAAAAACGCATC-3' (SEQ ID NO:1936) 5'-CGATCTTGATCCTAATTCA- 3' (SEQ ID NO:1937) 5'-ATCAAGTTGCCTATGCTGA-3' (SEQ ID NO:1938)
SEQ ID NO:865	5'-TTAACACTTTGATTATG CGG-3' (SEQ ID NO:1939) 5'-GGATTATGCGATTGTTTAC AAG-3' (SEQ ID NO:1940)	5'-GTCTTAGCAAAATGGC GTC-3' (SEQ ID NO:1941) 5'-AATGAGCGTAAGAGAGCC TTC-3' (SEQ ID NO:1942)
SEQ ID NO:677	5'-CTTATGGGGTATTGTCA-3' (SEQ ID NO:1943) 5'-AGCATGTGGGTATCCAGC-3' (SEQ ID NO:1944)	5'-AGGTTGTTGCCTAAAGACT-3' (SEQ ID NO:1945) 5'-CTGCCTCCACCTTGATC-3' (SEQ ID NO:1946)
SEQ ID NO:764	5'-ACCAATATCAATTGGCACT-3' (SEQ ID NO:1947) 5'-ACTTGGAAAAGCTCTGCA-3' (SEQ ID NO:1948)	5'-CTTGCTTGTCAATATCTAGC-3' (SEQ ID NO:1949) 5'-GTTGAAGTGTGGTGCTA-3' (SEQ ID NO:1950)
	5'-CAAGCAAGTGGTTGGTT TAG-3' (SEQ ID NO:1951) 5'-TGGAAAGAGCAAATCATTC AAG-3' (SEQ ID NO:1952)	5'-GCCCATATAACAAAAAGCC CAT-3' (SEQ ID NO:1953) 5'-CTAAAACCAAAACCACCTTGC TTGTC-3' (SEQ ID NO:1954)
Vector Primers	5'-GTAAAACGACGCCAG-3' (SEQ ID NO:1955)	5'-CAGGAAACAGCTATGAC-3' (SEQ ID NO:1956)

5 *Results*

To establish the PCR error rate in these experiments, five individual clones of SEQ ID NO:649, prepared from five separate PCR reaction mixtures from *H. pylori* strain J99, were sequenced over a total length of 897 nucleotides for a cumulative total of 4485 bases of DNA sequence. DNA sequence for the five clones was compared to the DNA sequence of SEQ ID NO:649 obtained previously by a different method, i.e., random shotgun cloning and sequencing. The PCR error rate for the experiments described herein was determined to be 2 base changes out of 4485 bases, which is equivalent to an estimated error rate of less than or equal to 0.04%.

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DNA sequence analysis was performed on four different open reading frames identified as genes and amplified by PCR methods from a dozen different strains of the bacterium *Helicobacter pylori*. The deduced amino acid sequences of three of the four open reading frames that were selected for this study showed statistically significant
5 BLAST homology to defined proteins present in other bacterial species. Those ORFs included: SEQ ID NO:649, homologous to the val A & B genes encoding an ABC transporter in *F. novicida*; SEQ ID NO:865, homologous to lipoprotein e (P4) present in the outer membrane of *H. influenzae*; SEQ ID NO:677, homologous to fecA, an outer membrane receptor in iron (III) dicitrate transport in *E. coli*. SEQ ID NO:764 was
10 identified as an unknown open reading frame, because it showed low homology with sequences in the public databases.

To assess the extent of conservation or variance in the ORFs across various strains of *H. pylori*, changes in DNA sequence and the deduced protein sequence were compared to the DNA and deduced protein sequences found in the J99 strain of *H. pylori* (see Table
15 10 below). Results are presented as percent identity to the J99 strain of *H. pylori* sequenced by random shotgun cloning. To control for any variations in the J99 sequence each of the four open reading frames were cloned and sequenced again from the J99 bacterial strain and that sequence information was compared to the sequence information that had been collected from inserts cloned by random shotgun sequencing of the J99 strain. The data
20 demonstrate that there is variation in the DNA sequence ranging from as little as 0.12 % difference (SEQ ID NO:764, J99 strain) to approximately 7% change (SEQ ID NO:649, strain AH5). The deduced protein sequences show either no variation (SEQ ID NO:764, strains AH18 and AH24) or up to as much as 7.66% amino acid changes (SEQ ID NO:649, Strain AH5).

25

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Table 10
Multiple Strain DNA Sequence analysis of *H. pylori* Vaccine Candidates

J99 Seq. ID #:	649	649	865	865	677	677	764	764
Length of	248 a.a.	746 nt.	232 a.a.	696 nt.	182 a.a.	548 nt.	273 a.a.	819 nt.
Region								
Sequenced:								

<u>Strain Tested</u>	AA identity	Nuc. identity	AA identity	Nuc. identity	AA identity	Nuc. identity	AA identity	Nuc. identity
J99	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	99.63%	99.88%
AH244	95.16%	95.04%	n.d.	n.d.	99.09%	96.71%	98.90%	96.45%
AH4	95.97%	95.98%	97.84%	95.83%	n.d.	n.d.	97.80%	95.73%
AH5	92.34%	93.03%	98.28%	96.12%	98.91%	96.90%	98.53%	95.73%
AH15	95.16%	94.91%	97.41%	95.98%	99.82%	97.99%	99.63%	96.09%
AH61	n.d.	n.d.	97.84%	95.98%	99.27%	97.44%	n.d.	n.d.
5155	n.d.	n.d.	n.d.	n.d.	99.45%	97.08%	98.53%	95.60%
5294	94.35%	94.37%	98.28%	95.40%	99.64%	97.26%	97.07%	95.48%
7958	94.35%	94.10%	97.84%	95.40%	n.d.	n.d.	99.63%	96.46%
5640	95.16%	94.37%	97.41%	95.69%	99.09%	97.63%	98.53%	95.48%
AH18	n.d.	n.d.	98.71%	95.69%	99.64%	97.44%	100.00%	95.97%
AH24	94.75%	95.04%	97.84%	95.40%	99.27%	96.71%	100.00%	96.46%

n.d. = not done

5 VI. Experimental Knock-Out Protocol for the Determination of Essential *H. pylori* Genes as Potential Therapeutic Targets

Therapeutic targets are chosen from genes whose protein products appear to play key roles in essential cell pathways such as cell envelope synthesis, DNA synthesis, transcription, translation, regulation and colonization/virulence.

- 10 The protocol for the deletion of portions of *H. pylori* genes/ORFs and the insertional mutagenesis of a kanamycin-resistance cassette in order to identify genes which are essential to the cell is modified from previously published methods (Labigne-Roussel et al., 1988, J. Bacteriology 170, pp. 1704-1708; Cover et al., 1994, J. Biological Chemistry 269, pp. 10566-10573; Reyrat et al., 1995, Proc. Natl. Acad. Sci. 92, pp 8768-8772). The result is a gene "knock-out."
- 15

*Identification and Cloning of *H. pylori* Gene Sequences*

- The sequences of the genes or ORFs (open reading frames) selected as knock-out targets are identified from the *H. pylori* genomic sequence and used to design primers to specifically amplify the genes/ORFs. All synthetic oligonucleotide primers are designed with the aid of the OLIGO program (National Biosciences, Inc., Plymouth, MN 55447, USA), and can be purchased from Gibco/BRL Life Technologies (Gaithersburg, MD, USA). If the ORF is smaller than 800 to 1000 base pairs, flanking primers are chosen outside of the open reading frame.

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Genomic DNA prepared from the *Helicobacter pylori* HpJ99 strain (ATCC 55679) is used as the source of template DNA for amplification of the ORFs by PCR (polymerase chain reaction) (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). For the preparation of genomic DNA from *H. pylori*, see
5 Example I. PCR amplification is carried out by introducing 10 nanograms of genomic HpJ99 DNA into a reaction vial containing 10 mM Tris pH 8.3, 50 mM KCl, 2 mM MgCl₂, 2 microMolar synthetic oligonucleotide primers (forward=F1 and reverse=R1), 0.2 mM of each deoxynucleotide triphosphate (dATP,dGTP, dCTP, dTTP), and 1.25 units of heat stable DNA polymerase (AmpliTaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA)
10 in a final volume of 40 microliters. The PCR is carried out with Perkin Elmer Cetus/GeneAmp PCR System 9600 thermal cyclers.

Upon completion of thermal cycling reactions, each sample of amplified DNA is visualized on a 2% TAE agarose gel stained with Ethidium Bromide (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994) to determine that a single product of the expected size had resulted from the reaction.
15 Amplified DNA is then washed and purified using the Qiaquick Spin PCR purification kit (Qiagen, Gaithersburg, MD, USA).

PCR products are cloned into the pT7Blue T-Vector (catalog#69820-1, Novagen, Inc., Madison, WI, USA) using the TA cloning strategy (Current Protocols in Molecular 20 Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). The ligation of the PCR product into the vector is accomplished by mixing a 6 fold molar excess of the PCR product, 10 ng of pT7Blue-T vector (Novagen), 1 microliter of T4 DNA Ligase Buffer (New England Biolabs, Beverly, MA, USA), and 200 units of T4 DNA Ligase (New England Biolabs) into a final reaction volume of 10 microliters. Ligation is allowed to proceed for 16 hours at 16°C.
25

Ligation products are electroporated (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994) into electroporation-competent XL-1 Blue or DH5- α *E.coli* cells (Clontech Lab., Inc. Palo Alto, CA, USA). Briefly, 1 microliter of ligation reaction is mixed with 40 microliters of electrocompetent cells and subjected to 30 a high voltage pulse (25 microFarads, 2.5 kV, 200 ohms) after which the samples are incubated in 0.45 ml SOC medium (0.5% yeast extract, 2% tryptone, 10 mM NaCl, 2.5 mM KCl, 10 mM MgCl₂, 10 mM MgSO₄ and 20 mM glucose) at 37°C with shaking for 1 hour. Samples are then spread onto LB (10 g/l bacto tryptone, 5 g/l bacto yeast extract, 10 g/l sodium chloride) plates containing 100 microgram/ml of Ampicillin, 0.3% X-gal, and 100 35 microgram/ml IPTG. These plates are incubated overnight at 37°C. Ampicillin-resistant colonies with white color are selected, grown in 5 ml of liquid LB containing 100 microgram/ml of Ampicillin, and plasmid DNA is isolated using the Qiagen miniprep protocol (Qiagen, Gaithersburg, MD, USA).

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To verify that the correct *H.pylori* DNA inserts had been cloned, these pT7Blue plasmid DNAs are used as templates for PCR amplification of the cloned inserts, using the same forward and reverse primers used for the initial amplification of the J99 *H.pylori* sequence. Recognition of the primers and a PCR product of the correct size as visualized
5 on a 2% TAE, ethidium bromide stained agarose gel are confirmation that the correct inserts had been cloned. Two to six such verified clones are obtained for each knock-out target, and frozen at -70°C for storage. To minimize errors due to PCR, plasmid DNA from these verified clones are pooled, and used in subsequent cloning steps.

The sequences of the genes/ORFs are again used to design a second pair of primers
10 which flank the region of *H.pylori* DNA to be either interrupted or deleted (up to 250 basepairs) within the ORFs but are oriented away from each other. The pool of circular plasmid DNAs of the previously isolated clones are used as templates for this round of PCR. Since the orientation of amplification of this pair of deletion primers is away from each other, the portion of the ORF between the primers is not included in the resultant PCR
15 product. The PCR product is a linear piece of DNA with *H.pylori* DNA at each end and the pT7Blue vector backbone between them which, in essence, resultes in the deletion of a portion of the ORFs. The PCR product is visualized on a 1% TAE, ethidium bromide stained agarose gel to confirm that only a single product of the correct size has been amplified.

20 A Kanamycin-resistance cassette (Labigne-Roussel et al., 1988 J. Bacteriology 170, 1704-1708) is ligated to this PCR product by the TA cloning method used previously (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). The Kanamycin cassette containing a *Campylobacter* kanamycin resistance gene is obtained by carrying out an EcoRI digestion of the recombinant plasmid
25 pCTB8:kan (Cover et al., 1994, J. Biological Chemistry 269, pp. 10566-10573). The proper fragment (1.4 kb) is isolated on a 1% TAE gel, and isolated using the QIAquick gel extraction kit (Qiagen, Gaithersburg, MD, USA). The fragment is end repaired using the Klenow fill-in protocol, which involved mixing 4ug of the DNA fragment, 1 microliter of dATP,dGTP, dCTP, dTTP at 0.5 mM, 2 microliter of Klenow Buffer (New England
30 Biolabs) and 5 units of Klenow DNA Polymerase I Large (Klenow) Fragment (New England Biolabs) into a 20 microliter reaction, incubating at 30°C for 15 min, and inactivating the enzyme by heating to 75°C for 10 minutes. This blunt-ended Kanamycin cassette is then purified through a Qiaquick column (Qiagen, Gaithersburg, MD, USA) to eliminate nucleotides. The "T" overhang is then generated by mixing 5 micrograms of the
35 blunt-ended kanamycin cassette, 10 mM Tris pH 8.3, 50 mM KCl, 2 mM MgCl₂, 5 units of DNA Polymerase (AmpliTaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA), 20 microliters of 5 mM dTTP; in a 100 microliter reaction and incubating the reaction for 2 hours at 37°C. The "Kan-T" cassette is purified using a QIAquick column (Qiagen, Gaithersburg, MD, USA). The PCR product of the deletion primers (F2 and R2) is ligated

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to the Kan-T cassette by mixing 10 to 25 ng of deletion primer PCR product, 50 - 75 ng Kan-T cassette DNA, 1 microliter 10x T4 DNA Ligase reaction mixture, 0.5 microliter T4 DNA Ligase (New England Biolabs, Beverly, MA, USA) in a 10 microliter reaction and incubating for 16 hours at 16°C.

5 The ligation products are transformed into XL-1 Blue or DH5- α *E.coli* cells by electroporation as described previously. After recovery in SOC, cells are plated onto LB plates containing 100 microgram/ml Ampicillin and grown overnight at 37°C. These plates are then replica plated onto plates containing 25 microgram/ml Kanamycin and allowed to grow overnight. Resultant colonies have both the Ampicillin resistance gene present in the
10 pT7Blue vector, and the newly introduced Kanamycin resistance gene. Colonies are picked into LB containing 25 microgram/ml Kanamycin and plasmid DNA is isolated from the cultured cells using the Qiagen miniprep protocol (Qiagen, Gaithersburg, MD, USA).

Several tests by PCR amplification are conducted on these plasmids to verify that the Kanamycin is inserted in the *H. pylori* gene/ORF, and to determine the orientation of
15 the insertion of the Kanamycin-resistance gene relative to the *H. pylori* gene/ORF. To verify that the Kanamycin cassette is inserted into the *H. pylori* sequence, the plasmid DNAs are used as templates for PCR amplification with the set of primers originally used to clone the *H. pylori* gene/ORFs. The correct PCR product is the size of the deleted gene/ORF but increased in size by the addition of a 1.4 kilobase Kanamycin cassette. To
20 avoid potential polar effects of the kanamycin resistance cassette on *H. pylori* gene expression, the orientation of the Kanamycin resistance gene with respect to the knock-out gene/ORF is determined and both orientations are eventually used in *H. pylori* transformations (see below). To determine the orientation of insertion of the kanamycin resistance gene, primers are designed from the ends of the kanamycin resistance gene
25 ("Kan-1" 5'-ATCTTACCTATCACCTCAAAT-3', and "Kan-2" 5'-AGACAGCAACATCTTGAA-3'). By using each of the cloning primers in conjunction with each of the Kan primers (4 combinations of primers), the orientation of the Kanamycin cassette relative to the *H.pylori* sequence is determined. Positive clones are classified as either in the "A" orientation (the same direction of transcription is present
30 for both the *H. pylori* gene and the Kanamycin resistance gene), or in the "B" orientation (the direction of transcription for the *H.pylori* gene is opposite to that of the Kanamycin resistance gene). Clones which share the same orientation (A or B) are pooled for subsequent experiments and independently transformed into *H. pylori*.

35 *Transformation of Plasmid DNA into H. pylori cells*

Two strains of *H. pylori* are used for transformation: ATCC 55679, the clinical isolate which provided the DNA from which the *H. pylori* sequence database is obtained, and AH244, an isolate which had been passaged in, and has the ability to colonize the mouse stomach. Cells for transformation are grown at 37°C, 10% CO₂, 100% humidity,

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either on Sheep-Blood agar plates or in Brucella Broth liquid. Cells are grown to exponential phase, and examined microscopically to determine that the cells are "healthy" (actively moving cells) and not contaminated. If grown on plates, cells are harvested by scraping cells from the plate with a sterile loop, suspended in 1 ml of Brucella Broth, spun down (1 minute, top speed in eppendorf microfuge) and resuspended in 200 microliters Brucella Broth. If grown in Brucella Broth liquid, cells are centrifuged (15 minutes at 3000 rpm in a Beckman TJ6 centrifuge) and the cell pellet resuspended in 200 microliters of Brucella broth. An aliquot of cells is taken to determine the optical density at 600 nm, in order to calculate the concentration of cells. An aliquot (1 to 5 OD₆₀₀ units/25 microliter) 5 of the resuspended cells is placed onto a prewarmed Sheep-Blood agar plate, and the plate is further incubated at 37°C, 6% CO₂, 100% humidity for 4 hours. After this incubation, 10 10 microliters of plasmid DNA (100 micrograms per microliter) is spotted onto these cells. A positive control (plasmid DNA with the ribonuclease H gene disrupted by kanamycin resistance gene) and a negative control (no plasmid DNA) are done in parallel. The plates 15 are returned to 37°C, 6% CO₂ for an additional 4 hours of incubation. Cells are then spread onto that plate using a swab wetted in Brucella broth, and grown for 20 hours at 37°C, 6% CO₂. Cells are then transferred to a Sheep-Blood agar plate containing 25 20 micrograms/ml Kanamycin, and allowed to grow for 3 to 5 days at 37°C, 6% CO₂, 100% humidity. If colonies appear, they are picked and regrown as patches on a fresh Sheep-Blood agar plate containing 25 micrograms/ml Kanamycin.

Three sets of PCR tests are done to verify that the colonies of transformants have arisen from homologous recombination at the proper chromosomal location. The template for PCR (DNA from the colony) is obtained by a rapid boiling DNA preparation method as follows. An aliquot of the colony (stab of the colony with a toothpick) is introduced into 25 100 microliters of 1% Triton X-100, 20 mM Tris, pH 8.5, and boiled for 6 minutes. An equal volume of phenol : chloroform (1:1) is added and vortexed. The mixture is microfuged for 5 minutes and the supernatant is used as DNA template for PCR with combinations of the following primers to verify homologous recombination at the proper chromosomal location.

TEST 1. PCR with cloning primers originally used to amplify the gene/ORF. A positive result of homologous recombination at the correct chromosomal location should show a single PCR product whose size is expected to be the size of the deleted gene/ORF but increased in size by the addition of a 1.4 kilobase Kanamycin cassette. A PCR product of just the size of the gene/ORF is proof that the gene had not been knocked out and that 35 the transformant is not the result of homologous recombination at the correct chromosome location.

TEST 2. PCR with F3 (primer designed from sequences upstream of the gene/ORF and not present on the plasmid), and either primer Kan-1 or Kan-2 (primers designed from the ends of the kanamycin resistance gene), depending on whether the plasmid DNA used

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was of "A" or "B" orientation. Homologous recombination at the correct chromosomal location will result in a single PCR product of the expected size (i.e., from the location of F3 to the insertion site of kanamycin resistance gene). No PCR product or PCR product(s) of incorrect size(s) will prove that the plasmid had not integrated at the correct site and that the gene had not been knocked out.

TEST 3. PCR with R3 (primer designed from sequences downstream of the gene/ORF and not present on the plasmid) and either primer Kan-1 or Kan-2, depending on whether the plasmid DNA used was of "A" or "B" orientation. Homologous recombination at the correct chromosomal location will result in a single PCR product of the expected size (i.e., from the insertion site of kanamycin resistance gene to the downstream location of R3). Again, no PCR product or PCR product(s) of incorrect size(s) will prove that the plasmid had not integrated at the correct site and that the gene had not been knocked out.

Transformants showing positive results for all three tests above indicate that the gene is not essential for survival *in vitro*.

A negative result in any of the three above tests for each transformant indicates that the gene had not been disrupted, and that the gene is essential for survival *in vitro*.

In the event that no colonies result from two independent transformations while the positive control with the disrupted ribonuclease H plasmid DNA produces transformants, the plasmid DNA is further analyzed by PCR on DNA from transformant populations prior to plating for colony formation. This will verify that the plasmid can enter the cells and undergo homologous recombination at the correct site. Briefly, plasmid DNA is incubated according to the transformation protocol described above. DNA is extracted from the *H. pylori* cells immediately after incubation with the plasmid DNAs and the DNA is used as template for the above TEST 2 and TEST 3. Positive results in TEST 2 and TEST 3 would verify that the plasmid DNA could enter the cells and undergo homologous recombination at the correct chromosomal location. If TEST 2 and TEST 3 are positive, then failure to obtain viable transformants indicates that the gene is essential, and cells suffering a disruption in that gene are incapable of colony formation

30 VII. High-throughput drug screen assay

Cloning, expression and protein purification

Cloning, transformation, expression and purification of the *H. pylori* target gene and its protein product, e.g., an *H. pylori* enzyme, to be used in a high-throughput drug screen assay, is carried out essentially as described in Examples II and III above. Development and application of a screening assay for a particular *H. pylori* gene product, peptidyl-propyl *cis-trans* isomerase, is described below as a specific example.

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Enzymatic Assay

The assay is essentially as described by Fisher (Fischer, G., et.al. (1984) *Biomed. Biochim. Acta* 43:1101-1111). The assay measures the *cis-trans* isomerization of the Ala-Pro bond in the test peptide N-succinyl-Ala-Ala-Pro-Phe-p-nitroanilide (Sigma # S-7388, lot # 84H5805). The assay is coupled with α -chymotrypsin, where the ability of the protease to cleave the test peptide occurs only when the Ala-Pro bond is in *trans*. The conversion of the test peptide to the *trans* isomer in the assay is followed at 390 nm on a Beckman Model DU-650 spectrophotometer. The data are collected every second with an average scanning of time of 0.5 second. Assays are carried out in 35 mM Hepes, pH 8.0, in 10 a final volume of 400 μ l, with 10 μ M α -chymotrypsin (type 1-5 from bovine Pancreas, Sigma # C-7762, lot 23H7020) and 10 nM PPIase. To initiate the reaction, 10 μ l of the substrate (2 mM N-Succinyl-Ala-Ala-Pro-Phe-p-nitroanilide in DMSO) is added to 390 μ l of reaction mixture at room temperature.

15 *Enzymatic assay in crude bacterial extract.*

A 50 ml culture of *Helicobacter pylori* (strain J99) in Brucella broth is harvested at mid-log phase ($OD_{600\text{ nm}} \sim 1$) and resuspended in lysis buffer with the following protease inhibitors: 1 mM PMSF, and 10 μ g/ml of each of aprotinin, leupeptin, pepstatine, TLCK, TPCK, and soybean trypsin inhibitor. The suspension is subjected to 3 cycles of freeze-thaw (15 minutes at -70 °C, then 30 minutes at room temperature), followed by sonication (three 20 second bursts). The lysate is centrifuged (12,000 g x 30 minutes) and the supernatant is assayed for enzymatic activity as described above.

Many *H. pylori* enzymes can be expressed at high levels and in an active form in *E. coli*. Such high yields of purified proteins provide for the design of various high throughput drug screening assays.

EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments and methods described herein. Such equivalents are intended to be encompassed by the scope of the following claims.

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RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS

(iii) NUMBER OF SEQUENCES: 1956

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: 8-mm cartridge tape
- (B) COMPUTER: SPARC station LX
- (C) OPERATING SYSTEM: SunOS Release 4.1.3
- (D) SOFTWARE: tar

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- (C) REFERENCE/DOCKET NUMBER: GTN-001C5PC

(xi) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (617)227-7400
- (B) TELEFAX: (617)227-5941

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1527 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1527
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

ATGTGTTCTC AGGAAATTTC ATCAAGCTTG CAAACCATTAA TTGCCGAACAA ATTTTCTATA	60
AATATCATCA CTCAGCTTGC TAATAAACTC ACACAAGTTA AAAATCTAAA TTTTTTGTGAG	120
AATAAGACCC ATACTATCAA GCTTAAACTC ATCCATAACG GACTGCACAT CCGCCCCCTA	180
AATTATGTCA GTAATCTTTT TTTCATCTA CAAACGCTTA TAGGGCTTAT CAGTCTGTTT	240
GGGATTATAT TTTCATTAG TATTTATCTA CCCTTTATAA TGATTTTGC AACAGTGCCT	300
TGTATTCTCA TTTCACCCA TATAGCAAAA AAACATAGTG CTTCCATAGA TAAACTCAA	360
GACCAAAAG AAAGCATGCA AAATTACTTA TACTCTGGAC TAGATAACCA AAAGAACAAAG	420
GACAAACCTAT TATTTAACTT CATGCTAAAT TTTCACCCATA AATTTATTGA AACAAAAAGAA	480
TTGTATCTCA ATAATTTTGT GAAAGTAGCC CAAAAAAACT TAATATTTCAC CATATATGCT	540
GATGTTTAA TCACCACTCT AAGTATTGCA CTATTTTTTC TAATGGTTT TATTATCCTT	600
TCAAAATTAA TTGGTGTGGG AGCAATTGCT GGGTATATCC AAGCATTAG CTCTACCCAA	660
CAACAACTAC AAGATTTATC ATTTTATGGA AAGTGGTTT TTGCTATCAA TAAATACTTT	720
GAAAATTATT TCTGTATTTC AGATTACAAA ATACCGAAAC CAGAAACACA AATCAAATTAA	780
GAAGAAAAAA TCCATAGCAT TACATTGAA AATATTAGTT TCTCTTATCC TAATTCAAAA	840
CITATTTCG AAAACTTAA TCTCTCTTTA CACTCTAATA AAATTTATGC ATTAGTCGGC	900
AAGAATGCTA GCGGAAAAAG CACGCTGATT AATTATTAT TAGGTTTTTA TACCCCAAAT	960
TCAGGTCAAA TTATCATTAA TAACAAATAC CCATTACAAAG ACTTGGAACT AAATAGCTAC	1020
CATCAACAAA TGAGTGCAT ATTTCAAGAT TTTTCTTTT ATGCTGGGTA TAGCATTGAT	1080
GATAATCTT TTATGCAAA CAATATCACT AAAGAGCAAT TGAAGCAAAA AAGAGAAATA	1140
CTAAAATCTT TTGATGAGAA TTTTCAAAAT TGTCTTAATG ATTGCAACAA CACACTATTT	1200
GGAGCGCAAT ATAATGGGT AGATTTTCT TTAGGTCAAA AGCAACGCAT AGCTACCATG	1260
AGACCCCTTT TAAAACCAAG TAATTGCATT GTTTAGATG AGCCAAGCAG CGCCATCGAT	1320
CCCATTATGG AAAAGAGTT TTAGATTT ATTTTAAAA AATCGCAATC TAAGATGGCT	1380
TTAATTATTA CACACCGTC GAATAGTGTCA AAGCAAGCTA ATGAAATTAT CGTGTAGAT	1440
CAAGGCAAAC TAATAGAACCA GGGCAACTT GAAACCCCTA TGAAAAAACCA GGGATTATTT	1500
TGCGAATTGT TTTGAAACACA ACAATAC	1527

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

ATGGAGCGCA AGACGCTCCA GAGCATTAA TGTTAATAA AAAAGAAAT GATGAGACCA	60
AAAGGTATTTC TAATGAATTG TTGCAGGSCT TGGAAACACC AGGTTCTTAA GCAAAGCAGC	120
ACAGGTATTAG TGGTGTTGAG CATTATCTCT TCTACAGGCC CCTTTATTTGG TTTGTTTGGG	180
ACGGTAGTTAG AAATTTTACA ACCTTTAAC AATTGGGCG CGTTAGGTCA AGCTTCCTTT	240
GGAGTGATCG CACCCATTAT TTCTAAGGC CGTATGCCA CCGCTGCAGG GATTTAGCA	300
GCCATTCCAG CCTATTCTTT TTACTTGATC TTAAAGCGCA AGGTGTATGA TTTATCGGTT	360
TATGTGCAGA TGCAAGTGG A TATTTGTCT TCTAAAAAA	399

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 474 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3

ATGCATGAAC GCATTGAAAG AGGTATTRGA AATAATGAAT GTAAAAGAAAT TTTTGGCAAT	60
GAACCTAAAC AAAGAAAGAC AAAATTGATT GAAGACATAG AACGGCGGTT CAAAGAATGC	120
GAGGAACAAT TCCGTGGAAG TGTAGGAAAA AATATTGAAC AACTTGAAGA AAGAGTTAAA	180
GATTCTCTAG CGATTATAAA ACACATCAAT AACCTTGGTC TTAATCCTAA TTCTAATTTT	240
AATATGGATA CGGGCATTGA TACAATAGGC TTATTTAGTT CAATAGGAGG TTTGGTGTG	300
CTTCTATTGA CGCTGTAGT AGGTGAGTTT GCGTTAAATTG CAGGAGTGGG TTTAGCATTA	360
GTGGGGTAG GTAAATCAAT ATGGAGTTT TTGATTTCAG ATTATAAAAA ATCCCAACAA	420
AGAAAAGAAG TGGATAAGAA TTACATCAA ATTGCGAAA ATTGTGCAG GATG	474

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

ATGCCTGGCG TGTATCAAAT GAGTATAGAG CCTCTTTAA AAGAATGCGA AGAATTAGTG	60
GGTTTAGGCA TAAAAGCCGT TTTATTGTTT GGCAATTCTA AACATAAGGA CGCTACAGGA	120
AGCCATGCGT TAAATAAGGA TCACATTGTC GCAAAAGCTA CGAGAGAAAT TAAAAAACGA	180
TTTAAGGATT TGATCGTTAT AGCGGGATTTG TGTTTTGCG AATACACCGA CCATGGGCAT	240
TGCGGGATTT TAGAAAACGC TTCTGTGTCT AACGATAAAA CGCTAAAGAT TTTAAATCTT	300
CAAGGGCTTA TTTTGCTGAA AGCGGTGTGG ATATTC	336

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 195 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

GTGGAAAACA ACAAGAGTTT AAAGCATGCG AATGAGTTAA GGGATAAGCG AGATGAATTA	60
GAGTTTCATT TGCGAGAGCT TTTCGGGGGG AATGTTTTA AAAGCAGCAT TAAAACCCAT	120
TCGCTCACAG ATAAGACTC AGCGGACTTT GATGAGAGCT ATAACCTTAA TATCGGGCAT	180
GGGYTCAATA TSATA	195

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1857 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

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(A) NAME/KEY: misc_feature
 (B) LOCATION 1...1857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

GTGTTTGTGG	CAAGCAAACA	AGCTGACGAA	CAAAAAAAGC	TAGTTATAGA	GCAAGAGGTT	60
CAAAAGCGGC	AGTTTCAAAA	AATAGAAGAA	CTTAAAGCG	ACATGCAAAA	GGGTGTCAT	120
CCCTTTTTTA	AAAGTCTTGT	TGATGGGGG	AATAGGTTGT	TTGGTTTCCC	TGAAACTTTT	180
ATTATTCTT	CTATATTTAT	ATTGTTGTA	ACAATTGTAT	TATCTGTTAT	TCTTTTCAA	240
GCCTATGAAC	CTGTTTGT	TGTAGCGATT	GTTATTGTGC	TTGTTAGCTCT	TGGATTCAAG	300
AAAGATTACA	GGCTTTATCA	AAGAATGGAG	CGAGCGATGA	AATTTAAAAAA	ACCTTTTG	360
TTTAAGGGCG	TGAAAAAACAA	AGCGTTCATG	AGCATTTTT	CCATGAAGCC	TAGTAAAGAA	420
ATGCTAATG	ACATCCACTT	AAATCCAAC	AGAGAAGACA	GGCTTGTGAG	CGCTGCAAAC	480
TCCTATCTAG	CGAATTAACAT	TGAATGTTT	TTAGATGATG	GGGTGATCCT	TACTAACAAAC	540
TATTCTCTTT	TAGGCACAAAT	CAAATTGGGG	GGCATTGATT	TTTTAACAC	TTCCAAAAAA	600
GATCTCATAG	AGTTACACGC	TTCTATTAT	AGCGTTTTA	GGAATTGTTG	TACCCCTGAA	660
TTCAAATTAT	ATTTTACAC	TGTTAAAAG	AAAATCGTTA	TTGATGAAAC	CAATAGGGAT	720
TATGGTCTTA	TTTTTCTAA	TGATTCATG	CGAGCCTATA	ATGAGAAC	AAAGAGAGAA	780
AGTTTTATG	ATATTAGTT	TTATCTCACC	ATAGAGCAAG	ATTATTAGA	CACTCTCAAT	840
GAACCCGTTA	TGAATAAAAA	GCATTTGCA	GACAATAATT	TTGAAGAGTT	TCAAAGGATT	900
ATTAGAGCCA	AGCTTGAAAAA	CTTCAAAGAT	AGGATAGAGC	TCATAGAAGA	GCTACTGAGT	960
AAATACCAAC	CCACTAGATT	AAAAGAATAC	ACTAAAGATG	GCATTATTAA	CTCCAAACAA	1020
TGCGAATTTC	ACAATTTCT	TGTGGGAATG	AATGAAGCCC	CTTTTATTG	CAACAGAAAA	1080
GACTGTATC	TCAAGGAAA	AATGCATGGT	GGGGTGAAG	AAGTTTATT	TGCCAATAAG	1140
CATGGAAAAA	TCTTAAATGA	CGATTGAGT	AAAAATATT	TTAGCGCTAT	TGAGATCAGT	1200
GAATACGCC	CTAAATCACA	GAGCGATTIG	TTTGATGAA	TCAACGCTCT	AGACAGCGAA	1260
TTTATCTTTA	TGCATGCTTA	TTCGCCTAAA	AACTCACAA	TTTAAAGGA	CAAACTAGCT	1320
TTCACCTCTA	GAAGGATTAT	TATTAGTGG	GGCTCCAAAG	AGCAAGGCAT	GACTTTGGGT	1380
TGCTTGAGCG	ATTAGTGGG	TAATGGTGAT	ATTACGCTAG	GCAGTTATGG	TAATTCTTTA	1440
GTGCTGTTG	CTGATAGCTT	TGAAAAATG	AAACAAAGCG	TTAAGGAATG	CGTCTCTAGT	1500
CTTAAACGCTA	AAGGTTTTT	AGCCAACCCA	GCGACTTTCT	CTATGGAAAA	TTACTTTTTT	1560
GCCAAACATT	GCTCTTTTAT	CACGCTTCT	TTTATTG	ATGTAACCTTC	TAACAATT	1620
GCTGATTTC	TAGCGATGAG	AGCGATGGCA	AAAAGACAA	TAACGCTTGG	1680	
GGCAATAGCG	TGATGACGTT	AAAAGCGAG	ATCAATTGCG	TTTTTATT	GAACTTCCAC	1740
ATGCCCACTG	ATTTGGTT	AGCTTCAGCA	GGACACACTT	TGATACTTGG	CTCAACCGGT	1800
TCAGGTAAGA	ACAGTGT	TGTCCATGAC	TCTAACGCT	ATGGGGCAAT	TTGCCTA	1857

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 330 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

GTGAAAACAT	CGTGTGTTGGT	TACAATAGGG	AGGATCCGGG	GCGTTTTAT	CATTAAGCG	60
CAGTTGTTGC	TTCTGTGAGGG	AGGTTTTATG	AATTTCACCG	CTTATAACAC	GAAGACGCCA	120
GGGCATTG	ATTGTTATGT	GCATAAGGG	CATACGGAAT	TAGGCGAGGG	TGAAAGGCTG	180
ATTTAAACTT	TATCCATGAA	ATTAGCGAA	GGGTTGCCTA	AAGAATGGAG	GGTTTCCCT	240

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AGCAATGAAT GGCCTAAGGA ATTTAATATT TTAGCTTAC CTTATGAAGT GTTGCAAAA	300
GAGCGCGGGAA GCTCTGGGC GAAGCATTAA	330

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 204 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...204
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8

TGCGCTAAAG ACATCATCAC CGAGTCTCAA AACCTTGCG CAAGAAAATT CCGCCGTTTG	60
TATGCGTTAT TGAAAGAAAA TGAAATGCTC ATTGCATCG GATCTTATCA AATGGGAAAC	120
GATAAAGAGC TTGATGAAGC GATTAAGAAA AAGGCTCTAA TGGAGCAATT TTTAGTGCAA	180
GATGAAAACG CTTTACYAGC CTTT	204

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1338
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

ATGAAATCAC GCCAACCTCG CGCACAAAGCT TACGGCTCC AAATGATGGT CAAACAGATC	60
GCTTTTTAG AAACCATTTT AGTGGAAAAC GAGCAAGACG CTTCGATTTT GGAAAATTCT	120
TTGATCAAGC AGCTCAAGCC TAAATACAAC ATTCTTTAA GAGACGATAA AACTTACCT	180
TATATTACCA TGGATTTTTC TATTGATTTTC CCTATCCCTT TAATCACACG AAAATCTTA	240
AAACAGCCTG GCGTTAATAA TTTGGCCCT TTTACGAGCG GGGCTAAGGA TATTTTGAC	300
AGCTTGTATG AATTGCTCCC TTTGGTTCAA AAGAAAATT GCATCAAGGA TAAAAAGGCA	360
TGCATGTTT ATCAAATAGA CGCTTGAA GCCCCATGCG AGGATAAAAT CACTAAAGAA	420
GAATATTAA AAATCGCTAA AGAATGTTA GAAATGATTG AAAATAAAGA CAGGCTCATC	480
AAAGAGCTTG AATTGAAAAT GGAGCGCCCTT TCTAGTAAC TGCCTTTGA AGAACCTTA	540

ATTTATAGGG ATAGGATTGC AAAAATCCAA AAAATGCCCA CTTTCACTTG CATGGATTTA	600
GCCAAACTCT ACGATTGGA TATTTTGCT TTTTATGGTG GGAACAACAA GGCGGTGTTA	660
GTGAAAATGT TCATGCGTGG GGGTAAATC ATTTCITTCAG CGTTTGAAAA AATCCACTCT	720
CTCAACGGGT TTGACACTGA TGAAGCGATG AAACAAGCCA TTATCAATCA TTACCAATCG	780
CATTGCGCTT TGATGCGCTGA ACAAACTTA TTGAGCGCTT GTTCTAATGA AACGCTTAAA	840
GAATTGCAAG AGTTTATCTC TCACCAATAT TCTAAAAAA TCGCTCTTAG CATTCCCTAAA	900
AAGGGTGATA AGCTCGCTTT AATAGAAATC GCTATGAAAA ACGCTCAAGA GATTTTTAGC	960
CAAGAAAAAA CCTCTAATGA AGATCGGATC TTAGAAGAAG CGCGATCGCT TTCAATTAA	1020
GAGTGCCTGC CTTATAGGGT AGAAATCTTT GACACAAGCC ACCATTCAA CAGCCAATGC	1080
GTGGGGGAA TGGTCGTGTA TGAAAACAAT GCATTTCAAA AAGACTCTTA TCGGGCGCTAC	1140
CATCTAAAG GCTCTAACGA ATATGATCAA ATGAGCGAAT TGCTCACCAAG AAGGGCTTTA	1200
GACTTTGCTA AAGAGCCACC GCCTAATTTG TGGGTGATAG ATGGAGGGAG GGCGCAATTAA	1260
AACATCCCTT TAGAAATTAA AAAAAGCAGC GGGAGTTTG TAGAAGTGAT CGCTATTCT	1320
AAAGAAAAAA GGGGATTG	1338

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

GTGAGTTTGG GGGCGTTTCA GGGGTATTAT GGAGGGCTAG TGGATTTAGT GGGGCAAAGG	60
TIGAGCGAAA TTTGGAGCGC GATCCCCATG CTTTTTTTAC TCATTGTGAT TTCTAGCGCG	120
TTCAATTCTA ATTTTTGGAT CATCTGTTT TTAGTCTTGC TCTTTAGCTG GATGGGGCTT	180
TCTCAAGTCG TGCGCACGGA GTTTTTAAAA GCAAGGAATA TGGACTACAC CAAAGCCGCT	240
AGAGCGTTGG GG	252

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

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(B) LOCATION 1...120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

ATGAGTGAAG CCTATTTTT ACACCATAAA AACCGTTCTC AAGTGTCTCT TAATGAACAA	60
GTTTAAACG TTATGAAACA AGTTCAATTG GATGAAAATT TTTGGAATGT TTCTCTTATG	120

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

GTGATCCTGA TATTTATCAT CGTGGTGGAA GATCAGAAAG GCATTTTCCC TATCGCAGCG	60
TCAAAAGAA AAAGCCAAAG CTCTGTGATC ATTGAAGACG TGTGCTTCAG CAAAGAGGAT	120
TTTGTAGAACG GGGCAAAAGC GATTGAGGGG CTTTTAAAAA AACATGGCTT TAAGGATAAT	180
GGCATTATTT TTGGGCATGC GTTAAGCGGG AATTTCACACT TTGTCGTTAC GCGGATTCTA	240
GAAAATGAAG CTGAAAGAAA AGCGTTTGAA AATTTAGTTT CTGAGATGTT TTTAATGGTG	300
AGCAAAAGCT CTGGCTCTAT TAAAGCGAA CATGGCACAG GCAGGATGGT AGCCCCTTT	360
GTGGAAATGG AGTGGGGAGA AAAAGCTTAT AAGATCCACA AACAAATCAA GGAATTGTT	420
GATCCTAATG GCCTTTTAAA CCCTGATGTG ATCATCACAA ACGATAAAAGA AATCCACACT	480
AAAAATTAA AGAGCATTTA CCCTATTGAA GACCATTGG ACATGTGCA	540
TTTTGTGAAA GGATCTGCC CAGTAAAGAT TTATCCTTAA CGCCACGACA ACGCATCGTC	600
ATCCACAGAG AGGTAGAGCG TTGAAAGAA AGGGTAAGTC ATGGTCATGA TGAAGATCAG	660
GTTTTACTAG ATGAGCTTTT AAAAGAGTCT GAATACTTAG CGCATGCCAC TTGCGCGGTG	720
TGCCATATGT GTTCCACTTT ATGCCCTTAA GGGATTGATA CGGGGAGYAT CGCTTTAAAT	780
CATTATCAAA AAAACCCCTAA AGGCAGAAAG ATCGCTTCAA AGATTCTAA ATCACATGCA	840
AACGACCACACGCGTCTT AAAARGCGCT TTCGTGGTTT CAAAAACTCA	900

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13

ATGAAAGAAA	AAAACTTTGT	GCCTTAGGA	ATCATGAGCG	TGCTTATTTT	TGGGCTTGGG	60
ATCGTGGTGT	TTTAGTGGT	GTTGCCCTA	AAAAATTCGC	CTAAAATGA	TTTAGTGTAT	120
TTCAAGGGTC	ATAACGAAGT	GGATTTAAC	TTAACGCCA	TGCTTAAAC	TTATGAAAAC	180
TTTAATCCA	ATTATCGTT	TTCAGTGGGT	TTAAAGCCTC	TTACCGAAAG	CCCTAAACC	240
CCCATTTGC	CCTATTTTC	TAAAGGCACG	CATGGGATA	AAAAAATCCA	AGAAAACCTT	300
TTAACAAACG	CTTGTATTT	AGAAAAGTCC	AACACGCTTT	ATGCACAATT	GCAACCGCTC	360
AAACCCGCTT	TAGATTGCC	AAATATCAA	GTGTTATTTAG	CGTTCTATCC	CAGCCAATCC	420
CAGCCCCAGAT	TATTAGGAAC	GCTTGATGT	AAAAACGCAT	CGGAACCTTT	AAAATTGTAT	480
TTGTTAGAGG	GCGATAAAAGT	GGGGCGCTAT	AAGATCCTTT	TTAAATTGT	TTTTAAAAAT	540
AAAGAAGAAT	TGATTTGGA	GCAACTGCTT	TTTTTAAGTA	GCATGGCTTG	TATGGGTATA	600
TCAATTTAA	AAAACGCTAA	AGCATTTTT	AAATACAAAA	TA		642

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14

ATGCCCATTA	AAGGCTCTTT	TTTAGCCAGA	AACCGCCTGG	TGATCGCTTT	AACCGATGCG	60
GTGATTATCC	CCCAAGCGGA	TTTAAAAAGC	GGCTCTATGA	GCAGTGCGAG	ATTAGCCCAG	120
AAATACAAA	AACCCTTGT	TGTTTACCC	CAACGCCGA	ATGAGAGCGA	CGGCACTAAT	180
GAGCTTTAG	AAAAGGGCA	GGCTCAAGGG	ATATTTAATA	TTCAAAATTT	TATAAACACC	240
CTTTAAAAG	ATTACCATTT	AAAAGAAATG	CCTGAAATGA	AAGATGAATT	TTTGAATAT	300
TGCGCGAAAA	ACCCCTAGCTA	TGAAGAAGCG	TATCTCAAAT	TTGGGGATAA	GCTTTAGAA	360
TACGAGCTGT	TGGGTAAAGAT	TAAGCGCATC	AATCATCTCG	TGGTGTAGC	A	411

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...816
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15

ATGGTAGTAG AATTAAAAAA CATTGAAAAG ATTATGAAA	ACGGGTTCA TGCTCTAAAA	60
GGCGTGAATT TGGAATTGAA AAAAGGGCATT	TGATAGGCTA TTCAAGGGCG	120
GGGAAATCCA CGCTCATTG CTTGATCAAT	TGTTTAGAGC GCCCCAGTTC	180
TTAGTCAATG GGGTCAATCT GTTAAACTTA	AAGCCTAAAG AATTGCAAAA	240
AAAATAGGCA TGATTTCCA GCATTCAAT	AGCGCCCAA CTAAAACGT	300
GTCGCTTCG CTCTAGAAAT CGCCCGATGG	GAAAAAACTA AGATTAATC	360
GAATTGTTGG AATTAGTGGG GTTAAAGAT AAAGTCATT	AAGGGTGCAT TTTATCCTAA	420
GGCGGGCAAA ACAACGAGT GGCGATCGCT	ACAGCTCAGC AGGAGTTAG	480
CTTTCGATG AGGCCACAT CGCTTTGGAT	CGAATTGCC TAATTGTTG	540
CTAACGGCA TTCAAAAAAA GTTTGATTTG	CGCATTCTAT TTTAACGCTT	600
GTGGTTAAAG AATTGTGCAA TCAAATGTTG	TCATCACACA CCAGATTGAA	660
GGCTCGGTGG AGAAAATTTC TGCTAACCTT	GTGATCAGCA GCGGCGAAAT	720
ATCAAAACG AACATGCGGA TCAAAATCG	CGTAGAAAGA ATTGCTTGGC	780
GAGCATTAG ACGAGCCGAT CATTCTAAW	CAAGACATTGTTGCTGTTTTAGGG	816

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...318
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

ATGGGGGCTT TGATAGCCAT	GTTCCTTTTA ATGCTCATTA AAAAGACTAT	CGCTTATAAA	60
GAAGATAAAA AGAGCGCGGC	TTTAAAGGTC GTGCCTTATT	TGGTGGCGTT GATGAGCTTA	120
GCCTTCTAGCT GGTATTTGAT	CGTGAAGGTT TTAAACGCC	TCTATGCGGT GAGTTTGAA	180
ATCCAGCTCG CTTCGGGTG	TGTCCTTGCG CTTTGATTT	TTATCCTTTT TAAAAGATTT	240
GTGTTAAAAA AAGCCCCGCA	ATTAGAAAAT AGCCACGAAA	GCGTCAATGA GCTTTTTAAT	300
GTCCCCCTTGCA	TTTTTGCC		318

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 471 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...471
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17

ATGATTAAAA	GAATTGTTG	TATTTTAAGC	TTGAGCGCGA	GTTTAGCGTT	AGCTGGCGAA	60
GTGAATGGGT	TTTTCATGGG	TGCCGGTTAT	CAACAAGGTC	GTATGGCCC	TTATAACAGC	120
AATTACTCTG	ATTGGCGTCA	TGGCAATGAC	CTTATGGTT	TGAATTCAA	ATTAGGTTTT	180
GTAGGCTTG	CCAATAATG	GTTTGGGCT	AGGGTGTATG	GCTTTTTAGA	TTGGTTAAC	240
ACTTCAGGGA	CTGAACACAC	AAAACCAAT	TTGCTCACCT	ATGGCGGCGG	TGGCGATTTG	300
ATTGTCATC	TCATTCCTT	GGATAAAATTC	GCTCTAGGTC	TCATTGGTGG	CGTTCAATTA	360
GCCGAAACA	CTTGGATGTT	CCCTTATGAT	GTCAATCAAA	CCAGATTCCA	CTTCTTATGG	420
AATTAGGCG	GAAGAATGCG	TGTTGGGAT	RCAGTGCCTT	TGAAGCGGGC	G	471

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 834 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...834
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18

ATGTATCGCC	ATGTGTTGAA	AGATTCTCC	CTAGATTTTA	GCAAAGAAAG	CGTTCAAGAG	60
CTGTTAAC	AGCTGGCTAA	AGACACTTTT	TTATTGCTTT	TGCTGTGTTT	AATCATTTA	120
ATGGTGGTGG	CGTTTTGTC	TAATGTCCTG	CAATTGGCT	GGCTCTTGC	CCCTAAAGTC	180
ATTGAGCCTA	AATTTTCTAA	AATCAACCT	ATCAATGGCG	TCAAAAACCT	TTTTCTTTA	240
AAAAGATCC	TTGATGGGAG	TTTGATCACT	TTAAAAGTTT	TTTGTAGCTT	TTTTCTGGGG	300
TTTTCATCT	TTCCCTTATT	TTTACGGGAA	TTAAACCATG	CGGCTCTTTT	GAATTGCAA	360
GGCAGTTGT	TGTGGTTTA	AACCAAGGCG	TTATGGCTCA	TTTCCTTCGCT	TTTATTITTA	420
TTTTTGTCT	TGGCTTTGCT	GGATTTAATC	ATCAAACGCC	GCCAATACAC	TAACTCTTTA	480
AAAATGACTA	AACAAGAAGT	TAAGGACGAA	TACAAACAGC	AAGAAGGAAA	CCCAGAAATC	540
AAAGCCAAA	TCCGCCAGAT	GATGGTAAA	AAAGCCACGA	ATAAAATGAT	GCAAGAAATC	600
CCCAAATCCA	ATGTCGTGCT	GACTAACCCCT	ACCCATTATG	CCGTCGCTCT	CAAATTGAT	660
GAAGAACACC	CTGTGCCTGT	GGTAGTGGCT	AAAGGCACGG	ATTATTTAGC	CATTAGGATT	720
AAGGGTATCG	CCAGAGAGCA	TGACATAGAA	ATTATAGAAA	ATAAAACGCT	CGCTAGAGAG	780
CTTATAGAG	ACGTGAAATT	GAACGCCACC	ATACCAGAAG	AATTGTTGA	CGGG	834

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...360
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19

ATGAATAACAA	GSCCCTTAAT	CGCTTACGCCTT	TTGCAAGCGC	CTTTCATGT	TTTACGGATT	60
AGAGAGCCAG	TTCTTTTCA	GCCTTTTAC	CCCAAAACAG	AAAAGCCTAA	TCGCCCTCAA	120
AAGTTCGCGC	ATGTTCTAG	CATGCCAGT	TTGGAATT	TAGAAAAATT	GGTGATCCGC	180
TACCTTTAG	AAGACAGAACG	CCTATTGGAT	TTAGCGGTGG	GTTATATCCA	TAGTGGGTA	240
TTCTTGCATA	AAAAACAAGA	ATTTGACGCT	TTATGTCAAG	AAAAATTGGA	CGACCCCTAAA	300
TTAGTTGCGT	TATTATTAGA	TGCGAATTAA	CCCCTAAAAA	AAGGGGGTTT	TGAAAAGGAA	360

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 678 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...678
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20

ATGGGGCAGG	CATTTTTAA	AAAAATTGTT	GGCTGTTCT	GTCTTGGTTA	TTTATTTTA	60
TCTAGCGCAA	TAGAAGCACT	AGCACTTGAC	ATTAAGAATT	TTAATCGTGG	TAGGGTGAAGA	120
GTGGTGAATA	AGAAGATTGC	TTATTTGGGA	GATGAAAAAC	CTATTACCGAT	TTGGACTTCA	180
TTAGACAATG	TTACCGTAT	CCAACCTGAA	AAAGATGAAA	CTATTTCTTA	CATCACAAACA	240
GGTTTCAATA	AAAGTTGGAG	TATTGTGCCT	AATTCTAATC	ATATATTCTAT	TCAACCTAAA	300
TCGGTAAAAA	CTAATCTCAT	GTTTGAAAAA	GAAGCAGTGA	ATTTTGCCCT	AATGACAAGA	360
GATTACCAAG	ATTTTTAAA	GACAAAAAAA	CTTATCGTAG	ATGCGCTGA	CCCTAAAGAA	420
TTAGAAGAAC	AAAAAAAAGC	TCTAGAAAAA	GAAAAAGAAG	CTAAAGAACAA	GGCGCAAAG	480
GCACAAAAG	ATAAAAGAGA	AAAAAGAAAG	GAGGAGCGTG	CAAAAAATAG	AGCCAATTAA	540
GAAAATCTCA	CTAACGCTAT	GAGTAACCCA	CAAAATTGAA	GCAATAACAA	AAATCTTAGC	600
GAATIGATCA	AGCAACAGAG	AGAAAATGAA	TTAGACCAA	TGGAACGAAC	TAGAGGACAT	660
GCAAGAGCAG	GCTCAAGC					678

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(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 150 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...150
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21

ATGAATACAG AAATTTAAC CATCATGTTA GTTGTCTCCG TGCTTATGGG ATTGGTAGGC	60
TTAATAGCGT TTTTATGGGG GGTTAAAGC GGTCAGTTG ACGATGAAA ACGCATGCTT	120
GAAAGCGTGT TGTATGACGC GCGAGGACT	150

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...390
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22

ATGTTTGTAG CGGCCGGGCT TGGGGCTTAT GCGATCGCGC TTTTCCACCT CTTTACGCAT	60
GCGTTCTTCA AATCCCTCCT TTTCTTAGGC TCAGGCAATG TCATGCATGC GATGGAAGAC	120
AATCTGGATA TTACTAAAAAT GGGCGCTTTA TACAAGCCTA TGAGGATCAC AGCTGTCTTT	180
ATGATTATAG GGTCACTGGC TTTGTGTGGG ATCTACCCCT TTGCGGGCTA TTTCTCCAAA	240
GACAAGATTT TAGAGGTCGC CTTTGGGATG CACCACCACA TTTTATGGTT TGTTCTTTG	300
ATTGGGGCGA TCTTTACCGC TTTTATAGC TTCAGACTCA TCATGCTGGT GTTTTTGCA	360
CCCAAACAAAC ATGAAATCAA CCACCCCCCA	390

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 549 base pairs

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(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23

ATGTTTATAT CTTCTTCTTA CACGCTGAGT TTTGTATGGC TTTTTTTAAT TTTCTTTTT	60
TTCAAAAATA AGCCATTGGG TTTGAGGTTT TCGCTCTCTTGATAAGCGT GATTTTAAGC	120
AATATCGCTT TGAAAGACTC CCTATCGCTC AATGAATTAAAGCAGTTT TAAGCAGTTT TACAGCCCCC	180
TTAACGCCCT TTAGCTGTCT TTTGATCCCTTGCTTATGCAA GCTTTTCTTG CCATATACTC	240
AAAAAGCCCC CTTTAGAAAC CTTGCAATCT TATAGCGTCA TGCTGTTTTT CAATCTGTTG	300
CTTGTGACAG ATATTTTGG GTTTTGCGCTT TTTCAATCT ACCATCATTTT CATGGCTTCT	360
CTGATTTTA GCGCGCTTT TTGCAGCAGT TTGTTTTGAGA GTAGCCCCCTT ATTAGGCGTG	420
ATCGCTTCTAG TGGCTTTATC CAGITCGCTT TTGATGCGTT CTAATTTCAGATTTAGAT	480
TCTTATTGG ATTTCCCATT ATTTCTTTT GTCTTTTTA AGACTTATA TCTTGCTAAA	540
AAAAGGTTA	549

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 705 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24

ATCCGCCCTAG ATTACGCCCT ATTCAACCAG CATTAGCAA ATAGCAGAGA AAAAGCTAAA	60
GCGTTGGTTT TAAAAAAACA GGTTTAGTC AATAAAATGG TGTTTCTAA ACCCTCTTT	120
ATCGTTAAAG AGGGCGATCA AATTGAACCTC ATCGCTCCCA ATCTATTCTGT TAGCAGGGCT	180
GGGGAAAAAT TAGGGGCTTT TTTAGAAGAT CATTATAG ATTITAAAGA AAAGGTTGTT	240
TTAGATGTGG GAGCGACTAA GGGAGGCTTT AGTCAAGTGG CTCTTTTAAA AGGGGCTAAA	300
AAGGTGCTTT CGGTGGATGT GGGGAAAATG CAATTAGATG AAAGTTTGAA AAACGACCAA	360
CGCATAGAAT GTTACGAAGA ATGCGATATT AGAGGGTTTA AAACGCCAGA AAAAATTGAT	420
TTAGCACTTT GTGATGTGAG CTTTATTTCT TTATATGTA TTTAGAAGC GATTTGCCT	480
TTAACCGGTG AATTTTAAAC GCTTTCAAA CCGCAATTG AAGTGGGCAG AACAAATAAAA	540
CGCAATAAAA AGGGGGTGGT GATGGATAAA GAAGCCATTG TGAACGCTTT AGAAAACCTT	600
AAAAACCATT TAAAAACAAA GGATTTCAA ATCTAACGA TCCAAGAAAG CTTAGTGAAA	660

GGGAAAAACG GGAATGTTGA ATTTTTTATC CATTCAAGC GAGCC

705

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25

ATGAGCCTAC CACCGGTTTG CATTITGAAA GATGTGAATC ACCTTTTACA AGTCCTRCAT	60
TCTTTGGTGG CGTTAGGCCTA TTCCATGCTA GTGATTGAGC ATAATTAGA CATCATCAAA	120
AACGCTGACT ACATTATAGA CATGGGGCCT GATGGGGGGG ATAAGGGCGG GAAAGTCATT	180
GCGAGCGCA CGCCTTAGA AGTGGCGCAA AATTGCGAAA AAACCCAAAG CTATACGGGA	240
AAATTTTAG CTTTGGAAATT GAAA	264

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26

ATGAAAATC GATCGCATGA AATACAAGGC GTATCACACA TTAAGAATAA TTATAAATTT	60
TTCACCAAAG AGCTTGACAA TTATATCAGC AAAGGGTATC GCATTGAAGA GATTATGGC	120
GGCTTTTGT GGCTCAAAT CGTAGCCATA GGTTTAGAGT TGGGCGAAGA CGATCCGCAA	180
GTGGTGTGG AGAGCATCAA CGCTACAGGC GTGCAATTAA AAGGGCTGGA TCTCATCCGC	240
AACTATTTGA TGATGGGGGA AAATYCTGAC AACCAAGAATC GTCTTTATAA TACTTATTGG	300
GTGCCCTTAG AAAATTGCGCT TGGTGAAAG GATTGAAATG ATTTCATCAA AACCTATTG	360
AGAACCTATT TTGAGGATAG AGTTACAAGA GGGAGAGCGC GAAGTGTATT ACGCGCTAAA	420
AGCCCACACC AGAGACAATT TCCC	444

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...321
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27

ATGGATACCA TAAAAAGCAT TCCCATAAGA ACTTTTATTT TACTCTATAA AAGCTCACCA	60
AAATGTGTTG TGTTGGCATC ATTACAGTG CTATTGTCG GCATTCCTYC ATCTCTGAAT	120
ATTCCTGTTA TGATAAAAATT GATTGATATT GTGGTGAATC TATTACAAAA GCATACGCAT	180
TTTGAATACA GCTTGCTGTT ACCAACTTTA CTACTATGGG GAGCCTTGCT GTTTTAACG	240
CATGTGTTCT CAGGAAATT TATCAAGCTT GCAAACCATT ATTGCCGAAC AATTCTAT	300
AAATATCATC ACTCAGCTTG C	321

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 408 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...408
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28

ATGATCTTTT ACACCACCAT TAAAGAGCCT TTAAAAAACCC TCCAATACCG CTATGCGCAA	60
TTTTTGGCA AGATCAAGCC TTGTTCTTC TTAGACTCTC TAAAATCATG CTTTTTCAA	120
ACCTATTCTT TTCTTTAAC GCGAAAACAA GATTTCAAAT CGCATTGCG CCATTTCAATT	180
GACAGCGCCC ATTCCAACGC CTTAGTGGGT AATTGTTATC GAGCCTTATT CATAGGGAT	240
AGCTTGAATA AAGACTTAAG AGACAGGGCT AACGGCTAG GGATCAACCA CTTACTGGCC	300
ATTAGCGGGT TTCATTTAGG GATTTTGAGC GCGAGCGTGT ATTTCCTTTT CTCTCTTTT	360
TATACCCCCCT TACAAAAACG CTATTTCCCT TACAGGAACG CTTTTTWA	408

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 162 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...162
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29

ATGAATAAAC CATTTTTAAT CTTACTCATA GCCCTAATTG CCTTTAGCGG CTGTAACATG AGAAAAATACT TCAAAACCCGC TAAACACCAA ATTAAAGCGA AGCGTATTTC CCTAACCAATT TGCAAGAAAG CATCGTTTCG TCTAACGTT ATGGAGCCAT TT	60
	120
	162

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...375
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30

ATGGCGGCCCT GGAACACTTT AGTAGAAAAA ATCATCGCTC CTAAACACAA GGTCAAAATT GGTTTGTGG GCAAGTATTT AAGCTAAAAA GAATCTTATA AATCCTTGAT TGAAGCCCTA ATCCATCGGG GGGCGCATCT GGATACGCAA GTCAATATTG AATGGCTGGA TAGCGAGAAAT TTTAATGAAA AGACTGATTT AGAGGGCGTT GATGCGATTT TAGTGCCGGG GGGCTTTGGA GAAAGGGGGA TTGAGGGCAA AATTGCGCC ATTCAAAGGG CTAGGTTAGA AAAACTCCCC TTTTAGGGA TTGTTTGGG CATGCAATTAA GCGATCGTTG AATTGTTGTCG CAAATGTTT AGGCTTGAAA GGGGC	60
	120
	180
	240
	300
	360
	375

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 747 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

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- (D) TOPOLOGY: circular
 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...747
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31

ATGACTAAAG CGTTTGTGCC	TTTAAGTTG TTAGTGAGCG	CGATTTTATT AGCGTTTCG	60
CTCATCTTAA TCCCCACTTC	TAAGAGCGCT TATTACGGGT	TTTTGCGTCA AAAAAAAAGAC	120
AAGATTGACA TTAACATCAG	AGCGGGTGA TTCGGGCAAA	AATTAGGCGA TTGGCTCGTG	180
TATGTGGATA AGACTGAAAA	CAATTCCAT GATAATTGG	TGCTTTTTTC TAATAAAAGT	240
CTCTCTCAAG AAAGCTTTAT	TTTGGCTCAA AAAGGCAATA	TCAACAATCA AAACGGCGTG	300
TTTGAATTGA ATTTGTATAA	CGGGCATGCG TATTTCACTC	AAGGCGATAA AATGCGTAAG	360
GTTGATTTTG AAGAATTGCA	TTTGCACAAAC AAGCTCAAGT	CTTTCACATTG TAATGATGCG	420
GCTTATTTCG AAGGCACGGA	TTATTTGGGT TATIGGAAAA	AAGCCTTTGG TAAAAAACGCT	480
AATAAAAATC AAAAACGCGG	TTTTCTCAA GCGATCTTAG	TTTCCTTGTG CCCTTTAGCG	540
AGCGTGTITT TAATCCCCTT	ATTTGGCATTG GCCAACCCGC	GATTCAAAAC GAATTGGAGT	600
TATTTCYAWG TCCTTGGAGC	GGTTGGGTW TATTTTTAA	TGGTGCATGT GATTTCTACG	660
GATTGTGTTT TGATGACCTT	TTTCTTCCCC TTATTTGGG	CGTTTATTTC TTATTTATTG	720
TTTAGAAAAT TCATTTAAA	GGCTTAT		747

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...258
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

ATGAGTAAGA GCGCGATTTT	TGTTCTTTCT GGCTTTTAG CGTTCTTGCT	CTATGCTTTC	60
TTATTATATG GTTGTGTTT	AGAAAGGCAT AATAAAGAAG CAGAGAAAAT	CCTTTAGAT	120
TTAAATAAAA AGGACGAACA	AGCCATTGAC TTGAATTAG AAGATCTGCC	AAGCGAGAAA	180
AAGAATGAAA AAATTRAAGA	AGTAACGGAA AACAGGACG ATTGTTAGA	GCCTAAAGA	240
AGAACCCAAA GAGGAGCC			258

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33

GTGATGGCTC AATCCTTGCT TGTTCATGCC	CCTTGCTCGC CCTAGCC	60
ATGATCAATC TTACACCTT TTTAAAGAA AAGAATTCA	TCCAATTGAA CGGGAAA	120
TATCTTGCTA TGCCAGCGAT TTATATTCTT TTAAGCATCG	CTCTTTGAG TGGGGTTTT	180
ATTTGGGCCGA TGCAACAATT TGAATTTCCTT TTAGCGCTG	TTGTCATGCT TTTGGGGTTG	240
TTGTTGATGC TCATTGAGA AATCAAACGC CATAAAAGCG	TGAAATTCGC TATCACTAAA	300
AAAGAAAGGA TGAAAGCTA TATCAAAAAA GCTAAATCC	TGTATTTTT AGAACGATT	360
CTTATCATCG TGTAAATGGG CATT		384

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34

GTGCGTAATG TGGTTTATT CATTTAACCA GCGATTTT TAGCGTTCAT GCTTTAGTG		60
AGTATTGCA TGCCCCATTA TAGCGTGGCT GTCATTTAGCG GGGTGGAAAGT CAAAAGAATG		120
AATGAAAATG AAAACACGCC CAATAATAAG GAAGTAAAAA CCCTTGCTAG AGATGCTTAT		180
TTTGTGAACTT CTTACGACCC TAAGGATCAA AAAAGCGTGA CCGTCTATCG TAACGAAGAC		240
ACCGCGTTTG GCTTCCCTTT TTATTTAAG TTTAATTCCGG CTGATATTTC AGCTCTCGCC		300
AAAGTT		306

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35

ATGTTTAAAA AAATCATTTT TTTGTGCGTT TTTTGATAG GGGGATTGT CATTCCACCC	60
CTTGAAGCCA TGCCTATTTT GCGCAATAAA ACCCCCCAAA AAAATTACCA AGAAGCCCAT	120
GAAAAGCTCT ATAGAACAT CATTAACCGC CAAAASSTCA CCCGTAAAAA AAGCGGGTGG	180
TATTTTTTAG GGGGGGTTGG CGCTGTAGAA GCCATTAAGG ACTATCAAGG CAAGGAAATG	240
AAAGATTGGA TGCCACGCTC AATT	264

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 384 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36

GTGCATTTA CGTGTATCTT TCTAACCTA TTAAATGGA TTTGCCAGC CAAAAACAAG	60
CAGGCGTGCA AAAAGGCCAC CAACCAGATC CATTCAAGGY YTGAAACAA TCCAGCAAA	120
TATCCCCCTT CAACTTAA CCCCTCAATC CAAGGGGTA TACAAGGGT GATGCAAGGT	180
TTTGGGGCTT TGAGCAGCAY YTTAGAAGYC CCCYTATTTG TTTTYAAGC AAAATGTGGG	240
TGGATTGGGG CCTTGAGCA TTATTTATCC CCTTTATATG GGTGGGGCAA GATTCACGAT	300
GGTGGCCATT GCGATTGAT GCAAAAGAC GCCAATGGAA GGGGTATCGG CTTGGAAAAA	360
GGTCTTCCAC CTTCAAGGG GCTG	384

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...324
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37

ATGCAGAACT TTTCTCTCG TTTAGAAGG TGGCGGTG	60
TTAGCAGCGA TTGATATTGA TGAAGTAACA GAAGCTCAAG	120
GATCAGTTAG TGAGCCTGAG CGATAAGCTT TTAGAAAAAG	180
ACCGATCACT TAAAAGATCT TAACGATTTG CATGAAAAAA	240
TTAGACCTA AGCCTAAGGG CAAAGAAGAT AGTCCTAAT	300
AAAACGGTTG AAATCGGAAG CGGT	324

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...354
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38

GTGATTTTAG CGTTCGCCTT TGGCATGAGT CTTCTTGGAT TAGCGGGCAT	60
ATTCTTTT TATCCACAGG CGTTCATATC CCTAGAAAAG AGGATATTTT ATGGATTCT	120
TTAATAGGGA TTAGCGGGAC TTTAGGCCAG TATTCTTAA CCTATGCTTA CATGAAACGCT	180
CCTGCTGGGA TCATCGCCCC CATTGAATAC ACCCGCATTG TTTGGGGGCT ATTGTTTGGG	240
CTGTATTTAG GCGATACATT TTTGGATCTT AAAAGCTCTT TAGGGGTGGC TTTGATCTTA	300
TGTCAGGCT TGCTCATTC CTTGCCGCT CTTTAAAG AATTAAAAAA AATT	354

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 162 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...162
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39

ATGATCTATT TAGGGAAGAA AAATTTAAC GCCCTTTGAA AGGGGGCGTA TTTAATGGAT	60
GAGCATTTTA GAAACCCCCC TTGGAAGAC AATTACCCG TTTTAATGGG ATTAATCTGG	120
CGTGTGGTAT ATCTAACTTT TTTCCAATC CAAAAAGCCA CT	162

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 864 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...864
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40

ATGCCGCACA AATCAAAGC GYAAACGCTT AAAGTCTTTT CAAAATTTTT CAGCAATTTC	60
AAAATCACTA AACTCAAAGA CAACCACGAA GAAGCCCACA AACTTTTTGG AGAAAATAGC	120
CGTAAAGCCC ATGACACTGA GATCATTAC TCCACTTGC AAGTGGTCCC CAGGTATTCA	180
ATAGAAACCG TGGCTTTAG TTGTTGATT TTAGCGGTG CTTACATCTT ATTCAAATAC	240
GGCGAAGCTA GAATGGTACT CCCTACCATC TCTATGTATG CCCTAGCGCT TTATCGATA	300
CTCCCTTCTG TAACTGGAGT GATCAGCTAT TATAATGAAA TCGCTTACAA CCAGCTTGCA	360
ACCAATGTTG TTTTAAAG CTTTCTAAAG ACCATCGTTG AAGAGGATTT AGTCCCTTTA	420
GACTTTAACG AAAAATCAC TCTCCAAAC ATTTCATTG CTTATAAGTC AAAACACCCG	480
GTTTAAAAAA ATTTCACCT CACCATTCAA AAAGGTCAAA AAATCGCTCT CATAGGCCAT	540
AGCGGGTSCG GAAAATCCAC GCTGGCGGAT ATTATTTATGG GGCTTACCTA CCCTAAAAGT	600
GGGAAATTT TTATTGATAA CACCCCTTTA ACCAGCGAAA ACAGGGCCTC ATGGCGTAAA	660
AAAATAGGCT ATATCCCCCA AAATATTAC CTTTTTGATG GCACTGTGGG GGATAATATC	720
GCTTTGGGA GTGCTATAGA TGAAAAACGC TTGATTAAGG TGTGCAAAAT GGCTCATATC	780
TATGATTTT TATGCCGAGCA TGAGGGCCTT AAAACCCAAG TGGCGAAGG GGCGCTAACG	840
TTAGCGCGG TCAAAAACAG CGCA	864

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 576 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

140

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...576
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41

ATGCTTGATA TATGGATAGA TATGATAATC TGTATTTTTT ATTTGCTCTT TTTTACGACT	60
CCTTACATTG TAGGCGATAT TTGCAATTG AAATTATCC GTCAAAAACT CTGGGAGAAG	120
CCTGTTTAC TCCCACAAAA GGATTATGAA GAAGCGGGAA ATTATGCTAT TAGGAAAATG	180
CAATTATCCA TTATTTCTCA AATTTAGAT GGGGTGATCT TTGCTGGTTG GGTCTTTTT	240
GGTTTGACGC ATTTAGAAGA TCTCACGGCAT TATTAAACC TTCTGAAAC GCTAGGTTAC	300
TTGGTGTTTG CTTTGTGTTT TTAGCGATT CAAAGCGTTT TAGCTTTACC CATTAGCTAC	360
TATACTACCA TGCATTGGAA TAAGGAATTG GCCTTTCTA AGGTGAGTTT ATCGTTGTTT	420
TTTAAGGATT TTTTCAAAGG ATTATTGCTC ACTTTAGGCG TGGGGTTGTT GTTGATTAC	480
ACTCTCATAA TGATCATTGA ACATGTGGAG CATTGGGAGA TCAGCTCGTT TTTTGTGCG	540
TTGTTTCA TGATTTGGC TAATCTTTT TTACCC	576

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 504 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...504
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42

ATGCTAAAAA AAATATTTT AACCAACACC TTAGGGATTT TATGCTCTAG GATTTTGCG	60
TTTTTACGGG ATTTAATGAT GGCCAAATTC CTAGGGCTG GGGGTGATAG CGATATTTTC	120
TTTGTGGCTT TCAAATTGCC TAATCTATTG AGGGCTATTT TTGCGGAGGG CTCTTTTCT	180
CAAAGCTTTT TACCGAGCTT CATACTGGAGT TCCATTAAGG GGGGTTTGC GAGTTTGGTG	240
GGGCTTATTGTT TTGTGGCGT TTATTCATG TGGTGTATAG TACTAGCGCT CAATCCCTTA	300
TGGCTAACCA AACCTCTAGC TTACGGCTTT GATGAAGAAA CGCTCAAACAT ATGCACCCCT	360
ATTGTAGCGA TCAATTGTTG GTATCTTTA TTGGTGTATA TCACCACTTT TTAGGGCG	420
CITTTACAAAT ACAAACACAG CTTTTTGCC GCGCTTATGC GCAAGCTTAC TCAATTATG	480
CATGATTTTA CCCCTTTGA TTTC	504

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 459 base pairs

141

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...459

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43

ATGAATTTAG AAGTGGCTCT AAAGGCCTTT GAAACGCTAT TGCCATGCAA TAAACAAGAA	60
GTTTTAAAAA ACCTAAAGCC CCTAGATTAA ATCGGCCGTT GCGAGCTTTT AAGCCCTAAC	120
ATTTTAATAG ATGTGGGGCA TAACCCCCAT AGCGCTAAAG CCTTAAAAGA AGAAATCAAA	180
CGCATCTTTA ACGCTCCAAT CGTTTTGATT TATAATTGCT ATCAAGATAA AGACGCTTTT	240
TTGGTGCTAG AAATTTAAA GTCTGTGGTT AAAAAGGTTT TGATTTAGA ATTGCATAAT	300
GAAAGAATTAA TCCAATTAGA AAAACTAAA GGATTTTAG AACCTTTAGG GTTAAACAC	360
GCCTTGTTCG AAGAACTGAA AGAAAATGAA ATTATTTGG TGTATGGCTC ATTCTGGTA	420
GCCAACGCTT TTTATGAACG CTATCCAAAG AAGAGGGAT	459

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...177

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44

ATGGCTATCG GGTTTCCGTT AGTGTGGGG ATTTTACTCA CCCTTTTAG CCGTTCTTAT	60
TGGCGTGAGT TTGGGGCGT TTCAGGGTA TTATGGAGGG CTAGTGGATT TAGTGGGGCA	120
AAGGTTGAGC GAAATTGGA GCGCGATCCC CATGCTTTT TTACTCATTG TGATTTC	177

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 666 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

142

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45

ATGAAGAAAA AAGCAAAAGT CTTTGTTG TGTTTTAAAA TGATTCTT GTTGTATTTG	60
GCGGTCTTTT TTTGTTGAG CGTATCAGAC GCTAAAGAAA TCGCTATGCA ACGATTGAC	120
AAACAAAACC ATAAGATTT TGAAATCCTT GCGGATAAAG TGAGCGCCAA AGACAATGTG	180
ATAACCGCCT CAGGAAATGC GATCCTATTG AATTATGACG TGTATATTCT AGCGGRTAAG	240
GTGCGTTATG ACACCAAGAC TAAAGAACG TTATTAGAAG GCAATATTAA GGTTTATAGG	300
GGCGAGGGCT TCTCGTTAA AACCGATTAT GTGAAATTGA GTTTGAACGA AAAATATGAG	360
ATCATTTTCC CCTTTTATGT CCAAGACAGC GTGAGCGGGA TTGGGTGAG CGCGGATATT	420
GCTAGCGGGA AGGATCAAAA ATATAAGATT AAAAACATGA GCGCTTCAGG GTGCAGCATT	480
GACAACCCA TTGGCATGT CAATGCCACT TCAGGCTCAT TTAACATGCA AAAATCGCAT	540
TTCATCAATGT GGAATCCTAA GATTTATGTC GGCGATATTG CTGTATTGTA TTGCCCCAT	600
ATTITCATGT CCACGAGCAA TAAAAGAACT ACCGGGTTTT TATACCTGAA GTTGGCACT	660
TCCMAC	666

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 159 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...159
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46

ATGCTGGATT TTGATTTGGT TCTTTTGGC GCGACTGGGG ATTTAGCCAT GCGAAAGCTC	60
TTTGTTCGC TTATGAAAT TTATATTCA TTATGGTT TAAAAACGAT TCTAGGATTA	120
TCGCATCGGG GCGTAAGGAG CTATCCAATG AAGAGTTT	159

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...327
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47

ATGCAAGATT TACCCCCATG CCCTAACCGC AACGACGCCT ACACCTACCA TGATGGCACG	60
CAGTCGTTT GCTCTAGCTG TTTGTATGAA TGGAATGGAA ATGAAATTAG TAATGAAGAA	120
TTGATCGTTA AAGATTGCCA TAATAATCTT TTACAAAATG GGGACTCGGT CATTCTCATT	180
AAAGATTAA AGGTTAAAGG CTCATCTTG GTGCTTAAAA AAGGCACTAA AATCAAAAAT	240
ATCAACCTTG TCAATAGCGA TCACAATGTG GATTGTAAAG TGGAAGGGCA GAGCTTGTCT	300
TTAAAATCTG ATTCCCTTAA AAAAGCT	327

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...219
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48

GTGGATGGGG CTATCATAAC AGGGAAATTAT GCCTTGCAAG CAAAACTCAC CGGAGCCTTA	60
TTTCAGAAG ATAAGGACTC GCCTTATGCT AATCTTGTAG CCTCTCGTGA GGATAATGCG	120
CAAGATGAAG CGATAAAAAGC GTTGATTGAA GCCTTACAGA GCGAAAAGAC CAGGAAATTC	180
ATTTGGATA CCTATAAGGG GGCGATTATC CGGGCTTT	219

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 711 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49

GTGTTTYCCA	TGCTGGTGT	GGTGTGAGC	GATAATTTT	TAGGGCTTT	CATTGGCTGG	60
GAAGGGGTGG	GGCTATGCTC	TTACTTGCTC	ATTGGCTTT	GGTATCATAA	AAAAAGCGCG	120
AATAACGCTT	CTATTGAAGC	CTTITGATG	AATCGAAC	CGGATTTAGG	CATGCTCATG	180
GGGATTATTT	TGATCTTTG	GAATTGGC	ACCCCTCCAGT	ATAAAGAAGT	CTTTAGCCATG	240
CTCAATAACG	CCGATTATTTC	CATGCTCTT	TACATTAGCG	TGTTTCTTTT	TATTGGCGCT	300
ATGGGGAAGA	GTGCTCAATT	CCCTATGCAC	ACATGGTTAG	CCAACGCTAT	GGAGGGGCCT	360
ACCCCTGTAT	CCGCTCTCAT	CCATGCARCG	ACGATGGTAA	CCGCTGGGGT	GTATCTAATC	420
ATCAGAGCCA	ATCCTTTGTA	TAGTGGGTG	TTTGAAGTGG	GTTATTTTAT	CGCATGCTTA	480
GGAGCGTTTG	TGGCTCTTT	TGGAGCGAGC	ATGGCTTTAG	TCAATAAGGA	TTTAAAACGC	540
ATCGTGSYAT	ATTCACGCT	TTCTCAATT	GGGCTATATG	TTTGTAGCGG	CCGGGCTTGG	600
GGCTTATGCC	ATCGCGCTT	TCCACCTCTT	TACGCATGCG	TTCTTCAAAT	CCCTCCCTTT	660
CTTAGGCTCA	GGCAATGTCA	TGCATGCGAT	GGAAAGACAAT	CTGGATATTA	C	711

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50

ATGATGATAA	CCAAACAATC	GTATCAAAGA	TTCGCTTAA	TGCGGGTTTT	TGTGTTTCG	60
CTTTCGGCGT	TTATTTTAA	CACCAACGGAG	TTTGTCCCTG	TTGCACTTCT	GTCAGACATT	120
GCGAAAAGCT	TTGAAATGGA	GAGCGCAACA	GTGGGGCTTA	TGATCACTGC	TTATGCATGG	180
GTGGTGTCTC	TTGGCTCATT	GCCCTTGATG	CTGCTTAGCG	CTAAAATTGA	AAGGAAACGC	240
TTATTGCTTT	TTCTTTTATT	TTCAGCCATA	TCCTTTCCGG	T		291

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 840 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...840
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51

ATGAAACTGA GAGCAAGTGT TTTAACCGGT GTGGCAATTTC	TGTGCTTAAT TTTAAGTGCG	60
TGCAGTAAC ATGCGAAAAA AGTGGTGAAG CAAAAGAACCC	ATGTTTATAC GCCTGTGTAT	120
AATGAACGTAGA TAGAGAAGTAGA TAGTGAGATC	CCCTTAAATG ACAAACTCAA AGACACACCA	180
TTCATGGTGC AAGTGAAGTT GCCAAATTAC AAGGACTATT	TGTTGGATAA TAAACAAGTT	240
GTACTAACTT TCAAACITGT TCACCAATTCT AAAAGAGATTAA	CGCTCATAGG CGATGCCAAT	300
AAGATCCTCC AATACAAGAA TTACTTCCAA GCTAACGGGG	CAAGATCTGA CATTGATTTT	360
TACTTGCAAC CCACCTTGAA TCAAAAGGGT GTGGTGTATGA	TAGCGAGTAA CTACAATGAT	420
AATCCCCAACAA ACAAGAAAA ACCACGACC TTTGATGTGT	TGCAAGGAAG TCAGCCAATG	480
CTAGGAGCTA ACACAAAAAA CTTGCGATGGC TATGATGTGA	GTGGAGCAAA CAACAAGCAA	540
GTGATCAATG AAGTGGCAAG AGAAAAGCT CAGCTAGAAA	AAATCAATCA GTATTACAAG	600
ACTCTCTTGC AAGACAAGGA ACAAGAATAT ACCACTAGGA	AAAATAACCA ACGAGAAATT	660
TTAGAAACAT TGAGTAATCG TGCAAGTTAT CAAATGAGGC	AGAATGTGAT TAGTTCTGAG	720
ATTTTTAAGA ATGGCAACATT GAACATGCAA GCCAAAGAAG	AAGAAGTTAG GGAGAAAGCTA	780
CAAGAAGAAA GAGAGAATGA ATACTTGCAG AATCAAATCA	GAAGTTTGCT CAGTGGTAAG	840

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...174
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52

ATGTGGTTAG ATCACATCGC TAAAGAGATC AGAAGTTTAG TGGAAAACGA TATTGAAGTG	60
GGTATTGTGA TTGGTGGAGG CAATATCATT AGGGGGGTAA GCGCGGCTCT AGGGGGGATC	120
ATTAGGCGCA CCAGTGGGA TTATATGGGC ATGTTAGCCA CCGTGATTAW GCGG	174

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...372
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53

GTGCATAACT TCCATTGGAA	TGTGAAAGGC ACCGATTTTT	TCATGTGCA TAAAGCCACT	60
GAAGAAATTT ATGAAGGGTT	TGCGGACATG TTTGATGATC	TCGCTGAAAG GATCGTTCAA	120
TTAGGACACC ACCCCCCTAGT	CACTTTATCC GAACCGATCA	AACTCACTCG TGTTAAAGAA	180
GAAACTAAAA CGAGCTTCCA	CTCTAAAGAC ATCTTAAAG	AAATTCTAGA GGACTACAAA	240
CACCTAGAAA AGAATTAA	AGAGCTCTCT AACACGCCG	AAAAAGAAGG CGATAAAGTT	300
ACCGTAACCTT ATGCGGACGA	TCAATTAGCC AAGTTGCAAA	AATCCATTG GATGCTAGAA	360
GCCCCATTAG CT			372

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...270
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54

ATGAATAAAA CCATAAAAGC CGCCGCCCTA	GCCTATAACA TGGGGCAAGA TCATGCCCA	60
AAAGTGATCG CAAGCGGGGT	GGCGAAGTG GCTAAAAGGA TCATTCAAAA AGCTAAGGAA	120
TACGATATAG CGCTCTTTTC	TAACCCCATG CTGGTGGATT CGCTCTTAAA GGTGGAATTAA	180
GACTGCGCGA TACCTGAAGA ATTGTATGAA	AGCCTGGTGC AAGTGTAAAA ATGGCTAAC	240
AGCGTGGAAA ATAACCGCGCA	AATGTCCAAG	270

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 633 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

147

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55

ATGGGGAAAA	TTTCAGCGCA	TTTACCCCAT	GAAATCAGAA	ACCCCGTAGG	CTCTATCTCT	60
CTTTTAGCTT	CGGTGTTATT	AAACCATCGG	AACGAAAAAA	CTAAACCCAT	TGTTGTAGAA	120
TTGCAGAAAG	CTTTATGGCC	CGTAGAAAAG	ATCATTAAAG	CCACCTTGCT	TTTTCTAAA	180
GGCATTCAAG	CCAACCGCAC	CAAGCAAAGT	TTGAAAACGC	TAGAGAGCGA	TCTCAAAGAA	240
GCCCTAAACT	GCTACACTTA	CTCTAAAGAC	ATTGATTTTC	TTTTAATT	TAGCGATGAA	300
GAAGGGTTTT	TTGACTTTGA	TTTAATGGGG	ATTGTGTTAC	AAAATTCTT	GTATAACGCC	360
ATTGATGCCA	TTGAAGCCCT	AGAAGAGAGC	GAACAAGGTC	AGGTCAAAT	TGAAGCGTTC	420
ATTCAAAATG	AATTATTGTC	CTTCACCAT	ATTGATAATG	GCAAGGAAGT	GGAAAATAAA	480
AGCGCTTAT	TTGAGCCTT	TGAAACCACT	AAATTAAGG	GGAATGGCTT	AGGGTTAGCC	540
CTGCTTTG	AACTCGTTAA	AGCCCATGAA	GGGAGCATTG	CGCTATTAGA	AAATCAAAGAA	600
AAAACCTTTC	AAATTAAGAT	TCTTAACGCT	TCT			633

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56

GTGTCAGAAT	TTCATCAAGT	TTATGACCCCT	TTGGGTAATA	TTTGGCTGAG	CGCTCTTGTG	60
GCCTTAATTGC	CGATTTGTT	ATTTTCTTA	TCTTTAATGG	TTTTTAAACT	CAAAGTTAT	120
ACAGCGGCCT	TTTTGAGCGT	GGCCTTATCA	GCCATTATTG	CGGTTTTAGT	GTATAAAATG	180
CCTGTTAGCA	TCGGTGGGTT	AAGCTTCCTT	TATGGCTTTC	TTTATGGCCT	ATGGCTATTG	240
GCTTGGATCA	TTATTGCCG	GATTTTTTA	TACAAACTCA	GCGTTAAATC	CGGCTATTG	300
GAAATCTTAA	AAGAAAGCGT	TCAGTCCATC	ACTTTAGATC	ACCGCATTTT	AGTGATTG	360
ATTGGCTTTT	GTGGCTTC	ATTTTAA	GGGGGATCG	GCCTTGGAGG	GCCTATTGCC	420
ATCACACGGG	CGATTTAGT	GGGGTTGGGG	TTAACCCCTT	TGTATTCTGC	TGGGTTATGT	480
TTGATCGCTA	ACACCGCTCC	TGTGGCTT	GGCGCGGTGG	GTATCCCTAT	AAGCGCGATG	540
GCGAGCGCGG	TAGGGGTGCC	AGCGATCTTA	ATTCAGCCA	TGACGGTAA	AATCCTCTT	600
TTTGTGAGCT	TGTTAGTGCC	GTTTTTTATT	GTGTTK			636

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57

ATGAAATTAA AAATGGCTAA GGATTATGGT TTTGTTTG GCGTCAAAAG AGCGATAACAA	60
ATCCCTGAAA AAAATCAAAA CAGCTTGATT TTGCTCTCGC TCATTCTATAA CGCTAAAGAA	120
ATCAATCGTT TGGAAAAAAA TTTCATGTG AAAATTGAAG AAGATCCTAA AAAAATCCCT	180
AAAAATAAGA CGCTGATCAT AAGAACCCAT GGCATTCCTA AACAGGATT AGAATACTTG	240
AAAAATAAGG GGGTTAAAAT CACTGACGCG ACTTCCCCT ATGTGATCAA ACCTCAGCAA	300
ATTGTGGAAT CCATGAGTAA AGAAGGGTAT CAAATCGTGC TTTTGGGGGA CATTAAACCAC	360
CCTGAAGTCA AGGGCGTGAT CAGCTATGCC ACTAACCCAGG CTTTAGTCGG CAATTGTTA	420
GAAGAATTGC AAGAAAAAAA ATTGCAACGG AAAGTGGTT TAGTCTCTCA AACCACCCAA	480
GCAAAACCCA AAACCTTGC AAATCGCTTC TTATTTGGTG GARGRTGCAC TGAAGTGCCT	540
ATTTTT	546

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 672 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58

ATGGATCATG AGTTTTGAT TACCATGGT TTGAGCTTT CTITAGCTTT GATTACCACC	60
CTTATTTAC TCCCTATAGG GATTTTTTA GGCTATTTTA TAAGCCTTAA ACGCAATCTT	120
TAAACGAGCT TAACAGAAAC GCTTGTTAT ATGCCCTTAG TTTTACCCCC AAGCGTGCTA	180
GGGTTTATC TTCTTTAACT TTTCGCGCT TCTTCTTTT TGGGAGCGTT TTTACAAGAT	240
GTGTTAAATG TGAAACTCGT TTCTAGTTCA AAGGGCTTA TCTTAGGGAG CGTGATTTT	300
TCCTGCCCT TTATGGTAAG CCCTATTAAA AGCGCGTTAA TTTCCTTGCC CACTTCTTTA	360
AAAGAAGCCA GTTATAGCTT GGGTAAAGGG GAATACTACA CCCTTTTTT TGTCTACTC	420
CCTAACATCA AACCCAGTGT GTTGATGGCT ATCATTACAA CTTTTATGCA CACTATAAGT	480
GAATTGGCG TGGTGATGAT CCTTGGGGCT GATATATTAG GGGAAACAAG AGTGGCTAGC	540
ATTACGATCT TAAACGAAGC TGAAGCACTC AATTATTCTA AAGCCCATCA ATACGCCCTA	600
ACGCTCACGC TTATTAGTTT TAGCCTCTTG TTTGTTACCC TATTTTAAA TAAAAAACAA	660
AGCTCGTTT TA	672

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 420 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...420
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59

ATGCATCCTA TAATGTTTGC CTATATCGCT AACCGCGCTCG CTCAAGCTAG AAAGATCAAC	60
GGAAACACTTT GCATGGCGTT TCAAAAAATA TCTCAAGTCA AAGAATTAGG CATTGATAAA	120
GCAAAGAGTT TGATAGGCCTA CCTTTCTCAA GTGATTATCT ACCCCACAAA AGATACTGAT	180
GAATTAATAG AATGTGGCGT CCCATTAAGC GATAGTGAAA TCAATTCTT ACACAACACG	240
GACATGAGAG CCAGACAAAGT GCTAGTAAAA AATATCGTTA CAAACGCTTC AGCTTTTATT	300
GAAATTGATT TAAAAAAAGAT TTGCAAGAAC TACTTTATAT TCITGATAGC AATGCTGGTA	360
ATAGAAAAAT CCTCAATGAT CTTAAAAAAG CAAACCAAGA AACTTATAAG GAAGAGTATT	420

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...219
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60

ATGTGCCTGA CAGGCCGGCTT GATGCGTTGG CTCAAATCGG TAAAGCCTGA ACCAATCTTG	60
CATTCTGTGG TGGAAATTGT GGATATTGCC GGATTGATTA AGGGGGCGAG CAAGGGGGAG	120
GGTTTAGGCA ATCAGTTTT AGCCAATATC AAGGAATGCG AAGTGATCTT GCAAGTGGTG	180
CGCTGTTTG AAGATGACAA TYATCACGCA TGTGAACGA	219

(2) INFORMATION FOR SEQ ID NO:61:

150

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...276
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61

ATGCATGTTG	CTTGTCTTTT	GGCTTTAGGG	GATAACCTCA	TCACGCTTAG	CCTTTTAAAA	60
GAAATCGCTT	CCAAACAGCA	ACAGTCCCTT	AAAATCCTAG	GCACTCATTT	GACTTTAAAA	120
ATGCCAAGC	TTTTAGAACAT	TTTGAATCA	TTCCTGTTTT	TGAAAATATC	180	
CCTGTTTTT	ATGACCTTAA	AAAACAAGGC	GTTTTTGGG	CGATGAAGGA	240	
TTATTAAAGC	AATTAAAAAA	CATCAAATCA	AACGTT		276	

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 615 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...615
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62

ATGAAAAAGA	AGCCATTGAT	GTGGCGTATC	TGTGCGTTAA	GGAGACTTCT	TCTAGGGTTC	60
AAGAGAGAGA	GAGAGTTATT	AAGCTTCGCT	AAACATTGGA	ATATCCCAAC	GATTGTCGTT	120
TTCACACACA	CTCAAGCCGA	AGCCGGCGAT	CCCTTGTCC	AAGAAACTAA	AGGGATCATA	180
GACGAAGAAT	GGGGGTTTAA	AGGTTTTGTC	AGAGCCTATG	TGAGGGTCAA	TTCCGTTGCC	240
TTTTCATTTA	GGGGGTTGAA	AGTCCCTGTT	GAAGCTTGTAG	AAGAATTGGT	AGATGAAACG	300
AAAAAAATGCC	TTCAGACGC	TGAAAAAAAT	AAGAAAAGGC	ATTTCTTGAG	TATTCAAAGA	360
GTAAAGATT	AAGAAAGAAA	ACAGGCTATG	ATAGAGGAAT	GTAAAACCAT	TATCCATGTT	420
GCATCAGGCG	CTGCAGGAGT	TGCTGGCTT	ATCCCCATAC	CTTTTAGCGA	TGCGCTCGCT	480
ATCGCACCCA	TTCAAGCAGG	GATGATCTAT	AAAATGAATG	ACGCTTTGG	AATGGATTG	540
GATAAAATCTG	TGGGCGCGAG	TTGGTCGCA	GGATTGTTAG	GCGTAAACTG	TCGCGCAAGT	600
GGGGAGGACT	CTCGT					615

(2) INFORMATION FOR SEQ ID NO:63:

SUBSTITUTE SHEET (RULE 26)

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...123
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63

GTGCTTGGCG TGTTYAATT AAGGGGCAAT GTCTCCCT TGATCAGTT GCGTTAAAG	60
TTTGGCTTGA AAGCGAAAA ACAAAACAAA GACACTCGTT ATTTGGTGGT ACGCCATAAC	120
GAT	123

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 657 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...657
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64

GTGAAAAGCG TTTTAGCGA AGAAAAAGAA ACGCCTGTTA CTAAGAAAA CGGCTTTAT	60
TTGATCGCTT ATGACCCCCCT AGATGGGAGT TCAGTGATGG AGCCGAATT CTTAGTAGGC	120
ACGATTATAG GGGTTATGA AAAGGATTAT AAGGCCAAA ATTTAGTTGC AAGCCTTAT	180
GTGGTTTTG GGCATAAAAT AGAATTGGTG GTGGCTTAC AAGAAGTTA TCGTTACGCT	240
TTTTATCAA ACAAGTTCA TTTTATAGAA ACCATCGTT TAGAAAATAA GGGTAAAATC	300
ATCGCTAGCG GAGGCAATCA AAAGGATTT TCYTTGGGCT TAAAAAAGGC TTTAGAAGGG	360
TTTTTTGCAG AAAATTACCG CTTCGATAC TCAGGATCTA TGTTGGCTGA TGTCCATCAT	420
GTGTTGGTTA AAAAGGGCGG AATGTTTCC TACCCGAAA AGAAATTGCG AAAGCTTTT	480
GAAGCTTTTC CTTAGGCCTT GATGGTTGAA AAAGCTAAAG GGGAGCGTT TTATTTTGAT	540
AAGGGGGTTA AAAAGCGTTT GCTAGATCAA AGCGTAGAAA GCTACCATGA AAAAAGCGAA	600
TGCTATTTAG CCAGCCCGCA TGAAGCTCAG ATTTAGAAA AACATTTAAA GGGAGAA	657

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 564 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...564
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65

ATGAAAAGCA	TTGGAGAAGT	GATGGCGATA	GGGGCAATT	TCTTAGAAGC	CTTACAAAAAA	60
GCCTTATGCT	CTTGGAAAAA	CAATTGGCTA	GGGTTTGAAT	CGTTAAGCAA	AGATTTAGAG	120
GCGATAAAAAA	AGGAAATCCG	CCGGCCCAAT	CCCAAACGCT	TGCTCTATAT	TGCTGATGCG	180
TTCAGGTIGG	GGGTTCTGT	GGATGAAGTG	TTTGAATTAT	GCCAGATTGA	CAGGTGGTTT	240
TTATCTAAA	TTCAAAACT	AGTCAAAGCA	GAAGAGGGCA	TCAATTCTAG	CGTTTTAACG	300
GACGCCAAAA	AATTGAGAGG	GCTTAAAAT	TTAGGCTTTA	GCGATGCCAG	GATTGCCACT	360
AAAATCAAAG	AAAATGAAAAA	TTTAGAGGTC	AGCCCTTTG	AAGTGAATT	AGCTAGATCT	420
AATTACAAA	TCGCGCCCCA	TTTGAAGAA	GTGGACACTT	GCGCGGCGGA	GTTTTTATCG	480
CTCACGCTTA	TTTGTATTCC	ACCTATGCC	CTAACCTTT	GCCCCCTATT	GGAAACAAAC	540
AAGAAAAAAC	AGAAAAGAAA	ATCC				564

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 693 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...693
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66

ATGTTGGGA	ATAACCAGTT	ACAGCTTCAA	ATCAGTCAAA	AAGATTCTGA	GATTGCGGAG	60
TTAAAAAAAG	AACTCAATCT	CTATCAAAGC	CTTTAAATT	TGTGCTTGCA	TGAGGGTTTT	120
GTAGGTATTA	AAAACAATAA	AGTCGTTTT	AAAAGCGGGA	ATCTTGCAAG	CTTAAACAAAT	180
TTAGAAGAAC	AAAGCGTTCA	TTTTAAAGAA	AAACGAGAAA	CGCTTAATT	ACAAGGGTTT	240
TCTTATTCTT	TGAAAAGCCA	AAATATTGAC	GGCGTGCAGT	ATTTTTCATT	GGCTAAAAAA	300
ACAGGGGGTG	TGGGGGATA	CCATAAAAAT	GATTGTTTA	AGACTTTTG	CACGAGCTTA	360
AAAGAGGGCT	TAGACAACCC	GCAAGAAAGC	ATGCAGTATT	TCCATCAAGA	AACAGGCTTG	420
CTCTTGAATG	CGGCTAAAAA	TGGCGAAGAG	CATTCTAATG	AAGGATTAAT	AACCCTTAAT	480
AAAACGGGTC	AAGACATTGA	ATCGCTTAT	GAAAAGATGC	AAAACGCCAC	TCGTTAGCG	540

GAECTCCCTCA ACCAACGGAG CAATGAAATC ACTCAAGTCA TTTCTTTGAT TGATGATATT	600
GCAGAGCAAA CCAATCTCTT AGCCCTAAAC GCCGCTATTG AGGCCGCACG ACCGGTGAAC	660
ATGGCAGAGG GTTTCGGGTG GTGGCTGATG AGG	693

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 189 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...189

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67

ATGTGGGATTA TGTCTTCACT TTCTAGTTCA TTCTTTCAATT CGCTCTTCTT CATCAAATCA	60
AACCCTGGCC AACTCTAAA AGGTTGGGT TCAAAAAATCT TTTTCATAAA TAGAAAGTTT	120
GTTTAGCAC AGTATAATCC TAGCGTTCA ATTITATTT TACTCAATAG GGTGTTGGT	180
GTGGCGCTT	189

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 459 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...459

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68

GTGGCGCTA ACCCTGTGCC GCATGCGAA ATCTTGCAAT CAGTTGTGGA TGATTTGAAA	60
GAGAAAGGGA TCAAATTAGT GATCGTGTCT TTTACGGATT ATGTGTTGCC TAATTTAGCG	120
CTCAATGACG GCTCTTTAGA CGCGAATTAC TTCCAGCACC GCCCTTATTT GGATCGGTTT	180
AATTGGACA GAAAAATGCA CCTTGTTGGT TTGGCCAATA TCCATGTGGA GCCTTTAAGA	240
TTTTATTCTC AAAAAATCAC AGACATTTAAA AACCTTAAAAA AAGGCTCAGT GATTGCTGTG	300
CCAAATGATC CGGCCAATCA AGGCAGGGCG TTGATTTAC TCCATAAACAA AGGCCTTATC	360
GCTCTCAAAG ACCCAAGCAA TCTATACGCT ACGGAGTTG ATATTGTCAA AAATCCTTAC	420
AACATCAAAA TCAAACCCCT AGAAGCTGCG GTTATTGCC	459

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69

ATGGGGCTTG TTGCGAGCGG CATTAAACGAT	GAAGAGCTTT TAAAATGGCT TCAGGC	60
GGGTAAAAAA TGGGTCTTTC TTTCAAGTG	CTAGATGATA TTATAGACGT TACACAAGAT	120
GAAAAAGAAA CGGTAAACAC CGCATTTA	GACAGCGCTA AAAACAGCTT TGTGAATTAA	180
TTGGGCTAA AAAAGGCAGC GGTTACGCC	AAACTT	216

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 627 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70

ATGGGGTTTA ACCGCTTGGT GGATAGAGAC ATTGATAAGG ATAACCCAAG GACGAAAAAC	60
CGCCCGAGCG TGGATGGTAG GATCAGCGTT AAAGGCATGG TCATTTTTAG CGTTTCAAAC	120
GCTCTTTTGT TCGTGGGAGT GAGTTATTC ATCAACCCCT TAGCTTCAA CCTTTCTTA	180
CCTTTTTTAA TCATTTTAGG GGGTTATTG TATTCAGC GCTTTCTTC TTTGGCGCAT	240
TTCGTCGTGG GTTGGCTTT GGGTTTAGCC CCCATTGCAAG GAAGCGTGGC GGTGTTAGGG	300
GATATTCCCT TATGGAATGT CTTCCTGGCY TTAGGGGTGA TGTTGTGGGT GGCTGGGTTT	360
GATTTGCTCT ATTCTTACA GGATATGGAG TTGATAAAAG AAAGGGGCTT CTTTTCCATT	420
CCTAGCCAAT TAGGGAAAAA ATGGTGCTTG AATCTTCAA GGCTCTCGCA CCTTGTGGCA	480
CTGATCTGCT GGCTTTGTT TGTGAAATGC TATCATGGGG GGCTTTTGC GTATTTGGC	540
TTAGGGTTT CAGCCTTGAT CTTACTCTAT GAGCAGATT TAGTGGCCAG AGATTATAAA	600
AACATTCCCTA AAAGCCTTTT TTGTGAG	627

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...285
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71

GTTGGAGCAAA ATAAAATCAT TAAACTCTTC ACTGTGGCGA CTATGGCGAT GATGCC	60
ACATTGATTG GCACGATTWA TGGCATGAAT TTTAAATTCA TGCCGGAGTT AGAATGGCAA	120
TACGGGTATC TTTTGCGCT GATTGTCTG GCGATTCTA CGATTTGCC GGTGATTTAT	180
TTCAAAAAGA AAGGGTTGGT TGTAGCCTT CATGGAATT TTATCCTCAC TCTTAGACGC	240
TCTTTCTACA CCCCATGGCA TAGTCTCCCT GGCTACGCCA CGCTT	285

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...276
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72

ATGTTCGATT CAATCGTTTA TTTTTCAAT AAGAGCGGGT TTGTTACCAC GCTTGT	60
GTTGGATTT CGCTTTATTT GGTGATGACT TTATGGGTCT TTTTGTATAA AAGCATTGTA	120
TTAAAGATTG AACTCAGGCG CGAGATGCAA TCTTGTCTA ACATTCTAA TGGAGCGCAA	180
GACGCTCCAG AGCATTATAT GTTTAATAAA AAAAGAAATG ATGAGACCAA AAGGTATTCT	240
AATGAATTGT TGCAGGSCTT GGAAACACCCA GGTTCT	276

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 375 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73

ATGGCGATGC TYTATTGCA	TCGGTTATTG ATGCCGATT	TAGGAGCGAT TAAAGGGGG	60
GATATTGGCG AATGGTTCCC	TGATAATGAC CCCAAATACA	AAAACCCCTC TICTAAAGAG	120
CTTTTAAAAA TCGTGTTGGA	TTTTCTCAA AGCATTGGGT	TTGAATTGCT TGAAATGGGA	180
GCGACCACATCT TTAGCGAAAT	CCCTAAATTC ACTCTTACA	AACCGGGCAT TTTAGAGAAAT	240
TTGAGCCAAC TTTTGGGTTT	AGAAAAATCT CAAATCAGCT	TGAAAGCCAC TACAATGGAA	300
AAAATGGGGT TCATTGGCAA	ACAAGAAGGG CTGTTAGTCC	AAGCGCATGT GAGCATGCGT	360
TATAAACAAA AACTT			375

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3534 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...3534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74

ATGATACCAA ATTTAGATAT AGAAGGAGAA ACAATGACTA ACGAAGCCAT TAACCAACAA	60
CCACAAACCG AAGCGGCTTT TAACCCCGAG CAATTATCA ATAATCTTCA AGTGGCTTTT	120
ATTAAAGTTG ATAATGTTGT CGCTTCATTT GATCCTAATC AAAAACCAAT CGTTGATAAG	180
AATGATAGGG ATAATAGGGCA AGCTTTTGAG AAAATCTCGC AGCTAAGGGA GGAATTGCT	240
AATAAAGCGA TCAAAAATCC TACCAAAAAG AATCACTATT TTTCAGCTT TATCACTAAG	300
AGCAATGATT TAATGACAA AGACAATCTC ATTGATACAG GTTCTTCCAT AAAGAGCTTT	360
CAGAAATTTG GGACTCAGCG TTACCAAATT TTTATGAATT GGGTGTCCA TCAAAACGAT	420
CCGTCTAAA TCAACACCCA AAAAATCCGA GGTGTTATGG AAAATATCAT ACAACCCCT	480
ATCTCTGATG ATAAAGAGAA AGCGGAGTTT TTGAGCTCTG CCAAACAAGC TTTTGCAAGGA	540
ATTATCATAG GAAACCAAAT CCGATCGGAT CAAAATTCA TGGGCGTGT TGATGAATCT	600
TTGAAAGAGA CGCAAGAAGC AGAAAAAAAT GGAGAGCTA ATGGAGATCC TACTGGTGGG	660
GATTGGCTTG ATATTTTTT ATCATTTGTG TTAAACAAA AACAAATCTTC CGATCTAAA	720
GAAACGCTCA ATCAAGAACCC AGTTCCCTCAT GTCCAACCG ATGTAGGCCAC TACCACCACT	780

GACATACAAA	GCTTACCGCC	TGAAGCTAGG	GATTGCTTG	ATGAAAGGGG	TAATTTTCT	840
AAATTCACTC	TTGGCGATAT	GAACATGTTA	GATGTTGAGG	GAGTCGCTGA	CATTGATCCT	900
AATTACAAGT	TCAACCAATT	ATTGATCCAC	AATAACGCTC	TGTCTTCGT	GTTAATGGGG	960
AGTCATAATG	GCATAGAAC	TGAAAAAGT	TCATGTTGT	ATGAAACCAA	TGCTGGCTCT	1020
GAAGCTAGGC	ATGATTGGAA	CGCCACCCTT	GGTTATAAAA	ACCAACGAGG	CGACAATGTG	1080
GCTACACTCA	TTAATGTGCA	TATGAAAAT	GGCAGTGGGT	TAGTCATAGC	AGGTGGTGAG	1140
AAAGGGATTA	ACAACCCTAG	TTTTATCTC	TACAAAGAAG	ACCAACTCAC	AGGCTCACAA	1200
CGAGCATTGA	GTCAAGAAGA	GATCCAAAAC	AAAGTGGATT	TCATGGAATT	TCTTGCACAA	1260
AATAATGCTA	AATTAGACAA	CTTGAGCAAG	AAAGAGAAAG	AAAAATTCCA	AAATGAGATT	1320
GAAGATTTTC	AAAAAGACTC	TAAGGCTTAT	TTAGACGCC	TAGGGAATGA	TCACATGCT	1380
TTGTTTCTA	AAAAAGACAA	AAAACATTAA	GCTTTAGTTG	CTGAGTTGG	TAATGGGGAA	1440
TTGAGCTACA	CTCTCAAAGA	TTATGGAAA	AAAGCAGATA	AAGCTTTAGA	TAGGGAGGCA	1500
AAAACACTC	TTCAGGCTAG	CCTAAACAT	GATGGCGTGA	TGTTTGTG	TTATTCTAAT	1560
TTCAAATACA	CCAAAGCCTC	CAAGAGCTC	GATAAGGGTG	TGGGTGCTAC	GAATGGCGTT	1620
TCCCATTAG	AAGCAGGCTT	TAGCAAGGTA	GCTGCTTTA	ATTTGCCTAA	TTAAATAAT	1680
CTCGCTATCA	CTAGTGTGCG	AAGGCAGGAT	TTAGAGGATA	AACTAATCG	TAAAGGATTG	1740
TCCCCACAAG	AAGCTAATAA	GCTTGTCAAA	GATTTTTG	GCAGCAACAA	AGAATTGGTT	1800
GGAAAAGCTT	AAAACCTCAA	AAAAGCTGTA	GCTGAAGCTA	AAAACACAGG	CAACTATGAC	1860
GAGGTGAAAC	AAGCTCAGAA	AGATCTGAA	AAATCTCTAA	AGAAAACGAGA	GCGTTTGGAG	1920
AAAGATGTAG	CGAAAAAATT	GGAGAGCAAA	AGCGGCAACA	AAAATAAAAT	GGAAGCAAAA	1980
TCTCAAGCTA	ACAGCCAAA	AGATGAGATT	TTTGGCTG	TCAATAAAGA	GGCTAATAGG	2040
GATCGAGAG	CAATCGCTTA	CGCTCAGAAT	CTTAAAGGCCA	TCAAAAGGG	ATTGTCGTAT	2100
AAACTCGAAA	ATATCAACAA	GGATTGAAA	GACTTTAGTA	AATCTTGT	TGAATTCTAA	2160
AATGCCAAA	ATAAGGATT	CAGCAAGGCA	GAAGAACAC	TAAGGCCCC	TAAAGGCTCG	2220
GTGAAAGATT	TAGGTATCAA	TCCAGAATGG	ATTCAAAAG	TTGAAAACCT	TAATGCAGCT	2280
TTGAATGAAT	TCAAAATGG	CAAAAATAAG	GATTTCAGCA	AGGTAACGCA	AGCAAAAGC	2340
GACCTTGAAA	ATTCATTAA	AGATGTGATC	ATCAATCAA	AGATAACGGA	AAAAGTTGAT	2400
AATCTCAATC	AAGCGGTATC	AGTGGCTAA	CCAACGGGTG	ATTCAGTGG	GGTAGAGCAA	2460
GCGTTAGCCG	ATCTCAAAA	TTTCTCAAG	GAGCAATTGG	CTCAACAAGC	TCAAAAAAAT	2520
GAAGATTTC	ATACTGGAAA	AAATTCTGCA	CTATACCAAT	CCGTTAAGAA	TGGTGTAAAC	2580
GGAACCTCTAG	TCGGTAAATGG	GTATCTAA	GCAGAAGGCCA	CAACTCTT	AAAAAACTTT	2640
TCGGACATCA	AGAAAGAGTT	GAATGCAA	CTTGGAAATT	TCAATAACAA	TAACAATAAT	2700
GGACTCGAAA	ACAGCACAGA	ACCCATTAT	ACTCAAGTTG	CTAAAAGG	AAAAGCAAAA	2760
ATTGACCGAC	TCGATCAAAT	ACCAACTGGT	TTGGGTGATG	TAGGGCAAGC	AGCGAGCTTC	2820
CTTTGAAAAA	GGCATGATAA	AGTTGATGAT	CTCAGTAAGG	TAGGGCTTTC	AGCTAACCAT	2880
GAACCCATT	ACGCTACGAT	TGATGATCTC	GGCGGACCTT	TCCCTTGAA	AAGGCATGAT	2940
AAAGTTGATG	ATCTCAGTAA	CGTAGGCCCT	TCAAGGGAGC	AAAATTGAC	TCAGAAAATT	3000
GACAATCTCA	ACCAGGGCGT	ATCAGAACCT	AAAGCAAGTC	ATTTTGACAA	CCTAGATCAA	3060
ATGATAGACA	AGCTCAAAGA	TTCTACAAA	AAAATGTTG	TGAATCTATA	TGTTGAAAGT	3120
GCAAAAAAAG	TGCCTACTAG	TTTGTCAAGC	AAATTGGACA	ATTAGCTAC	TAACAGCCAC	3180
ACACGCATTA	ATAGCAATGT	CAAAATGGA	ACAATCAATG	AAAAGCGAC	CGGCATGCTA	3240
ACGCAAAAAA	ATTCTGAGTC	CCTCAAGCTC	GTGAATGATA	AGATAGTTG	GCATAATGTG	3300
GGAAGTGTCTC	CTTTGTGTCAGC	GTATGATAAA	ATTGGATTCA	ACCAAAAGAA	TATGAAAGAT	3360
TATTCTGATT	CGTTCAAGTT	TTCCACCAGG	TTGAGCAATG	CCGTAAGA	CATTAAGTCT	3420
GGCTTGTG	AACTTTTAAAC	CAATATATT	TCTATGGGAT	CTTACAGCTT	GATGAAAGCA	3480
AGTGTGGAAC	ATGGAGTCAA	AAATACTAAT	ACAAAGGTG	GTTTCCAAAAA	ATCT	3534

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75

ATGAAAGCGT	TGAAGACTTT	TTTAAAAAAA	TCCCTTATTTC	TGTTACTAGC	AATGCCCTTA	60
AACCACTTAA	ACGCTGTGGC	TATGATGTC	GATAATCTA	CGCAGAACGC	TTGGAATGGT	120
GCTAAAAGAG	CATGGGATGA	AAGCAAGTGG	GCTAACATT	TAGCCACTAT	TACTGAAAGG	180
ATCAAGCTCG	CTCAAGACAC	ATTAGATAGG	GCTAATCAGA	CGCTTAATTTC	CATCAACAAA	240
GTGAATGATG	TTTGAAACAA	AACCAATCAA	TTTCTAACAG	GCAGTATTTT	AAGCATCCCC	300
AATCCCATGC	AGTATGTCAGA	AAAATCCAA	AGTTTGCCCA	AGCAAGTTCA	AGCCAATACT	360
GAAAGGATCA	AAGAAAATGC	ACAAAATCAT	GATATACGCA	ATCAAAATTGC	AGCCAAACGC	420
ATCTCTGAAA	AATGCCCTGA	ACTCAATTGG	GATGTCAGTC	AAGACGCGAG	CCCTACAGAG	480
AAAAACTTAC	ACCAATTGTT	CACGAGCAAG	GGGAAAGAAA	GCGCTAACAC	AAAGGCTCTA	540
AAGGATTITG	CTAACGCCAT	AGGTAACACT	CAAATCAGCA	CGGCGAACGA	TTTAGGAGCT	600
GGACTTAGAG	GCAGAGCCCTT	ATTAGAATAC	ATTGCAATTTC	AAAAGGCAA	TTTACAAGCG	660
GCTAAAAAAA	TCCAATTATT	AGACAGCCAA	ATGACTTTAG	CTCTACTCAA	TAACGACTAT	720
ACGGCTTATG	AAAAACTTAG	AGCTGAAAAA	GAAGAATTAA	AAAGACAAAT	CGCTTCAAAT	780
GTGTATGCGA	AAAGTCAAACA	GCTTGTGTA	GCTTCCCAAG	ATAGAGCGTT	TAGTCAAATG	840
GATAATGAGT	TGGGCTTAA	AACTTTGGG	TTCAACGATG	AGAATGTTAA	AAAAGGTTAT	900
TGCAAGAAAG	AAAACAGAAA	TGGCAAAAGC	GAGTCATCC	CTAACATGCT	CAATGTTAAT	960
CGCTTAAAG	CGCAATTGTA	TGAGCTTAAT	TTAGATTATA	GTAGGGATAT	TGCTGGTAAA	1020
AAAGGTGAAG	CAGCCGCTAA	AGTGTCAAT	GACTACAAAC	ACCGATTCCA	ACAATTAAGC	1080
GTAGAAACTG	CTTTAGAAAT	CGCTCAAAAT	TTAAGTTITA	TGAATAAGAC	GCTAGGTTTA	1140
ATGGTGCAAA	TGCAAAGCTA	TGCAATTCAAG	CAACAAATGG	GCTATTGTA	AGATATTATT	1200
CCTGCTGACG	CCCTAAAAGA	TGACAAAGAG	CATCAAGAAA	ATCTTGAACA	AAAACAACAA	1260
GAAATAGAGA	AAAGTCTATAG	GGCTAAATTAA	GACGCTTATG	CTTTCCTAA	TGGTAGTGT	1320
GGAAAGGCAA	GTGGCGTGA	TTCAAATAGT	AATAATGAAG	CCCCAAGCTC	TGATAATATC	1380
CAGTCGTTA	ATCCGTAT					1398

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76

GTGATGGATG	CAGAAAATGG	GGAAATTGCTC	GTTGCAGGAA	GTTACCCCTGA	ATACAATTG	60
AACGATTTG	TAGGCGGGAT	CAGTCAAACAC	AAATGGCAAA	AACTCCAAGA	TGATATTAT	120
AACCCTTTAT	TAAACCGCTT	CGCAATGCCT	TGTATCCGCC	GGGATCTGTG	GTTAAAATGG	180
						189

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...1263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77

ATGAATTTTT TTGACACCCT TATGGGTATG	60
AGCTTGCCTG AACATGTGGG TAGCTTTTT CATGCACAAAC	120
ACTATTTTAT TTATGATATG GGCCTATAAG CGTGAAAG AGGGCGATAT	180
AAAACCGCTA TGGGTGTGGT TGTATTATA GCGTTGTAG GATTTATCAA	240
AAAAATCCTA ATGATTTAA CACTTATTT ATCAATACGA TATTCTACCC	300
CTAGCCATAC TTATCGCTCA AAGCCTAAAT GATGCCCTAG AAATCCCCAC	360
TTAACACTAAT TTAAGTCCTA GTGAAATTAT TAGCATAGGA AATTAGCCT	420
CAAGTGGCTA TGCAATGATA GTTAAATCTGT GGGATAATGC	480
TTTTGATGGT ATTAACATGT TTAATTGGCT CACAATGATA	540
CCTAAAATAA TTATGTTTT TTTAGTGATT TTAGGGCAAT TATTGTTTTT	600
CTTATTATTG TGTTATTAGT TACAGCAGAA ATTTTATGT GGTCAGCATT	660
GTATTGCCCT TAGGTTAAAT CCCCCAAACC AAAGGCATGT TATTAGCTA	720
CTCATTTCCC TTACTCTTAA TAAACCTTGT ATGATGTTAG TAGCTTTTT	780
TAATTATGGA ATAATCTATA AAGTCAATAC TTAAATCCCC ACTAACACG	840
AAGTCACACA AGGCTTTTAT GGCAATGCGG ATAAAATGGC	900
AAATGAGGGA AAAATTATTG ATGTCTTTGG CAATGCTTTA	960
GAAGGAGATT GGAACCTCTA TATAGCCCAT AGTTCTATTG TAGGTTTTT	1020
AACCATTATT GTTTAGGTT CTGTGATTTC TTTCCTTCTA GTCAACAGAG	1080
TGCCTGATT TATCAATAAT ATCTTGGCA CAAGTGGAGG CGTGGGGCA	1140
GTAAACAGAAA TGATGCAAA AATTGGCATG ACAATAGGCG GAGCTGTATT	1200
TGGGGTAGT GCAGTTATGG TTGCTAATCA AGTTAACCAA	1260
GCCTATCAGA GTGCTGGGG CGGACTAGCA GGACTTCAAG CTGGAGCTAA	1263
AGCTTTGGG CTTGGAGCAA TCAGTGGAGG GGCAAGTGCT ATGGCAAACC	
ACAGGAGTGT TAAAGCTGGG GTGAAACACT TTGTTAAAGT GGCTTGGAT	
TTGATAATGA TAAAATAAT AAA	

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78

ATGGATGAAC CAGAAACCAG TTTAGAGCAA AACGCTCTTA TAAGACTATC AAATCTCATA	60
AGCTTGCAGCA ACACCCAACA ACTTACAAGT ATCATGCCA CTCATGATCC TATTGTCTTA	120
GATAGTGCG AATGGGTATT GCTCCTAAG AATGCCAACA TTGCTCAATA CAAACCTTTA	180
AATTCTATAT TAAAATCTGT AGCTAAACT TTAAACTTTA AAGAAAAACC AACCAACAAA	240
GAECTTATTAG CGTTACTAAA GGATATT	267

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 711 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79

GTGAAACCT TAGGATTGTC TTCGCTTGGT GGGACTTTAG AATTTTACGA TTTTATCATC	60
TTTGTATTT TTACAAGTAT CATTGCCAAA CACTTTTCC CAAACACGCT TAGCCCTATC	120
TGGCTGAAA TCAACACTTA TGGGATCTT GCTGCAGGTT ATCTGGCGCG CCCGCTTGGT	180
GGCATAGTGA TGGCCCACCT TGGGGATAAA TTGGTCTGTA AAAACATGTT CATGCTCTCT	240
ATTTTATTAA TGGTAATCCC AACCTTGGCG CTAGCTTTGA TGCCAACCTTT TAATGATTIG	300
GTGGGTTTG GCGTGGGATAG CATGGGGCTT ACCCTAAAA ACGCTCATTA TCTTGGTTAC	360
ATAGCTCCTG TTTTTTRGTT RCTTGTAGG ATTGTCAAG GCGTCGCTGT GGGTGGTGAA	420
TTGCTGGCG CTGGGGTTT TGTCCATGAA CATGCCAAC AAGGACAAAA AAACACTTAT	480
ATCGGTTTT TAACCGCTTC CGTACTTTCT GGGATTTGC TTGGGAGTT GGTTTATATC	540
GGGATTTACA TGGTTTTGCA AAGCCTGTT GTGAAGATT GGGCTTGGCG GGTTGCCTTT	600
GGCCTGGAG GAATTTTGG TATCATTCT GTGTATTGAA GGCGCTTTT AGAAGAAACT	660
CCCGTTTTC AGCAAATGAA GCAGGGACGA TGCCTTAGTC AAATTCCCGC T	711

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1413 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80

ATCGC	AAAT TTTTGGATGG	GGCAAAAAGT GAGGTTTAA	AATA	CGATGT GATTTC	TTTT	60
GAT	ATTTTG ATACCCTCCT	TCTAAGACCT TTCA	AAAC CCACAG	ATTTTGAT	TAT	120
ATT	GAGACTA AATACAATAT	AAAGGTTT CATCAAGCAA	GGATCC	TGCG AGAAAT	CCA	180
TCC	CAGAAAAT TAAGTAAAAG	ACAAGACATT ACTCTAGATG	AAATTTATCA	TCAAATCCC	A	240
AA	AGAGTTTC ATTCA	TATAA GGGAGTAGAA ATCGCTACTG	AAAAGAGGT GCTTGT	TCCA	300	
AACTTGGAGA	TGTTAGAACT CTATCGTTTC	GCTAAAGAGA ACAATAAGAG	AGTGATTATT	GCAT	360	
GTATCAGATA	TGTATTAC	TTTAGAGGTT CTTGAAGATA	TTTTAATTTC	TAAGGGTTT	420	
GATGGT	TATAA CAAAGTTCTA	TCTTAGTAAC CATATAATGC	TCACTAAACA	TTCAAAAGGAT	480	
TTGTT	TAAGC ATGTTTAAA ACAAGAAAAT	ATTACTAATA CGCAGATATT	GCATATCGGT	540		
GATA	AAITCTT CGCAAGATGA	CGCTATGCC	AAAAGTTAG GCATACCAAC	GCTATTAGA	600	
AAAAGCGTGT	TGAAACATT AGAAGAAGTT	TTCCCTAAAT ACAAAACATT	TAATCCAACC	660		
AGTGTGCGC	AAAGTTTAT TTTAGGATCT	TTATGCGTTT	TTTATAAAAAT TTATATTCAA	720		
AAACATGAAA	AATTGATTA TTGGTTCTT	TTAGGAGCGA	TGCAGGCAGG AATTGCA	780		
GTTGCTTATT	GCCAGTTAT CTATAAGGAG	ATTCA	AAAATTTGA TACTTIA	TG	840	
TTTGTGCGC	GAGATGGTTA	TTTATTGCAA AAAATTTTA	ATATTTATA	TCCAAATTCA	900	
TATAAA	ACTA CTTATGTCTA	TGCTCCAGA	TTTTAAAAA AAGCGGTATT	TTT	960	
GTAGAGGGCG	AGAGTTGGA	AATTGCGT	TTTTAGAAG CGGAAGAAGA	AGTTAAAAG	1020	
AAGCAAATCA	CCACCAACCA	ACAGCGTAT GTATATCTCT	ATAGCAATT	TGAACATTGC	1080	
CGC	CATT	CGTTAAAATG TTAGATAAT	TACAGAAAAT ACTTGT	TTTC	1140	
GAAGCAAATA	TCGCTATTGT	AGATACGATT	ACTTTAGGCT	TTCTCGCA	1200	
CAAAAAGCTT	TAATAAAGA	AGTTTTGGG	TGCTATGTGG	AGGGTTAAC	1260	
TATGATTGCG	TGAGTTCTT	ACCTTTCA	CACCTAAAC	CCGTTTATT	1320	
GATT	TTATGG AGTTTTGCT	AAACAGCCT	GAATACCTA	TCATAA	1380	
GTTCCAATCT	TATCAAAAG	ACGTTTCATC	TTG	1413		

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81

GTGTTGAAAT	TCTTGAAGA	TTCCAAACAG	CTTAGCACGC	CTATGGAAA	GAGCGCGGTG	60
GGGATT	TTTGA	TTTCCAAGA	TATTGAGCC	ATTCCCATGC	TTTAATTTC	120
GGCAGTAAGG	ATTCTCATGT	CAATTGCTC	ATTCTTAAA	CCCTTATTTC	AGCGGGGATT	180
ATT	TTTAATTTC	TTTATTATT	GCCTGGAAA	AAAGGGCTA	ATCTCATCTT	240
AAACACACGC	GCTTGCCTGA	AATCTTAA	GGCACGGATT	TTAGTGATTG	TTGCAGCGC	300
GGCGGGGTTG	AGCCATT	TTGGGTTTC	TATGTCTT	GGGGCGTTCA	TTGTGGGCAT	360
GGCGATTTC						369

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82

ATGATTTTAG	CCCTTTTGAT	TTCTAAAGAA	AAAACGCATT	TAGAACGTT	GTATTATTTG	60
AGCTATGGCG	TGCTTTAGG	GGCGTGGCT	CAAATCTTAT	TACACTTTTA	TCCTTAGTA	120
AAATTAGGCT	TATGGGATT	ATTATTAAA	GGGTGTTGG	GTTTTAAGAC	AAAAATACA	180
AACAAAAAAAG	AATATCGTT	GAATAGGGCT	AAAAGGATC	TAAAAGCGTT	TTTCAAGCAA	240
TTCTTCCCCA	GCGTCTTAGG	CAATTCTAGC	GCTCAGATCG	CTTCCTTTTT	AGACACCACA	300
ATCGCTTCTT	TTCTGGCGAG	CGGGAGCGTG	TCTTATTGT	ATTACGCCA	TAGAGTCTTC	360
CAGCTCCCTT	TAGCCTTATT	CGCTATCGCT	ATCTCCACAG	CTCTTTCCC	TAGCATGCG	420
ATCGCGCTTA	AAAACAACCA	GCAGGATT	ATCTTACAAC	GCTTGCAAAA	GGCGTGGTT	480
TTTTGGTGG	GGGTTTGCT	TCTTGCAGC	ATTGGGGGGA	TAATGTTAAG	CAAAGAAATC	540
ACCGAACTT	TATITGAAAG	GGGGCAATT	AGCCCTAAAG	ACACCCAAT	CACTTCGCAA	600
GTCCTTTCGC	TCTATCTTT	AGGCTGCTC	CCTTTGGGC	TAACCAAAC	CTTTTCTTTA	660
TGGCTTATG	CGAAATTAGA	GCAAAAAAAA	GGGGCTAAA	TCTCTTTAAT	TTGCTTTTT	720
TTAGGTTTAG	CGGCTCTTT	GAGTTTAATG	CCTTTGTTAG	GGGTTTGGG	TTGCGT	777

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83

GTGCTAAAT	ACCTACRRT	GTTCATGTGT	GGGGATGCGG	TCATTATCAG	TAAGGCGGAC	60
ATGATTGAAG	TGTTTAATT	TAGGGTTCT	CAAGTCAG	AAGACATCCA	AAAATTAAG	120
CCTGAAGCGC	CCATTTTTT	AATGAGCTCC	AAAGACCTA	AAAGCTTGG	AGATTAA	180
AATTCCTTT	TAGAAAAAA	CGGTGAAAT	TACCAATCCA	CGCATTGTT	T	231

(2) INFORMATION FOR SEQ ID NO:84:

163

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 540 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...540

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84

ATGCTGCTT GCGCGGAAAG	GAATGAGACT TTAAAAAAAG	CGGTGCCTAT TGGTGTGGC	60
TTGATAGAGA GCGCGATCAA	TTTAACCGAGA ATGTCCTTA	AAAACCCCTGA TACAGAAAGC	120
CTTATTCTTA TAGGGAGCGC	GGGGAGTTAT AGCCCAGAAA	CGGAGATTTT GAGCGTGTTT	180
GAAAGCATTG AAGGCTATCA	AATTGAAGAG AGTTTAGGCC	ATTTAAACAG CTACACCCCT	240
TTGGATAATT TCATTACACAT	AGAAAATAA GAGCAGGCTC	TTTTGAAAG GGTGCGTGTG	300
AATAGCAGTA ACTACATCCA	CACCAGCGAA ATGTTTGCTA	AAAAAATGGT TCAAAAGGGC	360
GTTTATTAG AAAACATGGA	GTTTTTAGC GTCTTAAGCG	TGGCTAAAAT TTTTTCTTTA	420
AAGGCTAAAG GGATTTTTG	CGTGAGCAAT CATGTAGGGC	TTAACGCGCA TAAGGAATT	480
AAAGAAAACC ACGCCAAAGT	CAAACAGATT CTAGAAAACA	TCATTGATAG TTTGATAGTT	540

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 639 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...639

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85

GTGTATGAAG AAAGGATCAC	TCTGGCTTCT CAAGGGATCC	CTAAACGAG TAAAGTGGC	60
TTGAAATCT TTGACACTAA	AGACTTGGG GCGACTGATT	TTGATCAAAA CATCAAAC	120
ATTCGCGCCA TTGAGGGGGA	ATTGTCGCGC ACGATTGAAA	GTAAACCC CATTCTTAAA	180
GCCAATGTGC ATATTGCAAT	CCCTAAAGAC AGCGTGTITG	TGGCTAAAGA AGTCCCTCCT	240
AGCGCTTCAG TGATGCTCAA	GCTTAAGCCT GACATGAAGC	TTTCACCCAC TCAAATT	300
GGGATTAAAA ATTAAATCGC	TGCAGCTGTG CCTAAACTCA	CGATAGAAAA CGTAAAATC	360
GTGAATGAAA ATGGCGAATC	AATAGGCGAG GGCATATAC	TAGAAAATC CAAAGAATT	420
GCCTTAGAGC AATTGCGCTA	CAAACAAAAT TTGAAACA	TTTTAGAAAA TAAGATCGTC	480
AATATCTTAG CCCCTATTGT	GGGGRGTAAA AACAARGTRG	TCRCAARRGT CAATRCGGAG	540
TTTRATTTC	RCCAAAAGAA AAGCACCAAA	GAGACTTTG ATCCCAATAA	600
		TGTCGGTAAG	

GAGCGAGCAA AATTTAGAAG AAAAAAAAGA AGGCCTCC

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(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 444 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...444

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86

GTGATAARGA AAGGCTATAT AAGAGGAGAT CTTATCGTA TAGTTAGAAA TTTATTCTT	60
GTATCGTTG TGGCGTATAG TAGTGCCTTC GCACGGATT TAGAAACCGG AACCAAAAC	120
GACAAAAAGA CGGGTAAAAA ATTTTACAAA CTCCATAAAA ACCATGGCTC AGAACCCAG	180
ACTAAAAACG ATAAAAAAGCT TTATGATTTC ACTAAAAATA GCGGATTAGA AGGCCGTGGAT	240
TTAGAAAAACG GCCCTAACCT TAAAGCCAT AAAAAGCG ATAAAAAGTT TTATAAACAA	300
CTCGCTAAA ACAATATCGC TGAAGGGGTG AGCATGCCGA TTGTGAATT CAATAAAGCC	360
CTATCTTTG GGCCCTTATT TGAAAGGACT AAAAGCAAA AAACCCAATA CATGGACGGC	420
GGGTTGATGA TGCACATCCG TTTT	444

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 843 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...843

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87

GTGATGATCG ATCCCAAAT GGTGGAATT AGCATTATG CGGACATCCC TCATTTACTC	60
ACGCCCATTA TCACTGACCC TAAAAAAAGCT ATCGGGCTT TGCAAAGCGT GGCTAAAGAA	120
ATGGAGCGCC GATACTCTT AATGAGCGAA TACAAGGTTA AAACCATTGA TTCTTATAAT	180
GAACAAAGCCC AAAGTAACGR CGITGAAGCG TTCCCTATT TGATITGTGGT GATTGATGAA	240
TTAGCGGATT TGATGATGAC AGGGGGCAAA GAAGCGGAGT TTCCTATCGC TAGAATCGCT	300
CAAATGGGGC GAGCGAGCGG CTTGCACCTC ATTGTGGCGA CCCAACGCC GAGCGTGGAT	360

GTGCGTAACCG	GCTTGATTAA	AACCAACTTG	CCTTCAAGGG	TGAGTTTAG	GGTAGGCAC	420
AAGATTGATT	CTAAAGTGT	TTTAGACACC	GATGGGGCGC	AAAGCTTACT	AGGAAGGGC	480
GATATGCTCT	TTACCCCCCC	AGGAACAAAC	GGGTTAGTGC	GCTTGCATGC	CCCCTTGCC	540
ACTGAAGATC	AAATCAA	AATCGGGAT	TTTATTAAAG	CCCAAAAAGA	GGTGGAAATAC	600
GATAAAGATT	TCTTGCTAGA	AGAATCGCGC	ATGCCCTTAG	ACACCCCTAA	CTATCAAGGC	660
GATGACATT	TAGAAAGGGC	TAAAGCGGTG	ATTTTAGAAA	AAAAGATCAC	TTCTACGAGC	720
TTTTTACAAC	CCCAATTAAA	AATCGGCTAC	AACCAAGCCG	CCACCATTAC	TGACGAATT	780
GAAGCTCAAG	GCTTTCTATC	CCCAAGAAC	GCCAAAGGCA	ACAGAGAGAT	TTTGCAAAT	840
TTT						843

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88

ATGAATTTC	TTAAAATCCT	TTTAATGGAG	TTAAGAGCCA	TTGTTTCTCA	TAAGGGCGTT	60
TTATTGATCC	TTATAGGC	GC	TCC	TTAATC	TATGGCTTGT	120
AAAGACATCG	AAACG	AGCA	AAA	ATCGCC	TITG	180
AGGAATTAG	CCT	CATGGT	GCAAAGCTCC	AACCAAGT	AGATG	240
TCTATGCTGG	AAGC	AAAAA	GCTT	TTAATG	AAATCGCTTT	300
CCCTCTCATT	TTGAAGCCAA	TATTTATAAA	GAAG	AAAAAA	TTTATGGGAT	360
GAAGCCAAT	TACT	TTTGA	TTTATGGTGC	GTTAGCGAAT	GGGGTGGTGG	420
CGCCTTAAAC	GA				GGAGCATCAA	432

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...219

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89

GTGGGGGGCT TAGCCATGCT GGGCTTTTT TATAATATTG AAAAAATITC GCTGCCACA	60
CGCACGGCTT TCTCGCAATG CGGCCTAATW TATACGGTGC TCCTTTCCCC TTTGCTTTG	120
AAAGAAAAGC TCAAAAGAAG CGCGTTAATT TCCGCATGCA TCAGGCTAGT GGGGTGCTG	180
TTGATTTAG ATCCTAGCGT GGAAAATGTA GGACCTAGT	219

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 933 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90

GTGTGCTGGA CGGATTTGAT TCAAGGGCTT TTGATGATGA GCGCTTTAAT CGTGGTGCCG	60
ATTGTTATGA TAATCCATCT TGGAGGGATT GGAGAGGGGA TTAAAATCAT TAGAGAGATC	120
AAGCCTGAAA ACCTWTCTTT CTSGCAAGGC TCTAGCGTAG TCGCTATTAT TTCAAGCCTT	180
GCTTGGGGCT TAGGCTATT TGGGCAACCC CATATTTAG TGCGCTTCAT GTCTATCCGC	240
TCCATTAGAG ATGTGCTCAA AGCGACCACT ATGGGATTT CTTGGATGGT TATTTCTTTA	300
ATTGGGGCAT GCGTTATGGG GCTTTTAGGC GTGCTTATG TACATAATY TGACTTGAGT	360
TTAGAAAGACC CTGAAAAGAT TTTCATTGTA ATGAGTCAAT TGCTCTTAA CCCTTGGATC	420
ACAGGCATT TATTGAGCGC GATTITAGCG CGCGTGATGA GCACGGCCAG TTGCAACTG	480
CTTGTAAGCT CTTCTACCAT TGCTGAAGAT TTCTATGCGA CGATTITCAA TAAAACGCC	540
CCCCAAAAAT TAGTGATGAC GATTTCTAGG CTTCGGTTT TAGGGGTGGC TTGCATCGCT	600
TTTTTCATT CAACGGATAA AAACGCTAGC ATCCCTCAGCA TCGTGAGTTA CGCATGGCT	660
GGCTTTGGCG CGAGTTTGG CTCTGTGATT TTGTTTTCAC TTTTTGGTC AAGAATGACG	720
CCGATTGGCG CGATTGCTGG CATGCTCTCT GGGGCTAGCA CGGTGATTAT ATACGATAAA	780
TTTGGCAAAA GCTTTTTGGA TATTTATGAA ATCGTTCCGG GCTTTATTTG ACCGAGCGTA	840
GCTATTGTTG CGTTTAGTTT GTTTCTAGC GTGCGATCAG GCACTAAAGA GGCCTTGAA	900
ACCATGCTTA AAGAAATTGA GAGCTTAAAG CAT	933

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

SUBSTITUTE SHEET (RULE 26)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91

GTGGGGCTTT TTATCGTTT GTTTTAATT ATAATGAAGC ACCAAACCTC CCCCTATGCT	60
TTCACGCATA ATCAAGCCCT TGTCACTCAA ACCCCCCCCT ATTTCACGCA ACTCACTATC	120
CCTAAACCAA ATGACGCTTT AAGCGCGCAT GCGAGCTCTT TAATCAGCTT GCCTAACGAC	180
AATCTTTGA GCGCTTATT TAGCGGACT AAAGAAGGGG CAAGGGATGT GAAAATCAGC	240
GCGAATCTTT TTGACAGCAA GACTAATCGC TGGAGCGAAG CCTTCATTCT TTTAACAAA	300
GAAGAGCTTT CTCATCATTC GCATGAATAAC ATCAAAAAAA TTAGG	345

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92

ATGCTTGTAG GGCCAACAGG CGTGGGGAAA ACCGACGACTT TGGCTAAATT AGCCGCACGC	60
TATTCTAGAA TGCTGGCTAA AAAATACAAG GTGGCATTA TCACCTTACA CAATTATCGC	120
ATTGGGGCTT TGGAGCAATT GAGTTGGTAT GCTAATAAAA TGAAAATGAG TATAGAACG	180
GTGATTGACG CTAAGGATTG TGCTAAAGAA ATTGAAGCTT TGGAAATACTG CGATTTTATT	240
TTAGTGGATA CGACAGGGCA TTCGCAATAC GATAAGGAAA AAATTGCCGG TTTGAAAGAG	300
TTTATAGATG GGGGTTATAA TATTGATGTA TCCTTAGTGC TTTCGGTTAC CACTAAGTAT	360
GAAGACATGA AGATATTTA TGATTCCTT GGGGTGTTAG GGATTGACAC TTTAATCTTT	420
ACGAAATTAG ATGAGAGTAG GGGGTAGGG AATTGTTTT CTTTAGTGCA TGAAAGCCAA	480
AAGCTATCA GTTATCTTC TGTCGGCAA GAAGTGCCTA TGGATTGAA AGTGGCTACT	540
AATGAGTATT TAGTGGATTG CATGCTAGAT GGCTTAGTA ACCCTAATAA GGAACAAGCA	600

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

168

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93

GTGGGAGGAG	CGAGCTTTAT	TTCTGGGGC	AATGGCACGC	TTTATGGCTT	GAATGTGGC	60
TATGACCGAT	TGGTTAAAAG	CGTGATCCCT	GGGGTTATG	TGGCTTATGG	CTATAGCGGT	120
TTAACGGGA	ACATCATGCA	TCCTTGGCT	AATAATGTGG	ATGTGGGGAT	GTATGCGAGG	180
GCTTTTGTGA	AAAGAACGA	ATTCACTTTG	AGCGCAATG	AAACTTATGG	AGGCAATGCG	240
AGTCATATCA	ATTCTTCTAA	TCCTTGCTC	TCTGIGTIGA	ACCAACGCTA	CAACTACAAC	300
ACCTGGACAA	CGAGCGTCAA	TGGGAAATTAC	GGCTATGATT	TCATGTTCAA	ACAAAAAAAGC	360
GTGGTGCATA	AACCTCAAGT	GGGCTTGAGC	TATCATTTC	TAGGCTTGAG	CGGGATGAAA	420
GGTAATATGC	AAAATCCAGC	TTACCAACAA	TCGTCATGC	ATTCAAACCC	TTCTAACGAA	480
TCGGTTTAA	CGCTCAACAT	GGGGTTAGAG	AGCCGTAAT	ATTTGGTAA	AAATT CCTAT	540
TATTTTGTAA	CGGCGAGGTT	GGGTAGGGAT	CTTTTGTCA	AAGCTAAAGG	CGACAATGTG	600
GTGCGTTTG	TGGGTGAAAA	CACTTATTG	TACCGCAAGG	GGGAAATT	TAACACTTTT	660
GCGAGCGTGA	TCACAGGAGG	CGAAATGCAT	TTGTGGCGTT	TGATGTATGT	GAATGCCGG	720
GTGGGCTTA	AAATGGGCTT	GCAATACCAA	GATCTTAATA	TCACTGGGAA	TGTGGGCATG	780
CGAGTGGCGT	TT					792

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1017 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94

ATGGACGGCT	ATGGGTTAA	AATCCAAGAC	TTGGGCCAAA	AAACTCAAGT	TATCCAACAC	60
ATCTTTGCCG	GGGATGATGT	GACCCCTTTA	GAAGTCAAAG	AAAATGAATG	CGTTAAAATC	120
RTGACTCGAC	CGATGGTCCC	AAAGGAAATA	GAAACGATTG	TTCCCATAGA	ATGCATGCTA	180
GAGAGTCATA	AAGATTCGCG	CCTAGCTCT	AAAGATTITA	AAATTCAACG	TAATATCCGT	240
CAAAAGGGCG	AGAACGCTTC	TTTAAACAGC	GTTTTAGTCC	CTAAAATAC	CCGTTTGAAT	300
TATGCCATA	TCGCGCTCAT	TGCTCTCAA	GGGTTCAAAG	AAATCAAAGC	GTITAGAAAA	360
TTAAAAATCG	CTCTCTTATG	TAGGGCCGAT	GAATTAGTGC	CTTTAGGGCA	AAACGCCCTA	420
GAGTGCAGG	TTTATGATGT	TAATTCTGT	GGTGTTTTA	ACATGCTTAA	AAACTACAAC	480
ACGCATTTC	TAGGGTTTT	AAAAGATGAT	AAAATTTAC	AGCTTAAAAT	ACTTGAATTG	540
CAAGGCTATG	ATGTCATCT	TTCAAGTGC	GGGGTGAGCG	TAGGGGATAA	AGACTTTTT	600
AAAGACGCTT	TGAAAGAAAAG	AAACGCCCTT	TTTTATTACG	AAAAAGTCAA	TCTCAAACCT	660
GGAAAGCCGG	TAACCTTAC	CCAACCTAA	CAAAGCTTA	TTATAGGCTT	ACCGGTAAT	720
CCTTTAAGTT	GCTTACTGGT	TTTACGAGTT	TTGATTCTAC	CCTTATTGGA	GCGCTTATCC	780
TTAAATAAG	ATTTTAAATT	AAAACCTTT	AAAGCTCAA	TCAATGCC	TTAAAGCTT	840
AATAACAAAC	GGACCCATT	AATCTAGGC	AACTATTCAA	ACCACCAATT	CATTCCCTAC	900
ACCAACCGCT	ATGAATCAGG	AGCGATTCAA	GCCCTTGCGC	AAGTGGATTC	TATCRCTTTA	960
ATTGATGAAG	GACTGGGATT	GGTCAGGGC	GAAATTGAAA	TTTTAAGGTT	TGAAAAT	1017

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 438 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...438
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95

ATGCCATACG CCTTAAGAAA AAGATTTTC AAACGCCCTT TATTGTTTTT TTTAATTGTT	60
TGTATGATAA ATTTGCATGC CAAAAGCTAT CTGTTTCTC CTTTGCCCCC AGCGCACCAAG	120
CAAATCATTA AGACAGAGCC TTGCTCTTG GAGTGCCTGA AAGACTTGAT GCTGCAAAAT	180
CAAATCTTTT CTTTTGTATC CCAATACGAT GATAACAACC AAGATGAGAG CCTTAAACT	240
TATTACAAGG ACATCTTAAA CAAACTCAAC CCCGTATTCA TCGCTTCTCA AACTCCAGCT	300
AAAGAAAGCT ATGAGCCTAA GATTGAATTA GCGATTITAC TGCTAAAAA CGTGGTGGGC	360
CGTTATGCGA TTTTAGTGAT GAACACCCCTT TTAGCGTATT TTGAACACCA GAAACAAACGA	420
TTTCAATATC CAAGTCCTT	438

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...180
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96

ATGCCTATTA ACCCTCTCTA TCTTTCCCC AATCTTTTA CCGCTAGCAG TATTTTTTA	60
GGCATGATGA GTATTTTTA CGCTTCCAGT TACCAATTG TCATGGCGTG TTGGTTAGTG	120
GTGGCGAGTC TTATTTAGA TGGGCTTGAT GGGCGTGTG CAAGGCTTAC CAAACACCAC	180

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...699

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97

ATGCTTTCAAG	CCTTGCTTTC	TAAAATGGGG	ACTTACGCCT	TATTACGCCT	CTTGCTCCCG	60
CTTTTTCCCTG	AACTTTCAGA	AATTATTTTA	ACCCCCATAG	CCATTGTGGC	GCTGTGCATG	120
ATCATTTATG	GAGGTTTTCT	AGCCTAACGT	CAAAAAAGATT	AAAAAAACCT	CATCGCTTAT	180
AGCTCTTCT	CGCACATGGG	AGTCGTGGTG	CTTGGGGTTT	TTTCTTTCAA	TGTTGAAGGG	240
GTTCAGGGG	CGGTGTTTAT	GATGTTTGC	CATGGCGTTA	TCGTCATGGG	ATTATTTTA	300
CTCGCTGGTA	TCTTGGAAAGA	ACGGCCGAGC	AGTTTAGAAA	TCGCTCGCTT	TGGATCGATC	360
GCTAAAGCG	CTCCTGTTT	TGCAGCCTT	TTTATGATCG	TTTTAATGGC	GAATGTGGC	420
ATGCCCTTAA	GCATTGGTTT	TGTGGGAGAG	TTTTGARCT	TGTTAGGC	TTTGCCACT	480
TACCCCTCTT	TGGCTATCAT	TGCCGGACCA	AGCCTCATTC	TATCAGCGGT	TTACATRCTC	540
ACTTCATATA	AAGATGTGTT	CTTGGCAAC	TTAAAAAACCG	GGAACAACCA	AATCAGCGTG	600
TTTGAAGATT	TAAACGCTCG	TGAGGTAGGG	CTTTAAAGCG	TGATTTAGC	CTTGTATCTT	660
AATTTAGGG	ATTTATCYA	AAGCGCTTTT	AAAACCGAT			699

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...96

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98

GTGGAATTGA	TTAGCAATAA	CCCTAACGCC	AGCCAACAAT	CTATCGTTAT	TCCTTTGGAG	60
ACTTTTGCTT	TGGCGCGAGC	GTAAAGGG	ATCTTT			96

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99

ATGAAAATTT TTGGGACTGA TGGCGTGAGG GGTAAAGCAG GGGTGAAACT CACCCCCATG	60
TTTGTGATGC GTTTAGGCAT TGCTGCCGA TTGTATTTA AAAAACATTG TCAAACGAAT	120
AAAATTCTAA TCGGTAAAGA CACCAAGAAG AGCGGCTATA TGGTAGAAAA CGCTTTAGTG	180
AGCGCTCTCA CTTCATAGG CTATAATGTG ATCCAAATAG GGCCTATGCC TACCCCTGCG	240
ATCGCTTTTT TAACCGAAGA CATGCGCTGT GATGCCGGCA TTATGATAAG CGCGAGCCAC	300
AACCCTTTTG AAGACAATGG CATCAAGTTT TTCAATTCCCT ATGGTTATAAA ACTCAAAGAA	360
GAAGAAGAAA GAGCGATTGA AGAAATCTT CATGATGAAG AATTACTGCCA TTCTAGCTAT	420
AAAGTGGGCG AGAGCGTCGG TAGCGCTAA AGGATAGACG ATGTGATAGG GCCGCTATAT	480
CGCGCATTTG AAGCACTCTY TYCCCAAACA TTT	513

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100

GTGCGAGCCG TGTGTTGTCTT TGGTTTGAAA GCGGGCGTTTT GTATAGGGAT TTTTTTCTAT	60
GGCGCTTATT ATTCCTAGA TGAGTTTTTA ATCAAGCTC	99

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

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- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101

GTGAGGGAGCG GTAAAAGATT AGGCTATACC AATCACTGA TCACCGATAT TGTCAATATC	60
GGTATTGGGG GGTCAAGATT AGGCCTTTA ATGGTTTGCA CCGCCCTAA ACGCTACGGC	120
CACCCAAGAT TARRAATGCA TTTTGTGTCT AATGTGGAAT GGCACGCAGA TTTTAGACGT	180
TTTGGAAAAA ATCAACCCGG CCAGCGCGCT	210

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102

ATGAATCTTG TCTTTTTGTC GGCGCTCTA GGAGGGCTA TAGGGAGCTC GTTAAGGTAT	60
TTTGTGGGCA AAATGATGCC CAGTAAATT TTAATGTTTG AAAGTTTCCC TTTAGGGACT	120
TTTAGCGTGA ATCTCATAGG GTGTTTATC ATCGCTTTA TGGGGCATTT GGCGCTAA	180
AAAGTTTTTG GTGATGATT TGGAATTTC TTGTAACCG GAGTTTTAGG GGGTTTTACG	240
ACCTTTCTT CTTATGGTT AGACACTTTA AAACCTTGC AAAATCCCA ATACCTTGAA	300
GCCATITCCTT ATGCTTCTAGG CACTAACCTT TTAGGGCTTA TTGGGGTAGC TATCGTTGG	360
TTTTGGCTA AGAATTTCGT AGGCGTTAAT	390

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103

ATGTTGGAAA AACTGATTGA AAGAGTGTG TTTGCCACTC GTTGGTTGCT AGCCCCTTTA	60
TGCATTGCCA TGTCGTTAGT GTTGGTGGTT TTAGGCTATG TGTTCATGAA AGAGTTGTGG	120
CACATGCTCA GCCATTARA CACCATTAGT GAAACGGATT TGGTTTTATC AGCCTTAGGT	180
TTAGTGGATT TGTTGGTTCA TGGCCGGCT TGTTTGATG GTGCTGCTCG CCAGTTA	237

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104

ATGCACTATC ATTAACAAG TTTCAATATA ATACAAGATC TTTTTATAAC TTGTCATGTG	60
TTAAGGATCA AAATGCGCGT GTTTGTGTC TTTTTAGGGG TTTTTGTATC TAACGGCTTG	120
GCTCGTTTG GCTATGTGGT TTTAATCCCC CTACTCAITTT TATCAGGGAG TTTAACCCCA	180
CACCAAAGCT TCCAACGGGG TATTGCGGTG CTAATGGGCT ATGTTTTTGG GAGCTTTTA	240
ATCCAATTTC TAAGCCCCGT AATGTCATTA SAAAGCATCG CTAAAATCAG TTTTAAATTA	300
ACACTT	306

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105

GTGGATATGA AAGACGCTGT AGGGACTTAT AAACTAYTCA GGGCT

45

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3081 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...3081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106

GTGTGTTAG	ACCATCAGGT	TGGAGCAGGC	AAGACTTTGT	GCGCTATAGC	CAGCTGCATG	60
GAACAAAAAC	GCATGGGATT	AGTGAATAAA	ACGCTATTG	CCGTGCCTAA	CCATTAAACC	120
AAGCAATGGG	GCGATGAATT	TTATAAGGCT	TACCTTAACG	CTAATGTGTT	AGTTGTTGAT	180
AGCAAGGACA	CCACTGAAA	AGAAAGAGAA	CTTATTATTCA	ATCAAATCCC	TAACAAACAT	240
TATGACGCTG	TGGTTATCGC	GCACACCCAT	TTGGAATTAT	TGTCTAACCC	TAGAGGAATC	300
ATAGAAGAAT	TGAAAGAAGA	AGAGCTAGTG	AATGCTGAAA	AAAATTTGA	AAGGCAAGAA	360
TTAGCTTATA	AAAAATAACCC	TAGAGAAACT	AAAAAACCCA	ATGAAAGAGC	CTTTAAAAAC	420
AAAGTTCGATA	AAATCCGTG	TAATACGAT	GCGATTTAG	AAAAACAAGG	CTCTCATATT	480
GATATTAGTC	AAATGGGAT	TGACAATTG	ATTGTGGATG	AAGCCCACCT	ATTCAAAAT	540
CTAGCCCTTG	AAACTTCTAT	GGAAAAAATT	GCAGGACTTG	GTAACCAACA	AGGCTCTAAT	600
CGCGCTAGAG	ATTGTTTAT	AAAAACGCC	TACTTGCATC	AAAACGATAA	GAAAATCATG	660
TTTTTAACCG	GCACGCCAT	AGCTAATTCC	TTGAGTGAAA	TGTATCACTT	GCAACGCTAT	720
TTAACCCCCG	ATGTGTTAAA	AGAAAAGAGG	TTAGAATTCT	TTGATGATTG	GGCTAAAGACT	780
TATGGGAAAG	TGGTGAATGA	TTTGAAATT	GACACTTCCG	CTCAAAGTTA	AAAATGGTT	840
AATCGCTTT	CTAAATTAG	CGATGTGCA	GGCTTAAGCA	CCATGTATA	ACCTTTGCG	900
GATATTGTC	CTAATGATGA	TATTTAAAG	CATAACCCCC	ACTTTGTGCC	TAAAGTGTAT	960
GGGGATAAAC	CTATCAATGT	GGTGGTAAA	AGAAGCGAAG	AAGTGGCTCA	ATTCAATTGGA	1020
GTGGCTTAG	AAAATGGAAA	ATATAATGAA	GGCTCTATCA	TTGATAGGAT	GCAAAATGCG	1080
GAGGGCAAGA	AAAGCCAAA	AGGGCAAGAC	AATATCCTT	CTTGCACCC	AGACGCTAGA	1140
AAAGTGGCTT	TGGATTACCG	CTTGATTGAC	CCTAACGCTA	AAGTAGAAAA	AGAATTTTCT	1200
AAAAGCTATG	CTATGGAAA	AAATATCTAT	GAGAATTATT	TAGAAACTCA	TGCCACTAAA	1260
GGCACACAAAC	TTGGTTTCAT	AGGGCTATCC	ACACCCAAA	CCCATAGCCA	AAAAGTCAGT	1320
TTAGAAGCGC	TAGATAACGC	TCACGAAACT	GAAAATAAA	ATCCCCTAGA	AAAAGCTCAA	1380
GAACCTTTAG	AAAGCTTGTG	TAGTTATGAT	CAAAAGGGCA	ATCTTATCGC	TCCTAGCAAG	1440
AAAGAAATTAG	AGAACGAGCT	CAAAGAGAAA	GAAGCTAAA	GCGTCAATT	AGATGAAGAG	1500
ATAGCTAAAG	GCTGTTCGTT	TGATGTTAT	AGCGATGTT	TAAGGCATT	AGTCCAAATG	1560
GGTATCCCAC	AAAATGAAAT	CGCTTCATC	CATGACGCTA	AAACCGAAGA	GCAAAAGCAG	1620
GATTTGTTA	AAAAGCTCAA	TCGTGGCGGA	GTCAGGGTAT	TATTGGGAG	TCCTGCTAAA	1680
ATGGGCGTAG	GCACTAATGT	GCAAGAAAGA	TTAGTCGCTA	TGCATGAATT	AGATTGCCCA	1740
TGGAGACCTG	ATGAATTGTT	GCAAAATGGAA	GGGCGTGGGA	TAAGGCAAGG	CAATTTTA	1800
CACCAAAATG	ATCCTGAAA	CTTTAGAATG	AAAATCTATC	GTTACGCCAC	TGAAAAGACT	1860
TACGATAGCC	GTATGTGGCA	AATCATAGAA	ACTAAATCTA	AAGGCATAGA	GCAATTAGA	1920
AACGCGCACA	AATTAGGCTT	GAATGAATTA	GAAGACTTTA	ATATGGGTAG	CTCTAATGCG	1980

AGCGGAGATGA	AAGCAGAAGC	GACAGGCAAT	CCCTTGATTAA	TTGAAGAACT	CAAATTGAGA	2040
GCGGAGATTA	AAAGCGAAGA	ATCAAATAC	AAAGCCTTC	ATAAAGAGCA	TTACTTCAT	2100
GAAGAAAGCT	TAAAAAACAA	CGCTTCTAAA	TTGGATTATC	TAAAACAGGA	ATTGAAAGAT	2160
TTAGAACGC	TTCAAAGATC	CGTAATAATC	CCCACTCATA	CAGAGATCAA	GCTCTATGAT	2220
TTGAAAAATG	AAGAAAGTAA	GGATTATGAG	CTTATCAAAG	TTAACAGAGGT	AGAGCCTTTA	2280
AAAGAAAACG	CCTCTATGAG	TGAAGAATTA	ACGCCACAAGA	AACTCAAAGA	ACAAAACAAG	2340
CAAATAGCCG	AACAAAATAA	AGAAAAGCTA	GACGCTATTA	AAAAGCAATT	TGCAAGCAAT	2400
TTGAACACCT	TGTTTGTGAA	TGAAGAAGAA	GATTATAAGC	TTTTAGAATA	CAAGGGCTTT	2460
GTGGTGAATG	CTTATAAAAAC	TAAGTATCAA	GTGGAGTTTA	TTTTAACGCC	TAAAGACAAT	2520
CCCAATATTG	CCTATAGCCC	TAGCAATATG	TTTATAAAA	ACGATACTAT	CAACATGTTT	2580
AGCTCTTATA	ATTTCTGCGC	TGAGATCAAG	TTTGATGGGT	TTTTAAAAG	GTTGGATAAC	2640
GCTATCACTA	AACTCCCTGA	AAAATCAAG	GAATTAGAAA	ACTCCATTGA	AATCACGAAA	2700
AAAATATCG	CTAAATACAC	AAGATTAGTG	GAGCAAAAC	CTTCCTTACCC	ACGACTAGAA	2760
TACCTGCAAG	CTTTAAAATG	GGATCATAAA	ACTCTAATAG	ATGATTTAGC	TTAAATGAGC	2820
AAAGACAGAA	ATTATAAGCC	TGCGTTCAAC	CCTAAATCTA	AAGAAGTCTT	AAAGAATTG	2880
AACGCTGAA	AAAGAGCGAG	TTTAGAGAAT	GAGAGGGAAG	AGCAAGGGGT	TAAGGGAAC	2940
ACAAAGAGTC	ATGATGAAAT	AGAGCCAGCT	ACAGAACAAAG	TGATTGAAAAA	AGAAATAGAA	3000
AAAGGAGATG	AAATCGCTAA	TAATGTTGAT	TACTACCGAGA	ACGAACAAAGA	AGTGGAAATT	3060
ACTAAATCAA	TGGGTAGAAG	A				3081

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107

ATGGCCGAAG	AAGAAAAGAC	CGAACTCCCT	AGCCCCAAAAA	AAATCCAAAAA	AGCCAGAGAA	60
GAAGGCAATG	TGCCCTAAAAG	CATGGAAGTC	CTGGGGGTTT	TTAGGGTTAT	TGGCTGGCT	120
ATGAGTATT	TTTGTTTTTT	TTATATGGTG	GGTGGGATGG	CTTAGCGAG	ATGTATCGCC	180
ATGTGT						186

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108

ATGAAAACAC	TCGTGAAAAA	TACCATATAT	TCTTTTGCG	TATTGCTGT	TTTGATGGCA	60
GAAGATATAA	CAAGCGGCTT	AAAGCAACTG	GATAACACCT	ACCAAGAGAC	CAACCAACAA	120
GTGCTCAAAA	ACCTAGATGA	GATTTTTCA	ACCACTAGCC	CTAGCGCTAA	TAATAAAATA	180
GGTCAAGAAG	ATGCTCTAAA	CATCAAAAAA	GCGGCCATTG	CTTGAGAGGG	AGATTTAGCG	240
TTATGAAAG	CCAATTGGA	ACCGAATGAG	TTATTTTCA	TCTCAGAAGA	TGTGATTTTT	300
AAGACTTATA	TGTCTAGCCC	TGAACCTTTA	TTAACCTATA	TGAAAATCAA	TCCCTTAGAC	360
CAAAAGACTG	CTGAGCAACA	ATGCGGATA	TCCGATAAAG	TTTTAGTTCT	TTATTGTGAG	420
GGGAAGCTGA	AAATCGAGCA	AGAAAAACAA	AATAATAGAG	AGCGTTTAA	AACTTCTCTA	480
AAGGCATATC	AGAGCAACAT	TGGAGCTACA	GCTTCCTTA	TCACTGCTTC	ACAGACGCTT	540
GTAGAAAGCC	AAAAAAATAA	AAATTCATC	AAAGGAATCA	AAAAGCTTAT	GTTAGCTCAC	600
AACAAGGTCT	TTTAAATTAA	TTTAGAGGGAG	TTGGACGCAT	TAGAAAGATC	CCTAGAACAA	660
AGTAAGCGAC	AATACCTACA	AGAAAGGCAA	TCAAGTAAGA	TCATTGTTAA	A	711

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109

GTGAGCGAAA	AAGACAGGGC	GTTCCTTTTA	GGCAGCTTGT	CTTGCCTGGA	TTATGTTGTG	60
GTGTTTGGAG	AAGACACGCC	CATAAAATTG	ATTCAAGCCC	TAAAGCCTGA	TATTTTAGTC	120
AAGGGAGCGG	ACTACCTCAA	TAAAGAAGTC	ATAGGGAGCG	AGTTGGCTAA	AGAAACCCGT	180
TTGATAGAAT	TTGAAAGAAGG	TTATCCACA	ACCGCTATCA	TAGAAAAAAT	AAAAGGACA	240
CATAATGAT						249

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110

GTGTATGACA AATCCTTGTG TAAGACCATG GCGCTAGCGT TGAAGGCTTT AGGCCTTAAA	60
AGGGCGATGG TCGTTAATGG AGGGGGGACA GGTGAAATCG TGTTCCATGA CATTACGCAT	120
GCGTGCATAAT TGAAAAATAA CGAAATTAA GAGTATGATT TGAGCGCTAA AGATTTGRT	180
TTRCCCCCT CA	192

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 684 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111

ATGCTAGTAG AAATAGAGAA TTGACTAAA ACTTATGGGA GTTAAAAGC GCTAGACAAAT	60
ATCACTTGA AACTACCCAA ACAGCAATT ATAGGGCTTT TAGGGCCTAA TGGGGCGGGT	120
AAAACCACTC TGTAAAAAT TTAGCCGGA TTGAATTGTA ACTATCAAGG GGAAGTGAAA	180
ATTTTAAACC AAAAGATGG TATAGAGACT AAAAAGCG TGGCGTTTT AAGCGATGGC	240
GATTTTTAG ATCTAAATT AACGCCCTTA AAAGCGATCG CTTTTATATAA GGATTTTTT	300
ACCGATTTG ATGAATCAAA AGCCCTAAC TTGTTAAAAC GCTTCAGCGT GCCTTTAAA	360
AGAGAGTTCA AAGCCCTTTC AAAAGGCATG AGGGAAAAT TGCACTGAT TTAAACCCA	420
TCACGAAACG CTTCTTGTGTA TCTTTTGAT GAGCCGGTGG CTGGGATTGA CCCTAATGCA	480
AGAGAAGAGA TTTTGAGTT AATCGCTAAG GAGTTAGCC AAAACGCAAG CTTGCTAGTC	540
TCTACGCATT TGGTGGTGGA TGTGGAAAAG TATTTAGACA GCGCGATTTT TTAAAGAA	600
GCTAAAGTGG TGGCTTTGG GGATGTGGGG GAATTAAAAA AAGGGTATAG CAGTTTGGAG	660
GCAGCGTATA AAGAAAGTTT GAAA	684

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 819 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112

ATGAACAAGC	TTTTTTAGC	TTTTATGTT	GGGGGAATGC	TTTAAGTGC	TGATGCTTTA	60
AACGATAAGA	TTGAGAATT	AAATGGGGAG	CGATCCTACC	ACATGAACAA	GCTTTTTTTA	120
GAGCGTTTGT	TTAAAATCG	TAAGGATTTC	TATGAAATGG	GGCGTTTGA	TTCCCTAAAA	180
CTACTCAACA	CTCTCAAAGA	AAACGGGCTT	TTATCGTTA	ATTTTGACAA	ACCAAGCGTG	240
TTAAAATCA	CTTTCAAGGC	TTCAAGTAAT	CCCCTAGCGT	TTGCCAAAAG	CATCAACAAT	300
TCTTGAATA	TGATGGGTA	TTCGTATGTT	TTGCCATTAA	GAATGCAAAG	CTCTTCAGGC	360
GAGAATGTTT	TTTCATACGA	GCTTAAAACG	GAATACGTTT	TAGACCCCTAA	CATTTTGATA	420
GAGACGATGA	AAAGGCATGG	TTTTGATT	ATGGATATTAA	GACGGGTGTC	TTTAAAGGAG	480
TGGAATACG	ACTTTGCTT	ACAAAAGATC	AACCTCCCTA	ACGCGAGAGC	CTTAGTTTTG	540
AGTAGCGATC	CTGTGGAGTT	TAAGGAAGCG	ACGGGGAAAT	ATTGGCTGAG	CGTGAATCAA	600
AACCGCTATT	TAAAATAAG	CTCCAAATAAC	CCTTGTGGC	AACCCAAAAT	CATTTTTAT	660
GATGAAAATC	TTAAAGATCAT	TCAAATCATT	GCTAAAGAAA	ACAGACAAACA	AGAAATCGCT	720
CTTAACITGC	TTGATGGCGT	GCGTTTATC	CATATCACTG	ACGCAAAAAA	CCCTATCATT	780
TTAAAATG	GGATTAGCGT	GGTTTTGAT	GGCATGCCT			819

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113

GTGTCTCGCC CGTTCAAAAC GATCAAAAAA CCCCCACAAC CCCCT

45

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

179

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...201
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114

ATGATCGCTG TATTACCGCC CTTGGTTTCT ATGGGGAGCT TTGATGAGTG GATTTATAGG	60
GGGCTTGTGG CTTTAATGGT GAGCTGCTCT TGCGCGTTAG TGATTTCTGT GCCTTTAGGG	120
TATTTGGAG CGCTGGGAGC GGCGAGCCGA AAGGGGATTT TAATGAAAGG AGTCATGTT	180
TTAGAGGGTG CTTACCCAAA C	201

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 969 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...969
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115

GTGCAACACT TCAATTTCCT CTATAAAGAT TCTTTATTTT CTATCGCTTT ATTCACTTTC	60
ATTATCGCTC TTGTGATTTT ATTAGAACAG GCTAGAGCGT ATTTCACCCG AAAGAGAAAC	120
AAAAAAATTT TGCaaaaattt CGCCCAAAAT CAAAACGCCCT ATGCGAGCAG CGAGAATTAA	180
GACGAGCTTT TAAAGCATGC TAAAATTTCC AGTTTGATGT TTTTAGCTAG GGCgtattct	240
AAAGCCGATG TGGAATATGAG CATTGAAATC TTAAAGGGC TTGGAATTCG CCCCTTAAAA	300
GATGAAGAAA AAATCGCTGT TTTAGATTAA TTGGCTAAAA ATTATTITAG CGTGGGGTAT	360
TTGCAGAAAA CAAAAGACAC CGTGAAGAA CGTTGCTTTGCA TTGCGTATGAA TTAGAAAAAG ATTATTCAA	420
GGCGTTGTGA AGCTTTGCA TGCCTATGAA TTAGAAAAAG ATTATTCAA	480
ACTTTGGAAT GTTGGAAAGA ATTAGAGGTG CCTAAATTG AAACGATTAA AAATTACCTC	540
TATTTAATGC ATTAAATAGA GAATAAGGA GATGCGGCTA AAATCTTGCA TGTTTCAAAA	600
GCGTCGTTAG ATTGAAAAAA AATCGCTCTG AATCACTTAA AATCGCATGA TGAAAATCTT	660
TTTTGGCAAG AAATTGATAC AACCGAACCG CTAGAAAATG TGATCGATCT TTTATGGAT	720
ATGAATATCC CTGCTTTTAT TTTGAAAAAA CATGCCCCTT TGCAAGGACAT CGCGCGATCT	780
CAAGGGTTGC TTTTGGATCA CAAACCTTGC CAAATTTG AATTAGAGGT TTTACGGCT	840
CTATTGCAATAA AGCGAGTCG ACTTTGAAAT ACCGCTGCAA GCATTGCAA	900
CAAATCTTTC CTTTGAAAG CCATAGGTGT CCTGTGTGTT ACCAGTTAGC GTTTATGGAT	960
ATGGTGGCT	969

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

180

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116

ATGGAACACC TTACAAGGGG AATTAAGCAC

30

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117

GTGGTTATCT TAGGCTCRCA TGGCAAGGAA GAGTATTACG CTAGCAAGAT TGCAGCCCCC
ATTTTAAAG AAATCACCGA AATTTTAGTC CGTTACAATT ACCTATGCC CTCTATTGCG
ATTCAAAACG CTTTGAAAAA AAACCGCTTA AAA

60

120

153

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

181

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118

ATGAAAAAGG TTATTGTGGC TTTAGGCCTT TTGGCGTCG CAAATGTTTT AATGGCAACC	60
GATGTTAAGG CTCTTGTAAGG AGGTTGTGCC GCTTGCCATG GGGTTAACGTT TGAAAAGAAA	120
GCTTITAGGTA AAAGCAAAAT CGTTAACATG ATGAGCGAAA AAGAGATTGA AGAGGATCTT	180
ATGGCTTTA AAAGCGGTGC CAACAAGAAT CCTGTCATGA CCCGCAAGCT AAAAAAT	237

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119

ATGGGGATTG CAACCGAGTCT CATCAGTGAG GTTCTAAAGT TTTATTACGC TTTAAAATAC	60
CATGCGAAAT TTATGAGCTT GGGGGAGCTT GGGTGCTATG CGAGCCATTA TTCGTTGTGG	120
CAAAATGCA TAGAGCTCAA TGAAGCGATC TGTATTTTAG AAGACGATAT AACCTTGAAA	180
GAGGATTTA AAGAGGGCTT GGATTTTTA GAAAAACACA TCCAAGAGTT AGGCTATGCG	240
CGTTTGATGC ATTATTTGTA TGATGCCAGC GTGAAAAGTC AGCCT	285

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120

182

ATGCACCTTA	AAAGTGGGGC	TGTTTTATC	TCTGATGCGC	ATTTTTTGCC	CAAAAGCCCT	60
CATTTAATCC	ATACGTTAA	AGAACCTTTA	AGCCCAAAC	CCCCGCAAGT	CTTTTTCATG	120
GGCGATAATT	TCCATGTTCT	TGTGGCTAT	TTACCCCTAG	ATAAAGAGCA	GAAAAAAATC	180
ATTGATTTAA	TCCATGCGTT	GAGCGAAATT	TCACAAAGTCT	TTTACTTGA	AGGCAACCAT	240
GATTTTCCA	TGCGTTTTGT	ATTCAATTCC	AAAGTAATGG	TTTTGAGCG	CCAAAACCAA	300
CCCGCATTAT	TCCAGTATGA	TAACAAACGC	TTTTGCTAG	CCCATGGGGA	TTTATTCACTC	360
ACTAAAGCGT	ATGAATTATA	CATCACCGCAG	CTCACCTCCA	CTGGGCTAG	ATTTTTTTTA	420
ACTTTTTAA	ATTATTAAG	TTTTAAAACC	TTATACCCCTT	TT		462

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121

GTGCAACCGA	TGAAATCTAA	AAAACTTTAT	TTAGCTTTAA	TCATAGGGGT	TTTATTAGCG	60
TTTTAACCC	TATCTTCATG	GCTAGGTAAAT	AGCGGTTTAG	TGGGGCGTTT	TGGGGTGTGG	120
TTGCCGCAA	TCAATAAAAA	ATATTGGG	TATCTTTCAT	TGATTAATT	ACCCTATTTG	180
GCGTGGGTTT	TATTCCCTTT	ATACAGGGCT	AAAACCCCTT	TTACAGAAAT	CGTTTTAGAA	240
AAAACCTTATG	GGCATCTATT	AGGCATTTA	TCTTTACTCT	TTTGCAATC	TAGCCTGTTG	300
AATCAAGGGG	AAATCGGCAA	CAGCGCCGCT	TTGTTTTAC	ACCCTTTAT	AGGGGACTTT	360
GGGCTTTATG	TGCTGATAAT	GCTTATGGTA	TTTATCTCTT	TTTAATT	ATTCAAATG	420
CCCCCTAAAA	GCGTTTTTA	CCCTTATATG	AAACAAACAC	AAAGCCTTT	AAAAGAGATT	480
TACAAACAAT	GCTTGCAGGC	CTTCTAGCCCT	AATTITAGCC	TGAAAAAAGA	GGGTTTTGAA	540
AACACCCCAT	CAGATTCTCA	AAAAAAAGAA	ACCAACAACG	ACAAAGAAAA	AGAAAACCTC	600
AAAGAAAACC	CTATTGATGA	AAACCACAAC	ACCCCTAACG	AAGAATCGTT	TTTAGCGATC	660
CCTACCCCT	ATAACACGCC	CTTAAATAAT	TCAGAGCCGC	AAGAAGGCTT	AGTCCAATT	720
TCCCCACACC	CCCCTACCCA	TTACACATT	TACCTAAAAA	GAAACCGATT	TGATGATTG	780
ACTAACCCCA	CTTTAAAAGA	ACCTAACCAA	GAAACCAAAG	AAAGAGAAC	CACGCTAAAA	840
AAAGAAACGC	CCACCAACT	CAAACTTATC	ATGCCCATAT	CCGCATCCAC	ACAGAAAATC	900
ATGACAAAAC	RGAAAACAC	AAAACCCCTA	ACCACCCCA			939

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 957 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122

GTGATGTTAA	GTAGAGACAT	TGTCCAATAT	TCCAAGATCC	GCACCGAGTT	ATACGCCTAC	60
CTCACTTATT	TGTTTCGCA	CAATATCCGC	AACCACCTTC	CTGAAATCAC	TTTGGATTAT	120
TTAACACAGG	AAATCAGTAA	GATGCAAGCT	GAATCAA	TGGCAAAAAG	TTTTTTTGTT	180
TTAGACGCTA	AGGGCATGCT	CATGTTAAG	CCAAGCCAAT	TAAAGAGCA	GGGGCATAAG	240
GAAGGGCTAT	TAGAGCATGA	TTTAACAGAA	GGGATTGAAT	TAGAATCGCA	TGTCAGTTT	300
AGCGATAAGT	ATTATTTTTA	TCAAGCCGT	AATGAAAAGC	GTGCAATT	AACCGACCCC	360
TATCCTTCTA	AAAAAGGGAA	CCATTTGGTA	GTGAGCGCGT	CTTACCCGGT	GTATGATCAA	420
AATAACGATC	TAGCGTTTGT	GGTGTGCTT	CAAATCCCTT	TGAGGGTGGC	GATTGAAATC	480
AGCTCGCCTT	CAAAGTATT	TAAAACTTT	AGCGAAGGGA	GCATGGTCAT	GTATTTTATG	540
ATTTCTATCA	TGCTCACTT	AGTGTGCGCT	CTTTTATTG	TGAAATGCAT	TTCTAGCTT	600
TGGACAGCGA	TCGTGCAATT	TAGCAGTTT	GACATTAAG	AAGTGTTC	CCCCATTG	660
CTTTTAACCC	TAGCTTTAGC	CACCTTGAT	TTGGTCAAGG	CGATTTTGA	AGAAGAACTG	720
TTGGGTAAAAA	ATAGCGGGGA	CAACCACCAT	CGCATCCACC	GCACCATGAT	CAGGTTTTA	780
GGCTCTATCA	TTATCGCATT	AGCCATTGAA	CGCTTAATGC	TCGTGTTAA	ATTCA	840
AGCGAGCCGG	ATAAAATCAC	TTATGCGGTG	TATTGGCTA	TCGCGTGGC	GGTGT	900
ATCAGTTTGG	CGATTATGT	TAAATTGCT	TATAGCGTGT	TGCCCAAACG	AGAACGC	957

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123

ATGGTTATAC	ATGAAAAAAAT	CAAAAGCCGC	TTTTCTAGGA	ATGGTCTTT	AAGGAATAGG	60
GGCAGGCATT	TTGCATCTTC	AAGCGTGTAT	TTTTCTCAC	TTCTTGTCA	TACAGCGGTT	120
AATAGAAGTA	GTGCAGTTGC	TTGGTTATTG	ATGCC	TTGATTGG	GTGGTTTTG	180
ATTTCTTTA	GTGGGAATT	TGTAGCAGAC	ATGGCGTTTG	GC	TAAGATT	240
AAAACCCGCT	TTGGAATTTC	TATTGTGAGC	GGCGTTTCAC	TATTGCTTGG	CGCTTACCA	300
CGCTTTATT	TTTGTATGG	TTTGGCTT	TTAATTGGTG	GGCTGT	TTTA	354

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 276 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124

ATGTTTAAAA GCAGATTAAA TTCATGGATT TTATTAGGGA TTTTAGGGGT TTTAGTGGTG	60
GTTCCTGGG ATGTCATAAA ATACAAAATA GAAGATTGC AACATGATCA TTATCTATCA	120
CAAGTGAAG AAAGGGAAAGA ATATTATAAA AACCACATAG AAGAAGCTTT GAAAAAGGAT	180
AGCGAATGCT TTGAAAAAAGG AGGCATAAA GTGGATTGCT CGGCTGCTAT GAGAATAGCT	240
GCTGGTGAAA GAAATAGAAG AATGTTAGAG ATTAAA	276

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 414 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125

ATGGTATTT GGGGCCTGT TTTCTTTTA TGGGATCGAA CGGCATGGAA GCGCTTAATG	60
GTGTTTTGA ACAGCTTGAW TTYCATGCTT GCGCCCTGGA GTTTGGGGTC GTTTTTAGGG	120
GCATGGATCA AAAATGAAGC CCACACCACT CAAATCGTT TGATTTCTTC TTTGCCCTTG	180
ATTTTATGA TGGGTTTGT GTGGCTTTT GAATCCCTGC CCTCTTATIT GCAAGTCCTTC	240
GTTCAAATAG TGCCTGCTTA TCATGGGATC AGTTGCTCG GGCGATTGAA TCAAATGCAT	300
GCGBAATTAA TAGATGTTTC TATCCATTIT TACCGCCTTA TTGCGATTIT TATCGTGAGT	360
TTTATAGGGT GCGTGTCAA ACTCAGCTCT TTAAAGAAG CTTGTAAAAA CGCT	414

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 762 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...762
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126

ATGCATGAGC AAGGTTCTAT AAGCTTTRTA GGCCRACAGG GAGCTAAAAG ATTATTATAAC	60
ATACTCTACA AGCTCGCATT TAATGCTAAG TCTAATAAGA TTGCCCCTAGA TAGACATTAC	120
GCCAAAATGT TTTTGCAAGT TGTAGCAAGA ACTCTAATAAA AGAATGTCAA TATATTAGAA	180
GAGCAAGGTT TTATTGAAGT CATTAAAGGA AAACAAAGAT ACTTGTATGT GTATCTTAAA	240
GATTACAGAG AATTAGAATG CTTAGTGAAG AGCAAGATGG CTAAGTATGT GATGTATTAA	300
AGACAAATTC TTGATTATTG GGATAGAAAA AGGCCATTATG CTGGTATTAA TACGCTTAAA	360
AACCTAGCCT TTGCTAAGAC CAAAGAACG TTACCCAGAC ATTTAAACGA TAAAGACTTA	420
AAGAGTTTT TAAAAAACACT CTTAGACTAT AAGCCAGCTA CAAGCTTTGA AAAACGCAAT	480
AAGTGTATTTC TACTTATTGTT AATACTTGGG GGACTTAGAA AATGCGAAGT GTTAAACATA	540
GAATTAACAC ACATTCAAGT AGAAGAGCAA AACTACTTA TTGTTAAATTCA AGGTAAGGT	600
AGAAAAGAGA GAAAAGCTTA TATTAACAGA AGTTTGTAG AACCAAGCTT GAATGCTTGG	660
ATTAGTGATG ATTACAGACT AAAATATTTC AATGGAGCAT ATCTCTTAA AAAGGATAAG	720
CAAAAATCAC AAAATTCTTT AACGCTTTAT AATTATCCCC CT	762

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 555 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...555
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127

GTGGCTTTTA AAATTTTAAG TTTATGGTTA GGGGTGTTTT GTTTCCTTAG GGCTACGCAT	60
TTATACCTAG CGGAAGAACCC CAAATATAAA GACAATTTCAC CGCATTTCGA ATACGCTAAC	120
CCTAACGCTA GAAAGGCGG TGTTTGAGA AATGACGCTA TAGGGACTTT TGATAGCCTT	180
AACCCCTTTG CGCTTAAAGG CACTAAAGCC GAAGGCTTGG ATCTCATTAA TGACACTTTA	240
ATGGTGCTAA GCCTAGACGA ACCTTTGCA GAATACCCCT TAATCGCTAA AGACGCCGAA	300
GTGGCTAAGG ATAACAGCTA TGTGATTTT ACCCTAGATA AAAGAGCGAG ATTTCAGCAAT	360
AACGCTCCC TTGAGCGAG CGATGTGAAG TTGACTTTG ATACGATAAT GAAATTAGGA	420
TCGCCCTTT ATAGGCAGTA TTACCAAGAT GTTAAAAAGG CGGTTATCTT AGACAAGCAC	480
CATGTTAAAT TCATTTYCAA AACCACTGAA AATAAAGAAT TGCCCTCAT TTTAGGGCAG	540
TTGCAGATCT TTTC	555

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...198
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128

GTGGCCATGA TAGATTGCGC GATTATTGGA GGTGGTCTG CAGGTTTGAG TGCGGGGCTT	60
TATGCCACTA GAGGCGGTGT TAAAAACGCC GTTTTATTG AAAAAGGAAT GCCTGGGGGG	120
CAAATCACTG GCAGTAGTGA GATTGAAAAT TATCCGGGCG TTAAGGAAGT GGTGAGCGGA	180
TTGGATTTCAG TGCAACCA	198

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 546 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...546
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129

GTGGGGAAAA GCTTGAGATA CAGCTTGAAT TTAGATCTCA ATCAAAAAGC CGATTTGTTT	60
TTCACCGAAT TAGAGCCAAC AGGTCTCAGG CTCTCCCCCA TCATGAAACG CTTTACTATC	120
AAAGGCAGATT TTGATTTCAGG GCTAAAATCC TATGACATGA GCTACATGTA TGCAGGCTT	180
CAAGCTATAA CGCGGATCAG GAGATTACCC TTAGGGCTTT ATGATGGGT GCATGTCTAT	240
TCTAAACGC CCATGAAGGA TATTGAAAAAA TTACGCAACG CTTTAAAAAC AATCAACCAC	300
CATGGCATAG GCATTGAAGG GTGGTGGCAA CAAACGGGA ATTTCCTCTC GGCGATGGAA	360
TTGGAAAAAA GACCGTTATT CATTGTGCTC ATGCTCATTAA TTAAATGGC GTCTTTGAAT	420
ATCATCAGCT CGCTTTAAAT GGTGGTGTG AACAGCGTA AAGAAATCGC CCTACTCTT	480
AGCATGGGGA GCAGTCAAAAGAAGAAATCCAA AAAACCTTTT TTTATTGGG TAATATCATT	540
AGTTTA	546

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 741 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130

ATGAAAAAAA	CTTTTTTGAT	CGCTTGTAGCG	CTTACGGCTT	CTCTTATAGG	CGCTGAAAC	60
ACCAAATGGG	ATTATAAAA	TAAAGAAAAT	GGCCCGCACC	GCTGGGACAA	ATTGCACAAA	120
GATTTTGAAAG	TGTGCAAAAG	CGGTAAAAGC	CAATGCCCA	TCAACATTGA	GCATTACTAC	180
CACACGCAAG	ATAAAGCCGA	TTTGCATTTC	AAATACGCCG	CTTCTAAACC	TAAAGCGGTC	240
TTTTTCACCC	ACCATACTTT	AAAGGCTTCG	TTTGGAGCCGA	CTAACACAT	CAATTATAGA	300
GGGCATGACT	ATGTGTTGGA	TAATGTGCA	TTCCACGCC	CTATGGAGTT	TTTAATCAAT	360
AATAAAACCA	GGCCCTTGAG	CGCCCATTT	GTGCATAAAG	ACGCTAAAGG	GGCTTTGTTG	420
GTGTTAGCGA	TTGGTTTTGA	AGAAGGGAAA	GAAAACCCA	ACCTTGATCC	TATTTTAGAA	480
GGCATTCAAA	AGAAACAAAA	TCTTAAAGAG	GTGGCTTTAG	ACGCTTTCTT	GCCTAAAAGC	540
ATCAATTACT	ACCATTAA	CGGCTCTC	ACCGCTCCTC	CTTGCACAGA	GGGGGTGGCA	600
TGGTTTGTCA	TAGAAGAAC	TTTGGAAAGT	TCTGCCAAC	AATTGGCTGA	AATCAAAAAAA	660
CGCATGAAAA	ATTGCCCAA	CCAACGCC	GTCCAGCCTG	ACTACAACAC	CGTGATCATT	720
AAAAGCTCGG	CTGAGACCCG	C				741

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1266 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...1266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131

ATGAAAATT	CTTATTGGG	GCATGGAAA	ACCACTCTAG	CCCTAGGGCG	TTTTTTTAAA	60
AAAAACCATA	ATGAAGTCAA	ATTTTTTGAT	GATAAATTCC	CTGCATTTT	TAAGGATAGC	120
GAGGGTTTC	TTTGCTACCC	TAGTAAGGAT	TTTAACCTA	ATGATTCCCA	ACTAGAAATC	180
GTCAGCCCTG	GCATTAGTTT	CACGCACCT	TTACTCATGA	AAGCCAAGCA	TTTAATGAGC	240
GAATACCATT	ATATTGATAG	TTTGTGAT	CATTCTTCA	CGCCTACGAT	GATAAGTATT	300
ACCGGCAC	ACGGGAAAAC	CACCAAGACC	GAAATGCTA	CCACACTTT	AGAAGATT	360
AAGGCTGTGA	GTGGGGGGAA	TATCGGCACG	CCCTGATTG	AATTGTTGA	AAAACGATCG	420

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CCCTTGTGGG	TGCTAGAAC	AAGCTCCATT	TCTTGCATT	ACACTAATAA	GGCTTACCC	480
TTAATCTACT	TGCTCATCAA	TGTGGAAGCC	GATCATTGA	CTTGGCATTG	CAATTTGAA	540
AATTATTGAA	ACGCTAAACT	CAAGGTTTA	ACATTGATGC	CTAAAACCTTC	GCTCGCTATC	600
CTCCCTTAA	AATTCAAAGA	ACACCCATT	GTTCAAAACT	CCGAAGCGCA	AAAAATCTT	660
TTTGACAAA	GCGAAGAGGT	TTTAGAGTGT	TTAAAATCC	CTTCTAACGC	CCTTTTTTT	720
AAGGGAGCGT	TTTTATTAGA	CGCCGCTTTA	GCCCCTTATAG	TTTATGAGCA	ATTTTTAAAA	780
ATAAAAGAATT	AAAATGGCA	AGATTATAGA	GAAAAGCCC	TTAAAAGACT	GAACGCTTT	840
AAAATCGGCT	CCGATAAAA	AGGGATAAAC	AAGGCCGTTT	GTGGGTAGAT	900	
GACGCAAAG	CCACGAATAT	TGATGCCACC	TTACAAGCCC	AAAAAACCTT	AAAAACCAA	960
AAAATCCATT	TGATTTAGG	GGGCGATATT	AAAGGGGTCA	ATTTAACCCC	CCTTTTTGAA	1020
GAGTTTAAA	ACTATAAAAT	AAGCCTTAT	GCCATAGGAT	CAAGCGCTTC	TATCATACAA	1080
GCCTTACCGT	TAGAATTAA	TGTTTCTGT	CAGGTTGTT	TGAAGTTAGA	AAAAGCGTT	1140
CAAGAAATT	AAAGCGTTT	ATTACAAAAT	GAAGTCGCTT	TGCTTTCAAC	TAGCGCGGCC	1200
AGTTTGGATC	AATTTCTTC	GTATAAAGAA	AGGGGTGAA	AATTCAAAGC	GTGGTTTA	1260
AAAGAT						1266

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 162 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...162
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132

ATGAAAGAAA	TCATTGTCCG	CCTTGTGGC	CAGCCTAATG	TGGGGAAATC	GTCCTTAATC	60
AACGCTTGA	GTAACSCCCA	TTTAAAGTG	GGGAATTAA	CCGRGGTTAC	CGTGGATAAA	120
ATGGAAGTGA	GTTCGATCCA	WAAAGATCAT	CAARTSWYTM	TC		162

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133

GTGCATCGTT	TTTCTAGAAA	CCCATGGC	CA TCTGCAATC	GCGCTCGCTC	TTCGAGA	60
CTATCTCGCT	CATTAGTGAG	CGCGGTA	ACT TGGTGGTTGA	GCTTGTGCTT	TTCCGGTGGTT	120
AGTGCTTTAT	TTTCTTTAGT	CAGCTCGGT	GT ATTATGGG	TTAGCTCGGT	GTTTTCTCTT	180
TTTAGCCTT	CTTTTCTGT	TGTCAATTCT	CTTTTTCTT	CAGTCAGCCG	ATCTCTGGCT	240
GCTAATAAGC	GTGTTTTTC	TTTAGCTAAA	ATGCTTTT	CCGTTTTCAG	TTCTGCTTT	300
TCTTTAGTGA	GCTTGTATT	GT	TTGCCAT AAT			333

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134

ATGCAAAAAA	TGGGC GTTGT	CTCTTATTCC	GTGTTCAAG	CGTTGAAAA	GGCTTGAGT	60
CGGTTAAAG	AGGGCGTTCT	TTTGATTGTG	GATTCTTAA	GGCGTTTGAT	TATGGGGAGC	120
GCTTCAGTTA	AAGAATTGAG	TGGGTAATA	GGCATTGTTG	GGGCGTTAAC	CCATGCCAAT	180
AGCGT GAGCA	TGCTTTTGT	GT	TTTATCTA	TCAATCTAGG	GATTTTAAT	240
TTATTACCCA	TTCCAGCCTT	AGATGGGGCG	CAAATGCTAG	GGGTGTTTT	TAAAAATATT	300
TTTCATATCG	CTTGC CAAAC	GCCCATACAA	AATGCGTTGT	GGCTAGTGGG	GGTGGGGTTT	360
TTGGTTTTTG	TCATGTTTT	AGGGCTTTT	AATGACATTA	CTCGTTGCT	A	411

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135

GTGATGGCTT	TGTTGAAAAT	TAGTGCGTA	GTTCTGAGG	GGGAAGTTA	TACAGGAGAG	60
GTAAAAGCG	TTCGTGTC	AGGAGTGGAA	GGGAATTTC	GGGTGCTTTA	TGGGCATAGC	120
AACATGATCA	CCTTGCTCA	GGCGGGAGTC	GTTGAGATTG	AAACGAAAAA	CCAAAAGAG	180
CACATTGCTA	TCAATTGGGG	TTATGCAGAA	GTTACTAATG	AACGGGTGGA	TATTTTAGCC	240
GATGGAGCGG	TCTTTATTAA	AAAAGGATCA	GATGACAGAG	ATGATGCTAT	CTCTAGGGCT	300
AAAAAGCTTT	TAGAGGACGC	AAGCTCTGAC	AGGTTAGCGG	TCTCTAGCGT	GCTGGCTAAG	360
ATTGAGTC	TT					372

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136

ATGTATTCT	TGCTCTTACA	TTTGAATAAA	AAGACCGCTC	TTTAGGCAC	AAGAGGGTTT	60
TTTATCGACG	ACAAACACAT	CAAAGAAAAG	GGCTTGACCA	CGCCCACACTCT	TTTAGAGCTT	120
TATAGCGATT	TGGAAGAACG	GATTCGTTA	AAATGCGAAT	ACTTCATTAT	GGAGGTGAGC	180
TCCCATGCGA	TTGTCCAAA	CGCATCGCTG	GGCTTGATTT	CGCTCTTAAA	ATTCTCACCA	240
ATATCACAAG	CGATCATT					258

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137

ATGAAAACGA	ACTTTTATAA	AATTAAATTAA	CTATTTGCTT	GGTGTCTTAT	CATTGGCATG	60
TTAACGCTC	CGCTTAACGC	TGACCAAAAC	ACGGATATAA	AAGATATTAG	TCCTGAAGAT	120

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ATGGCGCTAA ATAGCGTGGG GCTTGTCT AGAGATCAGC TAAAAATAGA GATCCCTAAA	180
GAAACCTAG AGCAAAAGT GACCATACTC AATGACTATA ATGATAAGAA TGTTAATATC	240
AAGTTTGACG ACATAAGTT AGGGAGTTTC CAACCTAATG ATAATCTAGG TATCAATGCG	300
ATGTTGGGCA TTCAAAATCT TCTM	324

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 720 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138

ATGATTGATA SCCTTGATGG GGCAAAAGAT GCACAATTGA TAAAAAAAGC TTACGCGTTT	60
TTGTCTTAG GAGGCATGG CACGATTAA GGGGTTTAA GAATGACGCA TGCTCACAAAT	120
AAGCCATGCT TTGGGGTGGAG GATTGGGAAT TTAGGGTTTG TGAGCGCGGT TGAATTGAAC	180
GGGTGAAAG ATTCTTACA AGATCTCAAG CAAAACAGGA TCAAATTAGA AGAGCATTG	240
GCTTGGAGG GCCGTATTGG AAACACTTCT TTTTATGCGA TCAATGAAAT CGTGATCGCT	300
AAAAAAAAG CTTGTAGGGT TTTAGACATC AAAGCGTGCG CGGGCCATAC GCCCTTTAAC	360
ACTTATAAAG GCGATGGGCT TATCATTGCC ACGCCCTAG GCTCAACCAGC TTATAATTG	420
AGCGCTCATG GCCCCATTGT GCATGTTTA AGCCAAAGCT ATATTTTAAC GCCCTTGTC	480
GATTTTCTT TAACGCAACG CCCTTGTG TTAGGGGCGG AATTTTGCTT GAGTTTTGTC	540
GCTCATGAAG ACGCTCTTGT GGTTATTGAT GGGCAAGCCA CCTACGATTT AAAAGCCAAC	600
CAACCCCTAT ACATTCAAAA AAGCCCCAGC ACCACCAAGC TCTTACAAAAA AAATTCAAGG	660
GATTATTTA AAGTGCCTAA AGAAAAGCTG TTATGGGGGG AAAGCCCTAA CAAAAAAAGA	720

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 549 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...549
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139

ATGATACTGG GTTTGATAGG GGTTGTGGAA AAAATCTCTG CTTAGAAGC GCATATAGAA	60
GTGCAAGGGG TGTGTTATGG GGTGCAAGTT TCTATGCGAA CGGCTGCTTT GCTCCAAACG	120
GGCCAAAAAG CGCGTTGAA AATCTTACAA GTGATTAAG AAGATGCGA TCTTTTATAC	180
GGGTTTTAG AAGAGAGCGA AAAATTCTC TTGAAAGGC TTGAAAGAAAT CAATGGGTA	240
GGGGGGCGTA TCGCTTTCAG CATTCTTCA AGCTTTCGC CGAATGAATT TGAAAACATT	300
ATCGCTACTA AAGAAGTCAA AAGACTCCAG CAAGTCCCAG GCATAGGGAA AAAGCTCGCC	360
GATAAGATCA TGGTGGATTG GATTGGCTTT TTCATTCAG ATGAAAACAG ACCCGCGC	420
AATGAAAGTCT TTTAGCCCT AGAGAGTTG GGCTTTAAA GCGCTGAAAT CAATCCAGTT	480
TTAAAACCC TAAAACCCCA TCTCAGCATA GAGGCAGCGA TTAAAGAAGC CTTACAGCAA	540
CTGCGCTCT	549

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...462

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140

GTGGGGTTT TGTTTGCCTT TATGCGAAAA ATAACCTTTT GGAAACACC	60
CAAATAACCA TGCAATACAC CGCTGATGCG ATCGCTAAA GCCTTTAGA ATTAAATAAT	120
GCCTCTTCT TAGAGCCTTT AAAATCTTA GAAGAACGAT TCAAAACAC CCCCTTTGTT	180
TTGTTGGACG CAGACAACAG AGTCAAGTT TCTAATATCG GGGTGTGTTGT GGCCTCTTT	240
AAAAATGACG CCTTAATCAA AACCCCTTAT TTGCGCTTA AAAACAGGG CTTTACCTC	300
ACAGACACGG CCCCAACTAA CCGCTTAGGG GTTCTAAAA TCATTATTGC AGAAGAAGAA	360
ATTCAAAAAA TCTTATCCC CCTTTATAAA ATGATAGGCT ATGTTTTT GGGCGCGAGT	420
TTGTTTGTCG CGCTAATAGC CATGTTGGCTT TATAAAATCC CA	462

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 864 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141

GTGGTAATAA	TGATTTAGT	CTGCTTTTA	GCTGCTCG	AAGAGAGCTT	TATCAAATG	60
CAAAAAAAAG	CCCAAGAGCA	AGAAAATGAC	GGCTCTAAC	GCCCCAGCTA	TGTGGATTAG	120
GATTATGAAG	TCTTAGCGA	AACGATTTT	TTACAAAACA	TGGTGTATCA	GCCTATAGAG	180
GAAAGAACG	CCTTTTCCA	ACTGACTAAA	GATGAAGACA	ATTCTTTAA	CCCTGAAAAT	240
TCCGTGATTT	TACTGAATGA	GCCAAGCGAT	AATAGTAAA	AAAACCTACT	CTCATACCCA	300
AACGATCCC	ATAACAATGA	AGACAACGCT	AATAATAGTC	AAAAAAATCC	GTTCCCTTAC	360
AAGGCCAAA	AAAAACAAA	AAACCCAAA	CTCATTGAAT	ATTCCTAACCA	AGATTTCTAC	420
CCCCCTAAA	ATGGGGATAT	TATCATGAGT	AAAGAAGGGG	ATCAATGGTT	GATAGAAATC	480
CAATCCAAAG	CCTTGAAGCG	TTTTTAAA	GATCAAACCG	ATAAAGATCG	CCAGATCCAA	540
ACTTCACTT	TTAATGACAC	TAACCGCAA	ATCCGCAA	TTAAGGGCAA	AATTCTTCG	600
TATGTTTATA	CCACCAATAA	CGGTAGCTTG	AGTTAAGGC	CYTTTTATGA	ATCGTTTTG	660
TTAGAAAAAA	AGAGCGATAA	TGTTTATACG	ATAGAGAATA	AGGCTTCTAGA	TAATATGGAG	720
ATTTCAAAAGT	GTCAAATGGT	GTTAAAAAG	CATTCAACCG	ATAAATTAGA	CAGCCACAT	780
AAAGCCATCA	GTATTGATT	GGATTTAAA	AAAGAGCGCT	TTAAGAGCGA	TACGGAACTC	840
TTTTAGAAT	GTCTTAAGGA	AAAGT				864

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142

ATGGCCGCTC	CACTACTTGC	TCTGCCCTTT	CTTCTCTAAC	CTTTAGTGCT	TGGTGCTTTA	60
GCTGTCATAG	GAGTGGGTGC	TTACTTGAT	CCCAATAAGC	AAGATTCTTT	AGTTGTGCAA	120
GCAGATGGC	TTTATAGTGA	AATTCTGGG	TTTTCTCATTT	CGTTTTCTAG	CAAGATCTTG	180
AAAGGAATTG	GTGAGCCTTT	AGCCAATGTT	ATCCAACCTT	TGGTATGGT	TTTAGGAATG	240
CTTTTAATCC	TTTGTTATTC	CTTTAAACGC	TATCAAACAA	ATGATTTATT	TGAAATCAA	300
ACCTTTTTAA	TGCTTTTGT	GTTTGTAGGA	TACCTTCTT	TGTACCATT	TGCTTTTAAA	360
TCTGATGGTT	CTAGTAGCGG	TAATGGTCGC	TCCAGTTTTG	CCTTCAAAAA	TCATGTAACA	420
GAAATTTTG	ACACGCCG	TAACCTGCTA	AATGCTGGGA	TTTCTTAATGT	GGTTAAGGAA	480
TATCAACAA	ATAGTGCAAG	AGAACACAAG	AATATAGACA	CGCACCCACAG	TATCACTAAC	540
GCTAATTTTT	CATTCCATGT	CAGACAAATT	TTAACGAGTT	TGAATAAAACT	ATATGAAGAC	600
TTCAAAATT	ATAATGGACT	ATCGCTAAA	ACCCATTATTG	CAGCTGTTT	GTTATTAGTT	660
ATTTTAAAGGAT	TAGAATTGTT	TTTATTGTT	AAAGTTTCT	GTATGTTTT	TATGACTTAT	720
TTAGAAAAAA	TTATTTACTT	GTCTTTGGTT	ATTTTCTATGC	TACTGCTAGG	TTTTTTTCAG	780
CAGACTAGAG	TTTTTTAGT	GTCTTATGT	AAAAAAATT	TTTCATTGAC	TTTTTACATG	840
CCTTTGTGTT	TGCTATTAGT	GTTTATTCAAC	TCTTTGCAT	TACAATACGC	AATCAAAGTG	900
GGAGGGAGCA	ATGAAATAGT	GGCTAAATTT	GGCATTATTG	TAGCAATAGG	AATTTCACTG	960
ACATTATTTC	AAAAGTCCC	CGAAATGATT	AACGCTATCT	TTGGCACACA	AGGTGGTCTA	1020
ACGGATGCTA	AAAGCTTCAT	ATATCAAGGT	GTGCAAATGG	CTAGTGCTGG	AGCTGGAGCC	1080
ATAGCTGGAA	GTCTTAAGAG	TGTGGTCTGT	TCAGCATTTG	GTAGAACGCT	AGAACCTTAT	1140
AAACACGCAA	AATCTACGAT	AAACAGCACT	ACGGCTAACCA	TGAGAGACAT	GCCAGGACAT	1200
CCTGGTGT	GAAGGGTGT	GGAGACGATT	GAACCTCCCA	AGTCTCATAG	AGCTAGCAA	1260

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...216
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143

GTGTTAAAAT TTCAAAAATT ACCCTTATTG TTTGGTTCCA TTCTTTATAA TCAAAGCCCT	60
TTATTGGCTT TTGATTATAA GTTTAGTGGG GTAGCGGAAT CTGTTTCTAA AGTGGGGTTT	120
AACCATTCCA AACTCAATTG CAAAGAAGGG ATTTTCCCTA CAGGCCACCTT TGTAACCGCC	180
ACGATCAAGC TTCAAGTGRA TTYCAAATCT GCTCCC	216

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 615 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...615
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:144

ATGGGTAATC ATTTCCTAA ATTAGGATTT GTTTAGCGG CTTTAGGGAG CGCGATAGGT	60
TTAGGGCATA TCTGGCGCTT CCCCTATATG ACTGGGGTGA GTGGTGGGG TGCTTTGTT	120
TTATTGTTT TATTTCATC CTTAACGTT GGTGCGGCGA TGTTTATCGC TGAAATGCTA	180
TTAGGACAAA GCACGCAAAA AAATGTAACA GAAGCTTTA AAGAGCTTGA CATTAACCT	240
AAAAAAACGCT GGAAATACGC AGGGATCATG CTTATTCCTG GACCTTAAAT ACTGACTTTT	300
TATGGCACTA TTTTAGGTG GGTGCTTAT TATTTGGTGA GTATTAGTTT TAATTGCGCT	360
AGCAGTATCC AAGAATCTGA ACAAAATTT ACTCAAACCTT TGCACTATAG AGGGTTACAA	420
TCCATAGGGC TTTTTAGCGT TTTATTCATA ACCGGATGGA TTGTTTCTAG GGGGATTAAA	480
GAAGGCATTG AAAAATCTAA TTGGTTTA ATGCCCTTAC TCTTTGCCAC TTTTTTGTT	540
TTGCTTTTTT ATGCATGAG CATGGATTCT TTTTCTAAAG CTTTCCATTGATT CATGTTGATT	600
TCAAGCCAAA AGATT	615

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 984 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...984
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:145

ATGGAAAAAG	TTTGCCTGAG	CGCATGGGG	TTCCTAAGA	TTTTAGAAGA	AAGATTAAAA	60
GAAAATATG	GCGATGATTG	GGAAAAACAT	GTAAAGGCTA	AAGCAATAAA	CGAACAAAGAG	120
CTTGAAGAAC	AAGTCAAAGC	TAAAGCCAAA	GAGCAACAAA	AGACACAAAG	AGAAAAAAACA	180
CTCAATGGAT	TTTTAAAAAA	ACTTGCTTAA	AAAAGCGTG	ATATGTTACA	AAGCACTATG	240
TTATTTGATG	AAGTCAAAGA	AGCTGATGTG	CTTTTCAAG	CAGAGCGTAA	AATTGGCGAT	300
TGGATTTTA	GCAGTGCGGT	GTTCCTTTT	GCTCTAGCCC	TTATAGAAGC	CATTATTATT	360
GTATGCTTAT	TGCCGTTAAA	AGAAAAAGTG	CCTTATTAG	TAACCTTTTC	AAACGCTACA	420
CAAAATTTTG	CCATAGTCCA	AAGAGCAGAC	AAGAGCATCC	GTGCTAATCA	AGCGCTTGTG	480
AGACAATTGG	TAGCGCTTA	TGTTAATAAT	AGAGAAAATA	TTTCAAGTAT	AAAAGAGCAA	540
AACGAAATAG	CCCACGAAAC	CATTAGTTG	CAAAGCGCAT	TTGAAGTGTG	GGATTTTTT	600
GAAAAACTGG	TTTCCTTATGA	GCATAGCATT	TACACTAATA	TAAATCTAAC	ACGAAAAATT	660
AGCATTATCA	ATATGCCCTT	AATCAGTAAA	ACCCAAGCCA	ATATTGAAAT	ATCCGCACAA	720
CTTTTTCATA	AAGAAAAGT	AGAAAGCGAA	AAGCGTTATA	GAATAATTAT	GACCTTGAA	780
TTTGAACCTA	TTGAAATTGA	TACAAAATCT	GTTCCTCTAA	ACCCTACAGG	CTTTATGTGTT	840
ACAGGTTATG	ATGTAACTGA	AATTGCGATT	TTAAAAGATT	TAGATGAGAA	AAATAAAGTC	900
AAAGATGATG	GTGTGAAATC	TAGGATTATC	CATGTCGAGA	AAAAAGACCC	TCATATGAGC	960
CACTATAAAG	ATGTTAAGGA	GCAA				984

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...228

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146

ATGCTGCATA AGGCTAAGGT GGGCATCGTG TTTAGGCAG TTTTAGGGAT TTTTGGCGTG	60
TTTTATTGT TGTTTACTT GAGCGCGTTT TTAATGGTGG CTTTTAAAGA CACTAAACGC	120
ATGTTTATAA GCGTTTAAAT AGGGAGCGTG GTGTTCTTT GGAGCGATCT ATTGGTCTTT	180
GTAGGGTTTA AAAATATCAG CTTTGTGTTG GATATTGTT ATGAAATC	228

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147

ATCCCGTTTG TGAAAAACTG GATCTGGAGT TTAAAGATGG CTTCAGCGC GATTAGTGGG	60
GCTAGTGGGG TGGGAAAAG CGTCCTTATT GCGAGCCTTT TAGGGCGTT TGGGCTTAAA	120
GAGAGCAACG CTTCAAACAT TGAAGTGGAA TTGATCGCGC CTTTTTAAAGA CACGGAAGAA	180
TACGGCATTT TTAGAGAAGA TGACCATGAA CCTCTAGTTA TTACCGTGAT TAAAAAAAGAA	240
AAAACACGCT ATTTTTAAA CCAAACAAGC CTATCTAAA ACACGCTCAA AGCGTTATTA	300
AAGGGGCTTA TTAAACGCTT ATCTAACGAC AGATTCAGCC AGAATGAACt CAACGATATT	360
TTAATGCTCT CCTTATTAGA TGGCTATATC CAAAATAAA ATARGCGTT AGCCCCCTTT	420

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 924 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148

ATGCCACAAA ACCAGCTTGT GATCACCACATC ATTGATGAAT CAGGCTCTAA GCAACTCAAA	60
TTTTCTAAAA ATTTAAAACG CAACCTCATIC ATTCTGTTG TCATTCTTT ATTGATCGTG	120

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GGGCTTGGCG	TGGGGTTTTT	AAAATTTTA	ATCGCTAAAAA	TGGATAACGAT	GACAAGCGAG	180
AGGAATGCGG	TTTTAAGGGA	TTTGTAGGGT	TTGTATCAAA	AAAATTACGC	CCTAGCGAAA	240
GAGATTAAAA	ACAACGAGA	AGAGCTTTT	ATTGTGGGGC	AAAAGATCG	TGGGCTAGAA	300
TCCTTGATTG	AAATCAAAA	GGGGGCTAAT	GGGGGAGGGC	ATCTCTATGA	TGAAGTGGAT	360
TTAGAAAATT	TGAGCTTAAA	TCAAAAACAT	TTAGCACTCA	TGCTCATTC	TAATGGCATG	420
CCCCTAAAAA	CTTATAGCGC	TATCAAACCC	ACTAAAGAAA	GGAACCCACCC	CATTAAAAG	480
ATTAAGGGCG	TTGAATCCGG	GATCGATTIT	ATCGGCCAT	TGAACACGCC	TGTGTATGCG	540
AGCGCTGATG	GGATTGTGGA	TTTTGTGAAG	ACTCGTTCTA	ATGCCGGGTA	TGGGAACCTG	600
GTGCGCATTC	ACATGCGTT	TGGTTTCAGC	TCCATTATA	CCGACTTAGA	TCATGTCAT	660
GTGCAAGCTA	AAAGCTTCAT	CCAAAAGGG	CAGTTGATTG	GCTATAGCGG	GAAGAGCGGT	720
AATAGCGGGC	GGGAAAAAATT	GCATTATGAA	GTGCGGTTTT	TGGGTAAAAT	TTTAGACGCA	780
GAAAATTCC	TAGCATGGGA	TTTGGATCAT	TTTCAAAGCG	CTTTAGAAGA	AAATAAATT	840
ATTGAATGGA	AGAATCTGTT	TTGGGTTTTA	GAAGACATCG	TCCAGCTCCA	AGAGCATGTG	900
GATAAAGACA	CCTTAAAAGG	TCAG				924

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1017 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149

ATGATCACTG	GCTCTCACAA	CCCCAAAGAA	TACAACGGCT	TTAAAATCAC	GCTCAATCAA	60
AACCCCTTTT	ATGGCAAGGA	CATTCAAGCT	TTAAAAAAACA	CGCTTTAAA	CGCAAAGCAT	120
GAAATAAACG	CCCTAAAAGA	AAAGCAGAG	AAAGTCATG	CCCTAGAAGC	GTATCATCGC	180
TATTTGATCA	AGGATTTAA	GCATTTAAA	AATCTTAAAT	ACAAAATCGC	CCTGGATTIT	240
GGTAATGGCG	TGGGGCGGT	AGGATTAGAG	CCGATTTAA	AGGCTTTAAA	CATTGATT	300
ACCAGCCTTT	ATAGCGATCC	TGATGGGAT	TTTCCTAAC	ACCAACCCAGA	CCCTAGCGAA	360
GCGAAAAAACT	TAAAAGACTT	AGAAAAAACAC	ATGCGAGAAA	ACGCTATTIT	AATAGGCTTT	420
GCTTTTGATG	GGCATGCGGA	TAGGATTGCG	ATGCTAAAGCT	CTCATCATAT	CTATGCGGGC	480
GATGAATTAG	CGATTITATT	CGCTAAACCG	TTGCATGCTC	AAGGCATCAC	CCCTTTGTG	540
ATCGGCGAAG	TCAAATGCTC	TCAAGTGTG	TATAACGCAA	TCAATACTIT	TGGTAAGACG	600
CTCATGTATA	AAACCGGGCA	TAGCAATTAA	AAAATCAAGC	TCAAAGAAC	TAATGCCAT	660
TTTGGGGCTG	AAATGAGCGG	GCATATCTTT	TTTAAAGAAC	GCTATTITGG	CTATGATGAC	720
GCTCTTACG	CATGTTTAAG	GGCTTTGGAG	TTATTGCTTG	AACAAAGTCC	AAGCGACTTG	780
GAAAACACCA	TTAAAAAACCT	CCCCATTCC	TACACCACGC	CTGAAGAAAA	AATGCCGTG	840
AGCGAAGAAG	AAAAAATTGA	ATCATTCGC	AACTTACAAG	AAAGCGCTAA	AAACCCGCCA	900
AGCCATTTC	CTACAATCAA	AGAAATCATC	AGCATTGATG	GGGTGAGAGT	GGTTTTGAA	960
CATGGCTT	GGCTTATTGCG	CGCAAGCAAC	ACCCACCCCC	TATTTAGTC	GCCGCTT	1017

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150

ATGTCCAAGA ACCTTCAAAAA GAAGAACCCA AAGAAGAGTT TYCCACAAGC CCAGAAAGCC	60
ATAAGGGAGA TGAAAATGTT TGAAACCATT GCYTTTTATT TCTTGCAT CCTTAACCTTA	120
AGCATGGCGT TAGTGGTGTG CACAACCACA AATATCCTCT ATGCCATTAC CGCTCTCGCT	180
AGTAGCATGG TTTTTATTTTG TGCTTTTTTC TTTTTACTGG ACGCTGAGTT TTTGGGCGTG	240
GTGCAAATCA CGGTGTATGT GGGTGCCTGC ATTGTGATGT ATGCGTTTG CATGATCTTT	300
TTCACACTCG CTGAGAAGT AGTTGAACGC AACGAAAGCC CTAACATCTT GTGCGTTCTT	360
TCATTTGGCG TGGCGCTGTT GCTCACCTTG ATTAAAGCG CTCCTAGCAT TGSSGAAAAC	420
CTTCTAACGC AAGTCAAATC CAACGCTATT GATGCGCAA TYCCYAACAT TAAAGCGATT	480
GGTTATGTGC TTTTCAACCA TTACCTCATT CCCTTGAAAG CGGCGGCTTT AATGCTTTA	540
GTCGCTATGG TTGGAGGCAT CGCTACAGGG ATTCAAAAAA TCCATGGAA AAATCACACG	600
CAATTATATAA AGGAATCTCT A	621

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 753 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151

ATGGGTGCAA TTTTATCTAT TTTAAACTT GAAATCAAAT CTTATCTCAC CAATACAAGC	60
GGCCTATTTT GGACTTTTAT TTATCCTATT TTAATGCTCC TATTACTAAT TTTTGTTTT	120
TCAAAAATA CCACTGAAAT TTTTACTTT AATAACATTA TAGTCTAAAT GGGACTTCCTT	180
ATTATTCTA GCGCGATCTT TGGTCTCACCA CAAGCTATAA CAAGCTCTAG ATCGCATAAT	240
ATATTCTTAT TCTACATGCT ATCACCAAGCA ACTTCAAAC AAATAACTCT AGCATTAAATC	300
GCTTCAAGAC TAATCGTTGT AATCCTATAT GCTTTATCT TTATTGTTCT CTCTTTTAT	360
GCGCTCAATA TCATCACTAT TCTTAATTTT AAAGCGCTTA TTTTGGGTT TATTAGCATT	420
TTTTCAGCG CATTGTTTGT TTTTCTCTG GCAATTCTTG TAGCTAGAAT TTTTCAAAC	480
GAACAAAGCA TCTTAGGATT TTGTAATATC ATCAATCTCT ATGCGCTAAAT GTCTTGTAAAT	540
GTTTTGTTC CTTTGAATA CCTACCTAAT ATTGGTCAAT TATTATCAA AACATCTATT	600
TTTTACTACC TTAATCAACT TCTAAATCAA GCTTTCAAG GGATTGATAC TATACTGGTT	660
TTAGCAACTT CAACATTTT CATTATTGGT GGCAATTATTT TATTCTACT AAGCGCTAAAT	720
CGCATGTTAC TAACACCAAA AGAACCGATG CGT	753

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 207 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...207
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152

ATGGCAGGCA CACAAGCTAT ATATGAATCA TCTTCTGCAG GATTCTTATC GCAAGTCTCC	60
TCAATCATCT CAAGCACAAG TGGTGTGCCA GGGCATTTCAGGAATAGT AGCGGGCGCT	120
ATGACAGCAG CGATTATTCC TATTCTGTG GGATTACTA ATCCGAAAT GACCGYTATY	180
ATTRACCAA TAYAATCAA GCATCGC	207

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...336
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:153

GTGAGCCGTA TTTTAGGCTT GAGCGATGAT TTAGCGATGA CTTTATGCAG TGAATCCATC	60
CGCATTCAAG CCCCTATCAA AGGTAAAGAT GTCGTTGGTA TTGAAATCCC TAACAGCCAA	120
AGCCAAATTA TTATTTAAG AGAAATTTC GAAAGCGAAT TGTTTCAAAA ATCCAGCTCG	180
CCTCTAACCC TAGCTTCTAGG CAAAGACATT GTGGCTAACCC CTTCATCAC GGATTTAAAA	240
AAGCTCCCCC ACTTGCTCAT CGCCGGCACG ACAGGGAGCG GTAAGAGCGT GGGCGTGAAT	300
GCGATGATTT TATCCTTACT TTATAAAAAA CCCCCC	336

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:

200

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154

ATGGATGAAA GSCTCGTTTA	TGGGGTGATT TGCATGCCCA	GTCAGGTTTT TGCCAACACC	60
GGCACTAACG TGAGCATCAT	CTTTTITCAA AAAACGCCAA	GCGCAAAGGA AGTGATCTTG	120
ATTGACGCTT CCAAACCTCGG	CAGAAGATAAC ACCGAAAACA	AAAACAAAAAA AACGCGCTTA	180
AGGCCAAGCG ATATGGATTG	GATTTAGAA ACTTTCCAAA	ATAAAGCCCC AAAATCGGAT	240
TTTGCGCTC TGGTTTCTTT	TGATGAAATT ACAGAAAAAA	ATTATTCTCT AAACCCCCGG	300
CACTATTTCAT CTATAGAAGA	CACGAGCGAG ACAATCAGCC	AAGCGGAGTT TGAAAACCTTG	360
ATGCAACAAAT ATTCAAGCGA	ACTAGCGAGC CTTTTGATG	AAAGCCAAAA TTTGCAACAA	420
GAGATTTAG AAACCTTAAA	AGGGTTAGG TTGAG		456

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155

ATGAGAAGAA TTATTAAGAAA	CACACTTCA CGCTTAGGCT ATGAAGATGT	TTTAGAAGCT 60
GAGCATGGGG TGGAAAGCTTG	GGAAAAACTA GACGCTAATG CGGACACTAA	GGTGCTTATT 120
ACGGATTGGA ACATGCCCTGA	AATGAACGGG TTGGATCTCG	TTAAAAGGT GCGTGCGGAT 180
AACCGATTTA AGGAAATCCC	TATCATTATG ATCACCCACAG	AGGGCGGTAA AGCTGAGGTC 240
ATTACGACTT TAAAAGCGGG	CGTGAATAAC TACATTGTGA	AACCTTTAC CCCCCAAGTT 300
TTGAAAGAAA AATTAGAGGT	TGTTTTAGGG ACAAACGAT	

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 549 base pairs

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201

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...549

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156

ATGGCAGAAC	AACAAGAAAA	TACCGCGCAA	CAACCCAAA	AAAAAAGCAA	AGCCCTTTA	60
TTTGTCAATT	TTGGAAGCGT	GCTAGTGATG	CTTTTATTGG	TGGGGGTGAT	TATCATGCTG	120
C TTATGGGGA	ATAAGGAAGA	ATCTAAAGAA	AACGCTTCTA	AAAACACCCA	AGAAGTCCAA	180
GCTAATCCTA	TGGCGAACAA	GAATCAAGAA	GCCAAAGAAG	GCTCTAATAT	CCAGCAATAT	240
TTGGTGCTTG	GCCCTTTGTA	TGCGATTGAT	GCGCCTTTG	CGGTGAATT	GGTCTCTCAA	300
AATGGCAGAC	GCTACCTTAA	GGCTTCTATT	TCGCTAGAAT	TGAGCAATGA	AAAGCTTTG	360
AATGAAGTCA	AGGTAAAGA	CACGGCGATT	AAGGACACGA	TTATAGAAAT	TCTATCGTCT	420
AAAAGCGTGG	AAGAAAGTGGT	TACTAACAAA	GGCAAAACAA	AGCTTAAAGA	TGAAATTAAAG	480
AGCCATTGAA	ATTGCTTTT	GATTGATGGC	TTTATTAAAA	ATGTCTTTT	CACTGATTTC	540
ATTATCCAA						549

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...105

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157

ATGGGGTGT	TTAGCACCAT	TTGTTGTAAG	GGTTAACGC	TTAGCGTTGG	TGGATTTTG	60
G	TGATGATGA	GATTCTTAAT	ATTCAAAGAT	TTTGCAAAG	ATTTT	105

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2106 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
- (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2106
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158

GTGGCCGCTC	TTGTGGTTAA	AAGCGTAAA	ATTGATTATA	AACAAAGCAT	TCAATCTGAC	60
TCTCAACT	TGCAAGCGAS	CTTGAATCG	TTTGAAAATA	AAGAAGTGT	TGAGAATCAG	120
TATTTTTAG	TTTTAGAAAAG	CACTCACTCT	TTGCAATGGCG	TTTGGAGCA	TAAGAAAAAA	180
TCTTCATGC	ACGCTAATAG	AGAAAATTTC	AAGGATATT	TCTCTTATAA	AGCGCATTTT	240
TTGCAAGAAA	CTTTAAAAAG	CTTAGAAATC	CAGCTCAAAA	ACTATGCC	CAAACCTTTA	300
AACTCTAAAG	AGGTTTGAA	TTTTATGCA	GAATATATTA	ATGGGTTG	ACTCCCTTTA	360
AAACCCCTAG	TAGGGGCGTA	TTTGAGCGAT	AGCTTATATCG	CTAGTTCTAT	CACTTTGAA	420
AAAGATTATT	TCATTCAAGA	AAGCTTAAAT	CAAAACCT	ATAACCGCTT	GATTGGCATT	480
AAAGCTTATG	AGAGCGAAAG	GATCCTCT	ATAGCGGTG	GAGCGCTTTT	ATACCAAGAG	540
ACGCCCTTGG	ATATTATCTT	TTCCATAGAG	CCTATGACCG	TCAATAAAC	GCTGAGTTTT	600
TTAAAAGAGA	GGGCAAGTT	TAGCATGTCT	AATCTTGT	AAAACGAGCT	ATTAGAATAC	660
CAAGAATTAG	TCAAAACCAA	ACGATTATCC	ATGCAAAAT	TCGCCCTAAA	CGTTCTTATC	720
AAAGCCCCCA	GTITGGAGGA	TTTAGACGCT	CAAACCAGCT	TAATTTAGG	GCTTTTATTT	780
AAAGAAAACT	TAGTGGGGCT	TATAGAAACT	TTTGGCTTGA	AAGGGGGGTA	TTTTCCCTTT	840
TTCCTGAAC	GCATCCATT	AAACCAACCG	TTGCGTTTT	TAACCTCTAA	AGGCCCTAGCG	900
TGTTTGATGG	TGTTTGAAAG	GCAAAATTAA	GGTTTTAAGG	CTAATTCTATG	GGGAATAGC	960
CCTTGTAGCG	TGTTTAAAGA	TTGGATTAT	TCCTTTTTT	TATTCAATT	CCACAACCAA	1020
GAAGTGAGCC	ATAATAACCG	TAAGAAAATT	GCCAGAGTGA	ATGGGCATAC	TTTGTGTTATA	1080
GGGCAACCG	GAAGCGGTAA	AAGCACGCTG	ATTAGCTATT	TAATGATGAG	CGCTTTAAAA	1140
TACCAAAACA	TGCGCTTTT	AGCTTTGAC	AGGATGCAAG	GGTTGTATT	TTTCACCGAA	1200
TTTTTTAAAG	GGCAATTACCA	TGACGCCAA	TCTTTTGT	TCAACCCCTT	TTGTTTAGAG	1260
CCTAATTGTC	AGAATTGAGA	ATTTTGCAA	TCCTTTTTT	TGAGCATTT	GGATCTTGCC	1320
CCTTCAAGGG	ATAAGAAGC	CTTAGAAGAC	ATGAATGCGA	TTTCTGGCG	GATTAAGAGC	1380
CTTATGAGA	CCTTATACCC	CAAAGATTTC	ATTTGCTGG	ATTTTAAAGA	AACGCTTTAA	1440
AGAACCTCAT	CTAACCAATT	GGGCTGAGT	TTAGAGCCGT	ATTGAATAA	CCCCCTTTTT	1500
AACCTTIGA	ATGACGCCGT	CAACTCCAAC	GCTTTTTAA	ATGTGATAAA	CCTAGATGCG	1560
ATCACCCAAA	ACCTAAAGA	CTTAGGGCTT	TTAGCCTATT	ACTTGTGTTA	TAAGATCTTA	1620
GAAGAGTCTA	GGAAAAACGA	CAGCGCTTT	TTGGTTTTT	TAGACGAATT	AAATCCTAT	1680
GTGGAAAACG	ATTTGTTAA	CACTAAAATC	AACGCTTTAA	TCACGCAAGC	CAGGAAGCT	1740
AATGCCGTGG	TGGTGTGCG	CTTGCAGAC	ATTACCAAC	TTAGCGGGGT	AAAAACGCC	1800
CATAGTTTT	TAAGCAACAT	GGGGACTTC	ATTGGTATC	CGCAAAAAAA	CGCTAGGGAA	1860
TTGAAACACA	ATTTCAATGT	GCCTTGAGC	GAAGCTGAAA	TTTCTTTTT	AGAAAACACC	1920
CCTCTGTATG	CCAGGCAGGT	TTTGTCAAA	AACTGGGTA	ACGGGAGTTC	CAACATGATT	1980
GATGTGAGTT	TGGAGGGCTT	GGGGTGTAT	TTGAAAATCT	TTAACCTAGA	TTCCAGTCAT	2040
GTCAATAAAG	TGAAAGCGTT	ACAAAAAGAC	TACCCCTACAG	AGTGGCGTGA	GAACATTG	2100
AAGAGT						2106

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 879 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...879
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159

ATGCAAGAAC	ACTGGCAAGC	CGTCCAAGAC	ACCATTAAAG	TGGTTTCAGA	TGTGAAGCG	60
CGGAATTITG	CGGTGCGCAT	CACGGCTGAA	CCCGCAAGCC	CTGATTTGAA	AGAATTGAGA	120
GACCGCTAA	ATGGGATCAT	GSAYTATTG	CAAGAAAGCG	TAGGGACTCA	CATGCCAAGC	180
ATTTCAAAA	TCTTGAAAG	CTATTCTGGC	TTGGATTITA	GAGGGCGGAT	CCAAAACGCT	240
TCGGGTAGGG	TGGAATTGGT	TACTAACGCT	TTAGGGCAAG	AAATCCAAA	AATGCTAGAA	300
ACTTCGTCTA	ATTTTGCCAA	AGATCTAGCG	AACGATAGCG	CGAATTAAA	AGAATCCGTG	360
CAAATTTAG	AAAAGGCCTTC	AAACTCCAA	CACAAAAGCC	TGATGGAAAC	TTCCAAAACG	420
ATAGAAAATA	TCACCACTTC	CATTCAAGGC	GTGAGCTCTC	AAAGTGAAGC	CATGATTGAA	480
CAAGGGAAAG	ACATTAAAAAG	CATTGTAGAA	ATCATTAGAG	ATATTGCCGA	TCAAACGAAT	540
CTATTAGCCC	TAAACGCTGC	TATTGAAGCC	GCACGAGCCG	GCGAGCATGG	CAGAGGCTTT	600
GCGGTGGTGG	CTGATGAGGT	GAGGAAGCTC	GCTGAAAGGA	CGCAAAAATC	CCTCAGTGAG	660
ATTGAAGCCA	ATATTAATAT	TCTCGTTCAA	AGCATTTCAAG	ACACGAGCGA	AAGCATTAAA	720
AACCAGGTAA	AAGAACTAGA	AGAGATCAAC	GCTTCTATTG	AAGCCTTAAG	ATCGGTTACT	780
GAGGGCAATC	AAAAATCGC	TAGCGATTCT	TTAGAAATCA	GTCAGGAAAT	TGACAAAGTC	840
TCTAACGATA	TTTTAGAAGA	TGTGAATAAA	AAGCAGTTT			879

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 156 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...156
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160

ATGCCTAAAA	GTTCACCTT	ACCGACTTTC	GTGTGGTGT	TGTTTGTGGG	GGTTATCTTA	60
AGGAACGCTT	TGTCTTTTTT	AAAAATCCAT	ACCGTGTTTG	ACAGAGAGGT	TTCAGTTATA	120
GGGAATGTGA	GCTTGAGCCT	GTTTTAGCT	TACGCT			156

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 546 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...546
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161

GTGGGGCTTT TAAATTCTAA GGCGTCAAAA CCCTACCGCA AGATTTGCA AATGGTGT	60
CAAGACCCCT ACGCATCATT AAACCCCTCGC TTAAGCATTG AAAGCATTG AATAGAACG	120
TTCGCCTTTC CTTACCCCTAA AGCTTCACAA CAAGAATGGC ACCATTTAGC TGAACCTTGC	180
TTAGAAGAAG TGTGTTTAA CCCTGAATTG CTTAACCTTAC ACGCTTATGA GCTCAGCGGA	240
GGGGAGCGCC AAAGAGTGGC GATCGCTAGA GCGATTGCCT TAAACCTAG AATCATTCTT	300
TTAGATGAGC CAACCTCTGC TTAGACAAA AGCATTCAA AAAGCGTGT GGAATTATTG	360
TTGAAATTAC AAGAAAAGCA GGATTTGAGC TATTGTTTA TCAGCCATGA TTAGAGATGC	420
ATCAAAGCTT TTGCGATAG GGTGTTAGTG GTGAGTGAGG GGAAATCGT GGAAACAGGC	480
GCTATTGAAG AGGTGTTGCA AAACCCAAA CACGCTTATA CCAAGCGTTT GTTGAATCC	540
AGGCTT	546

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 753 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...753
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162

GTGAGTTGAA TTAAAGTTAG TGGTGATAAA AAAGTGATTG AGGTTTCTAT TCCTTTAACT	60
TCCATTTCAG GCAAAGCGCG TGTGAAATC AGACATGCCT TTAGCGATTA TGGTATTCA	120
ACAGCGACTA GAAAAATCCC TTTAGTTA AAGCATTATG TAGAGTGGCA GATCGGTTAT	180
GATGTCCTTAA TTAAAGATAA AGAAAAATTG GAACTCACTA CTTTAAAGA TGAAAAATAT	240
CATTTTTAG GGGCTAATAA TAAAGTAAA ACTCTTTATG AATTGAGCGA AATGATTAT	300
TACGCTAACG GATTGGGTTT AATCAGTTA GAAAATTAG AAAACTTTT AAAATTTTA	360
GAAAAACAAA AACAAATTAT AGAAGATAAT TTTATGATTA CAAGAGAAAG ATTTAGATCG	420
CATCAATTG GTGGCATGGA TTTGAACTC TCACGCATT CTTATCCTT GCTCATTCT	480
TCTTTGATG ATAATGAGTT GAGCGAAATA GTTATTAAGG ACAACAATA TGGCTCTAAA	540
ACCCAAGCCA TGCTGTATTG TTGCTTTCT ATTTGGAGT TAAAAACCCG TACCCCCCTA	600
TTAAACAGAA CGCCTATGCC CAAAGAACAT GCCCTTTGA TTATCCATGA AACCAACGCT	660
CTTGTGTTTT TAGAAATGCT TAAAATTGCT GGACTTTAA GCCAAGTGCA CCATAACGAT	720
GTGTTWAAGA TTTTWGAAA AATACTTCAA AAT	753

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(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...120
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163

GTGATCACGG CGTGTAA TAGYGAAAAA ACCATTGAAG ACACCATTCT TTCCGTGCCT	60
AATCAAACCTT ATAAAAACAT TGAATACATC ATTATAGATG GGGCTAGCGC GATAGCACTT	120

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...366
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164

GTGTTTGTAG GGCTTTATCA TGGGGCAAGC ATCTTGATT TAAAATTGA AGTCTATCTT	60
ACTATGCTAA TCCTCTTAAT GCCCCTTGTC GCTAGGATT ATATCAATT CCCAAAAACC	120
ACAGAAACCTT CGCATGGCTA TGCGAGATGG CCTAATGTTA AAGATATAGA ATGCTTTAAA	180
ATTTTAGCA AAGAGGGCTT TTGTAAAGTG GTGCATAGAT TAGGGGTGCA ATTTGATAAT	240
GGCTTTATTC TAGTAAATT TGGTTTCCA AAGCTTAGAA ATGTGTGCTA TGACAAGCCC	300
TTAGAACCGA TGATTGTTGC ACCCCCTGGT GCGGAAAAAC TGCAATGTGTG GCTTTGCCAA	360
ATTTAT	366

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

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(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165

ATGAAACGCC	TIGCTGTTCG	GCTTATTITG	GTGTTGGGAG	TGGTGTGGGG	GAAATCCTTG	60
CCTAAAGTGGG	CAAAGATTG	CTAAAAGAG	ATGCGGATTG	AAAAGACCCA	AACCAAAGAT	120
GAAAAAAATT	TAGTGTGTTG	GATGAGCGAT	ATATTGCTTT	CAGATATGGA	TTATAGCTTG	180
TCCTCAGCCA	GACAAACCC	CITAGAGAAA	GTGATGAAAG	CTTCAAGGG	GGATAGAATA	240
GAGATTAAGG	CTGGTGAAGCT	AAAGGCAC	TTTATTGATA	CGGATAAAAGT	TTATGTGCTT	300
CTAAGAACATCA	CTAAGAACCA	TGTCGCTTTA	ATGAATGAG			339

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166

ATGAACCCCC	AGATTCAACC	CGCCACTAAA	AAACCTTAA	AATCCCTTT	AGCCGCTAGT	60
TCAGGCAATT	TAGTGAATG	GTATGTTTT	TACCGCTTATG	CGTTCTTGC	TCCTTATTTC	120
GCTAAAGGAAT	TTACCCACAC	CAATGACCCT	ACTCTAGCGC	TCATCTCAGC	TTTTTAGTT	180
TTTATGCTAG	GGTTTTTCTAT	GGCCCTTTG	GGGAGTTTGT	TTTTGGTAA	ATTGGGGAT	240
AAAAAGGGGC	GTAAAAACTTC	CATGGTGTAT	TCCATTATCC	TTATGGCGCT	AGGCTCTTC	300
ATGCTCGCAT	TGCTCCCCAT	TAAAGAACAT	GTAGGGGAAT	GGGGCTTCTT	GTTTTATTG	360
TTAGCCAGGC	TTTACAGGG	CTTTAGCGTG	GGAGGAGAAT	ATGGCGTGGT	CGCCACTTAT	420
CTCTCTGAAT	TAGGCAAGAA	TGGTAAAAAA	GGTTTTTATG	GCTCTTCCCA	ATATGTAAC	480
TTAGTGGGAG	GGCAACTCTT	AGCTATTTT	TCGCTCTTAA	TCGTTGAAA	CGTTTACACG	540
CATGAGCAAA	TCAGCGCGTT	TGCTTGGCGT	TATTTATTG	CTTGTAGAGGG	TATATTAGCC	600
CTACTCTCGC	TCTTTTGTAG	AAATATCATG	GAAGAAACTA	TGGATAATGA	AGCGACTCCT	660
CAAAAAAAGA	CTAATGTAAC	TAATACAAA	GAACCCATA	TCAAAGAAAC	CCAAAGAGGC	720
AGTTAAAGG	AATTGCTAA	CCATAAAAAA	GCCTTAATGA	TAGTCTTGG	GCTAACTATG	780
GGAGGGAGTT	TGTGCTTTA	CACTTTACG	GTGTATTTAA	AAATCTTTT	AACCAACAGC	840
TCATCGTTA	GCCCTAAAGA	AAGCAGTTT	ATCATGCTTT	TAGCGCTCTC	TTATTCATC	900
TTCTTACAAC	CCTTATGCGG	GATGCTGCG	GATAAAATCA	AACGCACCCA	AATGCTGATG	960
GTTCCTGCGA	TCACAGGGCT	TATTGTAACG	CCTATTGTC	TTATGGTAT	CAAGCATGCC	1020

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ACTAGCGTGT ATGAAGCCCT ATTTATGAA ATACTCGCAT TGAGCAGCAT GAGTTTTAC	1080
ACTTGCATTG CTGGGGTTAT TAAGGCGGAA TTATTCCTG AACATGTGCG AGCGCTTGGC	1140
GTGGGTTTAG CCTATGCGAT CGCCAATGCG CTTTTGGAG GGAGCGCGAG TTATATAGCG	1200
TTAGAGTTCA AACAGCATGG TTTGAAGAG GGTTTGTGG GCTATGTCAT GTTGAGTATT	1260
GTTATCTTAA TGGTTATGGT TATCATATTG CCTAAAAAAA CCTATTGGA G	1311

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...285
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:167

ATGGACATTA GCATTTTAG AGAATACGAT ATTAGAGGCA TTACCCCCAC CACTTTAGAT	60
GAAAATACGG CTTTTAGTAT CGCGTGGAG TTGGGAAAAA TCATGCGAGA ATACGATAAA	120
AGCGTGTGTTG TAGGGCATGA CGCAAGGGTG CATGGCCCTT TTTGTTTGA AGTTTTGAGC	180
GCGGGGCTGC AATCAAGCGG CTTGAAAGTG TATGATTTAG GGCTAATCCC CACACCGGTA	240
CGCTAATTTG CGGCCCTTAA TGAAATAGAC AATATCCAAT GGGCC	285

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...306
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:168

GTGTGCGACA TTTTTCTGA TGGCGTTTA TTGGACAAAG CGTTAGTGAT TTATTTCAA	60
GCCCCCTATA GTTTCACCGG TGAAGATGTG TGGAAATCC AATGCCATGG AAGCCCCCTT	120
TTAGCGCAAR ATATCCTTCA AGCTTGCTTG AATTAGGGG CTAGGCTCGC TAAAGCGGGG	180
GAATTAGCA AAAAGCCTT TTAAACCAT AAAATGGATT TGAGCGAGAT TGAAGCGAGC	240
GTTCARCTCA TCCTTGTGA AGRTGAAAGC GTTTAAACG CTCTAGCCAG GCAGCTTCAA	300

GGGGGA

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(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...381
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:169

ATGTTTAAAA AAATGTGTTT GAGCCTGCTA ATGATAAGCG GTGTTTGTTG	60
GATTGGATT TCAAGCTGGA TTATCGCGCG ACTGGGGGA AATTCATGGG GAAAATGACG	120
GAECTCTAGTC TTTTAAGTAT CACTTCTATG AACGATGAAC CGGTGGTGAT TAAAAACCTT	180
ATTGTCAATA GGGGAAATTTC AGTCGAAGCG ACTAAAAAAAG TAGAACCCAA ATTGGCGAT	240
AAGTTTAAAA AAGAAAAAACT CTTTGATCAT GAATTTAAAT ACTCGCAACA GATATTTTAC	300
CGCTCTGGATT GCAAGCCTAA CCAATTGTTA GAAGTTAAAAA TCATCACCGGA CAAGGGCGAA	360
TATTACCATA AATTTCCTAA A	381

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1506 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1506
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:170

ATGACCTTGA AGCCATATCC AACCAAAGAG ACTGGTCTTG CTAGCCAATT ATCTGGGCAC	60
TGGTTTTTC AGCTTTCGTT ATTTAATAAA ACAAACTTA ATCCTAATAA AATTGGATT	120
CCTTTAGAGT TCAATAAAAG ATCAAAATAA AAGTTTGATA AAGATTTAGA AATCTATTT	180
GATAGTCATG AATCGTTCAA TATCTCTAAA AAATACTTGC AAGAAATAGA TCAAGAATCA	240
CTAAAAAAGA TCAAACAATC AAAAGATTTT TTTCATTC AAAAATAGA GAGTAAGCAT	300
GATAATAACG ATATACTGCA ACTTGAAATT TTTGAGAATG ATACAAGTT TCTTTTGCT	360
AAAGGAAGTT TTGCAGAAAT TTTAGAATAC AACATGCAAT TAAAAATAGA TTCTTTAATT	420

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ACAAAAGAAT TTAATAAGCT	TTTAGCGATC	GTTCAAGATA	GTCCCCAAGA	TAGTTACCAA	480
TTAAAAATTG	GTGTCCGACA	TAACAATAAG	CTTCTAGAG	AGAAATATAC	540
ATAAAACTTG	AAGTTTATGA	TTGCAGAAAA	TCCCACGATC	ACAATGAGCC	600
AGCCAGCAAA	GCACCCGGCTT	CCAATGGGG	TTTAATTCA	TGTTTGGCTT	660
GTGGGATCAC	ATTTTAGTTT	TAACCATAAT	ATTATCTATG	TCATGGACGA	720
CATTGAGCG	TGCCAGCCAG	AAAGGAGTTT	AGGAAATTTT	TAAAAGAATA	780
AATCATGTTA	CTTTTGTTTT	AGCCACCCAT	GACCCCTTTT	TAGTGGATAC	840
GATGAAATAA	GGATTGTGGA	AAAGGAAACA	GAAGGCTCTG	TAATTAAGAA	900
TATCCCCTAA	ATAATGCAAG	CAAAGACTCC	GACGTTTGG	ACAAAATCAA	960
GGAGTGGGCC	AGCATGTTTT	TCATAACCCC	CAAAACACC	GAATCATTTT	1020
ATCACGGATT	ATTGTTATTT	GAGCGCTTT	AAATTGTATT	TGCGTTACAA	1080
GACAACCCCA	TTCCTTTAC	TTTCTTACCC	ATTCAGGGC	TTAAAAACGA	1140
ATGAAAGAAA	CCATTGAAAA	ACTTTCGAG	TTAGACAATC	ACCCCTATTGT	1200
GATGACAGAA	AATGCGTTTT	TAACCAACAA	GCAACGAGCG	AACGATTTAA	1260
GAAGAAATGC	ATGATCCCCT	CACCATCTTA	CAACTCTCG	ACTGCGATAG	1320
CAAATTGAAG	ATTGTTTCAG	CGCAAACGAT	AGAAACAAAT	ACGCTAAAAA	1380
GAATTGAGCA	TGGTTTTAA	AACAAGGCTT	TTGTATGGCG	GAGAAGATGC	1440
CAAACAAAAA	GAAATTTTTT	AAAATTATTC	AAATGGATTG	CATGGGCTAC	1500
AAAAAC					1506

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...126
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:171

GTGTATTTTT	TTCTGGCATT	GAGCGGGGAA	AAAGCTTAC	TGCCCCGTAT	TGGCGGTTA	60
GAAAAAAACG	CGCTAGAACG	CGGGCTGTTA	AAGGGGGATA	GAATCCTTCT	ATCAACCAC	120
AAAAAAA						126

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1050 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172

ATGGAAAATT	TTAAACTCAT	CAACTTTTTT	ACCGGTCAAA	ACGATGCCGG	TAAAACCAAT	60
CTTTAGAAG	CTCTTATAC	CAACACAGG	CTTGTGATC	CTACTGCCAA	TCAAGTCAGT	120
CTTCCTCCTG	AACATGCCGT	GAATATTAGT	GAATTCAGAA	AAATCAAAC	CGATGCCGAC	180
AACCTAAAAA	CCTTTTTTTA	TCAAGGAAAC	ACCGCTAATC	CCATTAGTAT	CCGCACTGAA	240
TTTGAACATG	CTACTATCCC	TCTTACTATC	CAATACCCCA	CACAAACCAG	TTACAGCAAA	300
GACATCAATT	TGAATAGCGA	TGATGCTCAT	ATGACAACC	TTATAAACAC	AACAATAACG	360
AAGCCACAGC	TCCAATTTTC	CTACAATCCA	TCCCTTTCCC	CCATGACAAT	GACTTATGAA	420
TTTGAAGGC	AAAACCTAGG	TTAATCCAT	TCTAATTITAG	ATAAAATCGC	TCAAACCTAT	480
AAAGAAAATG	CGATGTTAT	TCCTATAGAA	TTATCTATTG	TTAATTCTCT	TAAAGCATTG	540
GAAAATTAC	AAATTAGCAAG	CAAAAGAAAAA	GAATTGATTG	AAATCCTACA	ATGTTTCAAC	600
CCTTAATATT	TAAATGCTAA	TACAATAAGA	AACTCTGTCT	ATATCCAAAT	CAAAGATGAA	660
AACACACCAGC	TAGAAGAAAG	TCCCCAAAGG	CTTTTAAATT	TGTTTGGTTG	GGGTTTTATC	720
AAATTCTTA	TTATGGTGAG	CATTCTTATA	GACAATCGTG	TCAAGTATCT	TTTTTATTGAT	780
GAATAGAAA	GCGGTTTGC	CCATACAAAAA	ATGCAAGAGT	TTTAAAAGC	TCTGTTAAG	840
TTAGCTCAA	AAATTACAGAT	TCAAATTTT	GCCACACGC	ACAATAAGGA	ATTTTTATTA	900
AACGCCATCA	ACACGATATC	CGATAATGAA	ACGGGAGTTT	TTAAAGACAT	AGCCTTGT	960
GAGCTTGA	AAAGAAAGCGC	TTCTGRCTTT	ATCAGACACA	GCTATTCTAT	GCTAGAAAAA	1020
GCGCTTATA	GGGGTATGGA	GGTTAGAGGC				1050

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173

ATGGATTTTA	AAAAATGCC	TAATTTGAA	AAAAATGTG	CGTTTCTTG	TTTCTCAAAT	60
TTGGTTTTAC	TTATTGAAAT	CCACTCTAA	GGACTACACA	TGCAAAAAAA	GAACCCCAAG	120
AACCCGCAAC	CGAATTAT	TAGCATCTTA	GATAAGGGCG	ATGTTGCAAC	AAACAATCCT	180
GTGAAAGACT	CAGACAAGGC	CAATAAAATA	CAAGAGCAC	TCCCTTATGT	CGTAAAAACG	240
CAAATCAATA	AAAGCAAGCAT	GATTTCTAGA	GATCCTATTG	ATGGGCAA	GTATTTAAGC	300
TTTGAAAAAC	GAGTCTATAA	GGATAATAGT	AAAGAAGATG	TCAATTCTT	TGCCAATGGT	360
GAGATAAAAG	AAAGTTCTCG	TGTTATGAA	GCGAATAAAAG	AAGGGTTG	AAGGCGCATC	420
ACTAAAAGAT	ACGATCTGAT	TGATAGAAAT	ATTGATAGAA	ATAGAGAATT	TTTTATAAAA	480
GAAATTGAAA	TTCTAACCC	CACAAACAGC	TTAAAAGAAT	TGAAAGAGCA	AGGGTTAGAA	540
ATCCAATTGA	CCCACCATAA	TGAAACGCAT	AAGAAGCCT	TAGAAAATGG	CAATGAAATC	600
GTAAAGAAT	ACGACCATCT	AAAGATATT	TACCAAGAAG	TAGAAAGAAC	AAAAGATGGT	660
GGATTGGTAA	GAGAAATAAT	CCCCAGTATT	TCTAGCGCTG	AGTATTCTAA	GCTTTACAC	720
AAACTGCCCT	TTGAATCAAT	AAACAAATGAA	ATACCAAAAC	TGAATACTAA	CGACAATGAA	780
GAAGTTAAA	AACTAGAAATT	TGAATTAGCT	AAAGAAGTGC	ATATTTTAAT	CCTAGAGCAA	840
CAATTGCTT	CAGCAACAAA	TTATTATTCT	TGGATAGATA	AAGATGATAA	TGCGAATT	900

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GCTTGGAAAA TGCATAGGCT	TATCAATGAA	AATAAACTCA	AAGAAAACCA	TCTCAGGCC	960
AATAACGCTA	ATAAGATTAA	GCAATTTC	TTTAATAATG	GTTCTATT	1020
AAAGAAGAAC	AAAGCGCTAT	ACAAGAAAAC	AGAGATTATT	CTTTAAGAAG	1080
AGTTTAGAAG	AAATCGCTCA	ACGAAAATT	GAATGCAA	AATACTATGA	1140
GTAAATGGTG	ATGGGAATAA	AAGAGAAATC	AAGCCTT	AAGAAATT	1200
AACAATTTC	AAAAAGCTTA	TAAGGAGCGT	TATGACAAT	TGGTAAGCTT	1260
ATCATTCAG	CTAAAGAGGG	TGCTAATGAG	CGACAAAATT	GACTGCAGCA	1320
CCTATTAAAA	ATACAATAGA	GACTAATACT	CTAAACAATA	TAACAATAAC	1380
ATAATCATCC	AAATT		TTATTCAAAA	TAATGATAAT	1395

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174

ATGGCGCTTG	AAAGTGGTTT	ATGGGATT	TGATGGCGTGA	TTTTTGACAG	CATGCATT	60
AAATATGAA	GGTTTAAGGC	GTTGTTCAA	AAGCATGGCA	ACGATAGTAA	AGAGGGTT	120
AAACAATTG	AAGTTTATCA	CTATCAA	ACTGGGATTT	CAAGGAATGA	AAAGATCCA	180
TATTTTATA	ACGAGATTT	AAAACCCCT	ATCGCTCAAG	AAGAAATAGA	TGCATTAGCC	240
CTAGAGTTG	GGCCTATCAT	AGAGCAAAAG	CTTTTGATA	GGGGCATT	GAATAGCGAR	300
GTGATGGCGT	TTATTGATAA	GCATTATCAA	AATTATATT	TCCATATCGC	TTCAGCGGCC	360
TTGCATAGCG	AATTGCAAGT	GTTGTGCCAG	TTTTTAGGG	TTACTAAGTA	TTTTAAGAGC	420
GTTGAAGGG	GTCCGCCTGA	AAACCCAAG	ATTATCGCTA	ATATCATTCA	AAAATACGCC	480
TATGACCCAA	GCCGTATGCT	AATGATAGCG	ATAGCGTCAA	TGATTATGAA	AGCGCTAAGG	540
CTAATAAAGT	GGCGTTTTG	GGCTATAACA	GCAAGTTT			579

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

212

(B) LOCATION 1...423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175

ATGCTCAAAA AAAAGATTGA TTTGCATAAA GATTCTATTA GGAAGCTCTT TTTTTATTAC	60
TTCATCCCTT TAGTTTTTC TATGATCTCA CTTCTACTT ACTCTATGGT AGATGACATG	120
TTTGTGGGCA AAAAAGCTGGG TAAAGAAGCT ATCGCTGCGG TCAATATCGC ATGGCCTATT	180
TTTCCAGGAC TCATTGCGTA TGAATTGCTT TTGGTTTTG GGGCAGCGAG CATTGTGGG	240
TATTTTTAG GTCAAAATAA AACCCATAGG GCTAGGCTTG TGTTTAGCAG CGTGTPTAT	300
TTTGTGCTC TAAGGCCTT TATTTGAGC ATGGCGTTAT TGCCCTTTAG CGAAAATATC	360
GCGCAGTTT TTGGGAGCAA TGACGCTTTA TTGAACATGT CAAACGCTAT ATTGAAATCA	420
TTT	423

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176

GTGAAATGTT TATTAATAAA AAAATCACTT CTATTTGCAC TGAAACCATT GCCGGACCTA	60
AAAACGACTA CCCCTATTTT AGCGCCTATG AGCGTGGTGG CTGGGAGGTT GRCTSCCAT	120
TTAGTCCAGC ATTATTTACT GGCTTAGAG CATGTTAAAG GGTTTATGGG TAAGGGGTC	180
ATACTAGGGG GTTTGTCGGG TGCSCAAAGG GCTAAAATCG TCGTAATTGG AGCCGGTGTG	240
GTTGGCATGG AGAGCCGAA AGTCTTAARC CAAATGGGR CTAAGTAAC GATTTTAGAA	300
TTAGACTACG CTAATTACA AAACCACCT TATTATCATT TGATGATT AGAAGTCTTA	360
AGCGTGAATG AAGCCAATAT CATTCAAGCC TTAAACGGGR CGGTGGGGCT AGTGGGAGCG	420
GTRCTGGTTA CARCGAGCCA AACCCCTAAA GTGRTCTAA GAAGGCATT AAAATAC	477

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

213

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...1128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177

ATGCTTGCAA AAATCGTTT TAGCTCATTG GTTGCCTTG GAGTTTGTC GGCTAATGTG	60
GAGCAGTTG GTTCATTTT CAACGAGATA AAAAAGAAC AAGAAGAAGT GGCCGCAAA	120
GAAGACGCTC TAAAGCTCG CAAGAACGCTC TTAAACAATA CGCATGATT CTTAGAACAC	180
TTCGGTTTA GAAAACAAA ATCAAGAG CTTGTGGATT ACAGAGCTAA AGTTCTTTA	240
GATTAGAAA ACAAGTACAA AAAAGAAAAA GAGGCTCTAG AGAAAGAGAC AAGAGGTTAA	300
ATCCTTACTG CTAAGTCAA GGCTTATGGT GATCTAGAGC AGGCCCTAA AGATAACCT	360
CTTITATAAGA AACITCTTC TAACCCTTAT GCTTATGTTT TAAACCAAGA AACATTACG	420
CAAGAACGATA AGGAGCGTT GAGTTATTAC TACCCCCAAG TGAAAACGAG CAGTATT	480
AAAAAAACTA CCGCTACAC TAAAGATAAG GCTCAGGCTT TGCTTCAAAT GGGTGTGTT	540
TCTTITAGATG AAGAGCAAA CAAAAAAGCG AGCCGATTAG CTTTATCTTA CAAGCAAGCG	600
ATTGAGAAAT ATTCCAATAA CATTCTAAT TTATTGAGCA GAAAAGAATT GGATAATATA	660
GATTATTACT TGCAGCTTGA AAGAAACAAA TTGACTCCA AAGCAAAAGA TATTGCTCAA	720
AAAGCCACCA ACACGGCTTAT TTAACTCG GAACGCTTGG CGTTTAGCAT GGCAGTTGAT	780
AAGATCAATG AGAAATACTT AAGGGGCTAT GAAGCTTTT CTAACCTGTT GAAAATGTC	840
AAAGATGATG TGGAGTTGAA TACTTTGACT AAAAACCTCA CCAATCAAAA ATTGAGTTTC	900
GCACAAAAAC AAAAATTGTT TTGTTGGTT TTAGACAGCT TCAATTGTA TACCAATCC	960
AAAAAACTA TATTAACAAA GACTAATGAA TACAATATCT TCGTAGATAG CGATCCTATG	1020
ATGAGCGACA AAACAACATAT GCACAAAGAA CACTACAAGA TATTTAATTCTT CTTCAAAACA	1080
GTGGTTCTG CATACCGGAA CAATGTTGCC AAGAATAACC CCTTGAA	1128

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178

ATGGATTTCG TAGGGTTTGA AGATTTAAA TGCAAAAGACA AAGAAAACCTC TCAAAAGTT	60
TTTGTGATCC GTAACGATAA GTTAGGCAT TTTATTTTAG YGATTCCCGC TTAAATCGCT	120
CTCAAGCATG CTTTTTCTAG AAAAGCGTA GAAGTGTATT TGGCGTGGT TGTGCCTAGC	180
TATACCAACCC CAATTGCTTT AGAATTCCCT TTCATTGATG AAGTTATCAT AGAAGACAAAC	240
CATTAGCCA CCACCCYCAA AAACCGCTCC ATTGACGCTC TTATCTTTT ATTTCATAAT	300
TTTAAAACG CAAACACTCGC TTTCAGTTG AGAAAATCCA TCCCTTATAT CCTAGCCCCA	360
AAGACCAAA TCTATTCTTG GCTTTATCAA AAGAGAGTCG GCCAAACCG CTCTTTATGC	420
TTAAAAACCG AATACGAATA CAATTGGAC TTAATCCATG CGTTTGTAA AGACTACGAT	480
CTCCCTAACG CTCAACTAA AAAATCGCA TGGAACTTA AAGACAAATC CAAAGAGCGA	540
TCCATCATCG CTICAAAACCT CAAAGCTTAT GTTGTCTAT TGTGGATTGG CGTGCATATG	600
CATAGCGGAG CGAGTTGCC CGTATTGCC GCTTCCATT TCATTGAGTT GATTGCAATC	660
TTGCATGAAA AATTAAGTTG TGAGATCATC CTTATTGCG GGCCAGGCAGA GAGAAAAGCC	720
ACAGAAGAAC TCCTTAAAGA AGTCCCTTC GCTCACCTCT ATGATACGAG CCATAGTTA	780
GTGGATTCTG CCAAATTGTG CGCGAATTAA AGCGCTCTA TCGGGAACGC TTCAGGCCCT	840
TTGCATGTGA ACGCTTATT TGACAAACAA TCTATCGGGT TTACCCCTAA CGAACTCACC	900
GCCTCTATTG CCAGATGGCG GCCTTCAAC GAACATTAG TAGGCATCAC CCCGCCTAA	960

GGCTCAAACG ATATGGGT TT GATTGACATT CAAAAAGAAA GCGAAAAGAT TATGGGATT	1020
ATCACAAAAA ATCTTTCTCA TCACATGCAA GAAAGA	1056

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...264
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179

GTGGGTGTCT TATCCCTCAA AATAGAGGCA ATTTCTAATT TTTATGGGT ATGCCTTTA	60
GGGGTGTGTT TAGCACTTTT TTATCTTTA GACGCCATT ATCTCATGCA AGAAAGGCTG	120
TTTACGGAGC AATACCAATG GCTAATAAAA AACCCGACTTA AAACCGATGA AAGGCTGTT	180
GAAGTCCTCC CTATTCTATCA AACTTGCCAA TCAACGCAAT TCTTATCGCC ATGCCTTCGT	240
TTAGTCTTTT CCCCTATTGG GCGT	264

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...315
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180

ATGTCTTTAG GGGCACTGGT CAGCTCACTC CTTTGCCATA AGTTAGAGGG GGCAATATTA	60
GATCTGAGAG CGTATCGTTT RARAGCTTAT TATCAGAAA ATAAAGATAC YTTGCTTATT	120
AAAGGCAAAA AACGCTTCT TTACAATTAT ATTAAGCCC ATATTGYTTT AAACCTGCTA	180
TGGACAAATTA GAAATCGCAC GTRATCATTG GGAAAATTAA CTCAAAATCC AACCGAACAA	240
CCGCCACGA ATAACCACAC CATTCAATGG AAAAACRGAA AACATTCTAA TGGACAGAAT	300
TTTAGTGATT GGTAT	315

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...228
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181

ATGAAAAAAA CAACCCCTCTT TGTATTGGGC TTATTATTCA ATAGCTCTTT AAGCGCTGTT	60
GATGGGATTT CTCAAACCGA GCCTTCTCT TTGAATTGG CTGAAGATAG CCTGCCTTTC	120
AACCATTCCTA ACGCCCCAAA ACTCTCTTT AAAAACGCAT GGAATAGGGT GTTGTCTAAT	180
CATGAAGGCT TGCATGCGCA GAATACGCCA TTAAGCGAGC GAGTAAAA	228

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...294
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182

GTGAAAAAAAG TAGAATCCAT GAATGTGGTG CCTTTCATTG ACATCATGCT TGTGTTGTTA	60
GTGATCGTGC TCACAACGGC GTCTTTTG TG CAAACTTCAA AGCTTCCTAT TAGCATTCT	120
CAAGTGGATA AGGATAGCAC TGATTCTAAA GATGTGTTGG ACAAAAAACA AGTTACGATC	180
GCTATTCTA ATAAGGGTTC TTTTTATTTT GACGATAAAG AAATCAGCTT TGAAAATTAA	240
AAACACAAGG TTTCCACTTT GGCTAAAGAC ACCCCTATTG TCTTGCAAG CGCA	294

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 486 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

216

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183

ATGGGATCTT ACACATTCCC TCTCATTTCG AAGCCAATAT TTATAAACAA AGTGCCTGTA	60
ACGATAGATT TTTATGCGAA CGCCAATTAC TTTTTGATTT ATGGTGCGTT AGCGAATGCG	120
GTGGTGGGGA GCATCAACCC CTTAAACGAT GAAATCAGGT TCAAACGCAA CGCCCAAATA	180
GAAGAAGCTG AATTAGGGAC AGACGGGATT AAGATTAAGC CTATCGCTTT GTATAACCCT	240
AGTGAGGGGT ATTTGAATTA CGCGCTCTCT AGCGTGTGTTA TTTTCATCTT ACACCAGGTG	300
ATGCTCATTTG CAAGCAGCAT GTTTACTAGC TCCAGGCCTT TGGAATTGGC CCTTTTAGAC	360
AAGAAACAAA TCGCTTTAAG GCTGTGCGCA AGACTCTTGG TGTTCATGGG GGGTTTAGC	420
GTTTTGTGTT TATGGTATTT TGGGGCGCTG TTTTCTTTT ATGGGATCGA ACGGCATGGA	480
AGCGCT	486

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184

GTGATTATGA CTAAGCTTGA TGGCACTTCT AAGGGCGGAG CGATTTARG CGTGCTGTAT	60
GAGTTGAAAT TACCCATTCT TTATTTAGGA ATGGCGAAA AAGAAGACGA TTTGATCGCT	120
TITGATGAAG AACGCTTTAT AGAAGATTTG GTTGATGCGG TGTTTGTTGA ACAAA	174

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...198
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:185

GTGTGTGGGG CTCATGGAAA GAGCAGTATC ACGGYCATGT TGAGCGCGAT TTGCCCCGCT	60
TTTGGASSGA TTATTGGGCG GCATTCTAAA GAGTTTGATT CCAATGTSSG AGAGAGCGCG	120
GATATGAGTT TGGTTTTGAA ASCCGATGAA AGTGATTCAA GTTTTTTAT TTTCCAACCC	180
TTTTTGCAGC ATTGTGCC	198

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...231
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186

GTGAATGAGT TAAAAAAACTC TAAGCAAGTT TTAGGGAATG GGAAAGCCGA TCTGAGCAAC	60
GAAAACACCA AGCTAAGGCA GACTAAAAAC RATCTGACTG AAAAAAAATCA AAGGCTAAC	120
ACAGAAAAAA CAGAATTAAA TAACAAGATT ACTGGGTTAG CCACAGAAAA AGAAAGGTTA	180
GCCGAGACA AGAAAAACCT AACTAAAAAGAA AGCAGACAAA GAAAACCTAA C	231

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 555 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187

ATGGATTTAC AACAAATTGA TGAGCTAGAA AATAAGTTG AAGAACAGA AGAACAGCC	60
CAAGATACCC CCCTAAAACA AGAGCCTAGC ACAAGGAAG TAAAAATCCC TAAAAAAAGG	120
GGCGTAAAAA AAAGCTTGTG AGATGAAGAT AAGAAAAAGA GCTTTAACAT TGCTTAGT	180
CCTTGTGTGA TAAAAGAACT TAATGAATT TTGCTAGAAT TTGGCTCATT TAAAGAGACA	240
CGAAGCACTT TTATTGAAGA AGCGCTTATT AGGCATTAA AACACAGAAA AAACACCAA	300
GAGCAAAAGC TTTTAAAGCA ACTAGAAGA TTACAAAACA AAGAAAAGG AATAATGAAA	360
ACAATGAACT TGAATGAAATT TTTTACCGAT AAGATAATCT ATAAAGACAC CCCTTAAAG	420
TTTAAGGATA CACTAGAACAGAAGAACAGC CAAGCTAGTT TAGTAGAGAA GTTAATCTTA	480
GCTAATATCT TAGCCAATAT GGTGTTGCT AAGATAAGCA ATGAGAATGC CCCTAAAATT	540
CTTATTTCA CGGCT	555

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188

ATGGGGTGCT ATGGGATAGG CATTAGCCGG TTGCTCAGCG TGATTTAGA GCACAAAAGC	60
GATGATCTAG RCTGTGTG GACGAAAAAT ACCGCTCCTT TTGATGTGGT GATCGTGGTT	120
TCTAACCTGA AAGATGAAGC GCACAAAAAA CTCGCTTTTG AAGTGTATGA AAGACTGCTC	180
CAAAAGGGCG TTGATGCGCT GTTAGATGAC AGAGACGCTC GTTTTGGGC GAAGATGAGG	240
GATTTGAAT TGATTGGGA ACGATTAGCC TTGATTGTTG GGAACCAAAC TTTAGAGAGT	300
AAGGAATTG AATGCATCAA ACGCGCTAAT TTAGAAAAGC AAACGATCAA AGACATAGGA	360
ATTAGAAGAA AAAATTAG AAATGTTAGC GAGCGAATAA GGGGAGGGAA TGGAAAAAYT	420
AGTGATTGGC TC	432

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189

ATGAAATAC ACAAACACA CCGCAAAATC AATGCCCTT TAGTTCTCT CGTTTAGCA	60
GGAGCGTTGA TTAGGCCAT ACCGAAAGAG AGTCATGCCG CCTTTTCAC GACC GTGATC	120
ATTCCAGCCA TTGTTGGGG TATGCCACA GGCAC TGCTG TAGGAACGGT CTCAGGGCTT	180
CTTAGTTGGG GACTCAAACA AGCCGAAGAA GCGAATAAAA CCCCAGATAAA ACCCGATAAA	240
GTTTGGCGCA TTCAAGCAGG AAAAGGGCTT	270

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 804 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190

ATGTCAGAAA AAGAAAGACT GAATGAAGTG ATCTTACAAG AAGAGAATAA TGGGAGTGGT	60
ACTAAAAAGG TGTGTTTGAT CGTGGCCATA GCCATTATCA TTTTGGCGGT GCTTTTAATG	120
GTGTTTGGA AAACCAACAG AGTCGCTCT AAAGAGACTT TTTTACAAAC CGATAGTGGC	180
ATGCAAAAAA TAGGCAACAC TAAAGATGAG AAAAAAGACG ATGAGTTGA AAGCTTGAAT	240
ATGGATTCTC CAAACAAAGA AGACAAGTT GACAAGTGG TGGATAATAT TAAAAAACAA	300
GAGAGTGAAG ATTCTATGCC CATTCAAAC GATCAAGCTC AAATGGAGAT GAAAACAACA	360
GAAGAAAAAC AAGAATCTCA AAAAGAATTAA AAAGCTGTTG AGCCTATTCC CATGAGCACT	420
CAAAAAGAAT CTCAGGCTGT GGCTAAAAAA GAAACCCCCC ATAAAAAGCC TAAAGTAGCG	480
CCAAAAGATA AAGAAGCGCA TAAAGRTAAA GCTAACATC CAGCTARGA GCCAAAAGTC	540
AAAAAAAGAAG CTCGTAAGA AGTTTCTAAG AAAGCTAATT CTAAAACCAA TCTTACTAAA	600
GGGCATTATT TCGAAGTGGG GGTTTTGCGCACACGCCA ACAAAAGCCTT TTTACAAGAG	660
TTTAATCAAT TCCCCCATAA AATTGAAGAT AGGGGGCTA CTAACGCTA CCTYATAGGY	720
CCTTATAAGA GCAAGCAAGA AGCCTTAATG CATGCCGATG AAGTCAGCAA GAAGATGACT	780
AAACCGGTTG TCATAGAAGT GCGG	804

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 513 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191

GTGGAATATT	ATGCCGTTAA	TTTCAGCGTG	TTGGATTGG	TCTTAATGGG	GAAAGCGACG	60
CATTGAATC	TGTCGCTAT	GCCTAAAGCT	AAGCACATTA	AAGAACCCAC	GAGCGTTTA	120
GAGCCCTTGG	ATTTAGAGTC	CTTAAAGAT	CAAGGCATTA	ACGATTTGTC	CGGCGGTCAA	180
AGGCAGATGG	TACTTTAGC	CAGAACGTTG	TTCGAAAGAA	CGCCCTTATT	GTTACTGGAT	240
GAGCCTACGA	GTGCCCTTAGA	TTTAAAAAAC	CAAGCCCTT	TTTTTGATGC	GATTAAGAT	300
GAGATGAAAA	AACGAGAATT	GAGCGTTTA	GTCAATATCC	ATGATCCAA	TTGGTTGCC	360
AGGCACTCCA	CGCATGTGGT	CATGCTAAA	GATAAAAAC	TTTTTTGCA	AGCTTCCACG	420
CCAATCGCTA	TGACTTCACA	CAATTAAAGC	GCCCTTATG	ACACGCCCT	ARAAGCGATC	480
TGGCATGATG	ATAAGCTTGT	GGTGTATGCG	TTG			513

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192

ATGATGGCAC	ATTCACITAT	TTGGTTTCA	AAAACATCAC	TCTCCAACCT	GCTTATTTTT	60
GTGGTTCAAC	CTGATGGGAA	ATTGAGCATG	ACTGATGCCG	CCATTGATCC	TAACATGACT	120
AATTCAAGGAT	TGAGATGGTA	TAGAGTTAT	GAAATTGAG	AGAAGTTAA	GCTCATTAAA	180
GACAAAGCCC	TTGTAACAGT	GATCAATAAA	GGCTATGGG	AAAATCCATT	GACAAAAAAT	240
TACAATATCA	AAAATATGG	TGAATTGGAG	CGTGTGATTA	AAAAGCTCCC	TCTTGTCAAGA	300
GATAAA						306

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...711
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:193

GTGCTGAATG AAGAGCAAA TTCATTAGAA GAAAAAGGGG GCGAAAACAA AAACGAAAAA	60
GAAACCCCCC TAAAGGGCAT TCATTCTAAA ATCCCTCTT TGAAGCAGGC TTGGAGCAG	120
ACGATTAGTA AAATCAAAG CTCTAAAGAG TTTTCAAAC AGCTTCTACA CAATAAAAAA	180
AAGCTTTATA TCGCGCTTGG AATATTGCTT TCACTCATCG CGCTCATTGT GGCTTGAGT	240
TTGTTACTAG GGCATAAAA AGAAAATAAA CAAACTCTT TACAAACTAA TACCGCCACC	300
ACCAATAACG AAACGCCTAA CGACACCAAT AACGCAGAAG CCGAAGGGCA AATAGAAAAT	360
TTAGACTTGC CTGATTTAAT CGGCAAAGAC TCTTGAAAA GAAACGATGA AAGCCAAGTG	420
GATCCGATGA TGCAAAAAGC GAGCCTTITG TATGAGCAAG GGCAAAAGA TGAAGCCTTG	480
CATTGTTTG ATAAGATCGC TTCTTTCTCG CAAGGGATTG CGAGCCATAA TCTAGGGGTG	540
ATTAATTCA AAGAAAAGGA TTTTAATGGG GCCTTGGATT TTGTTGATTC CAGTATCGCT	600
TCTAAAGAAA ACGCGACCGT GRGCGCGATT GATCCGTTAG TTACGGCTTA TCATTTGCAA	660
GATCCGGATT TGTATTATCA TTATCTAAAA ATTGTRAAGA GACACTTTGT A	711

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 675 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...675
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194

ATGAATACAA GTTTATTGAC CCAAGCACAG GTTTAAGCT CTAAAGAAAA TCAAATCCAT	60
CGCCTTTGT TAGAGCTTT AGAAGAGGCT AAGCTTCATT TTGAGCCTAA GCTTTATATC	120
ATTAACGCCC CTACATGAA CGCTTTTCGG AGCGGGTGGG ATGAATCTAA TTCCCTTATC	180
GCTCTTACAA GCGCTTTAAT AGAGAGGTTA GATAGAGACG AATTAAAAGC CGTGATCGCT	240
CATGAGCTCA GCCACATACG GCACAAACGAC ATCCGCTTGA CCATGTGCGT GGGGATTITG	300
AGCAATATCA TGCTATTGGT GGCTAATTTT AGCGTGTATT TTTCATGGG GAATCGCAAG	360
AATAGGGGG CGAACATTAGC CGGAATGATT TTATGGTTT TACAGATCAT TTGCTTTT	420
TTAACGCTCC TTTGCAAAT GTATTGAGC CGCACACGAG AATACATGGC CGATAGCGGG	480
CGGGCGTTTT TAATGCATGA CAATAAGCCC ATGATCAGAG CCTTACAAAA GATTCTAAC	540
GATTACACCA ACAACGATTA TAAAGAAAATA GATAAAAATA GCACCCGATC AGGGCCTAT	600
CTTTTAAACG CTGAAATGTT TAGCACCCAC CCTAGTATTA AAAATCGTAT CCAATCCTTA	660
AGAAAGCGTG TGATC	675

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1605 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1605
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:195

ATGTTTAATA	TTAAAAGGAC	TTTTTTAATA	ACGATCATAA	GTTTTTTCT	CATTGTTCC	60
AATTGGTGTGA	AAGCTATTGA	TTTGCCATT	GTTCAAATC	TCAAAATTTA	CCAAACAGTT	120
TATTGCATGC	TGATACCGAG	TTATGTTTTA	ACCAACAAAA	GTTTTGCAGA	TATTTTGACA	180
GGCTATACAT	CTATTGGTGC	ATCAGGGAGT	GGAAAGAGTT	CAGGGCAGGG	TGTGATCGAA	240
GCGCTTAGCA	CACCATTAGC	CACAAGTTA	GCCGCTAGCA	ATCTGGTGA	ATATTTGAAT	300
ACTTTAGTC	CTTTATGGGG	ATCGGCGTGG	GCAAGTGTG	CTACAGCTAT	ACAAGGTTT	360
GCTCTAACGC	CATCAAGTGC	CTGTAATT	GGTGTGAACG	CATTGATAAA	AAAAAACATA	420
GATGTTATCCA	TGGATAGGGT	ACTAGACAAAT	TTGAGCAACA	AGATTCAAGAA	TTTTACCAAA	480
GGCGGTGTTG	AGGACAATGT	GAAAGGCAAT	ATTCTTTAC	AAATAATTGG	CTCAATAACC	540
GCTCAAGCTT	CTACGAATAT	TACAGCTAT	GGTTTAAATT	GGCTGATTGG	TAAAGAATT	600
ACTGCAAATA	AACTGCAAA	CAACACTATA	GCCATGCTTG	CTTTTGCCTGC	ATTAGAATCT	660
GTTGTCAAAG	GAGCGGACGC	TGCTGTTCTT	CCTGCATATG	GTGTAGTCAA	TCTGCCTGAT	720
ATTATCATAG	GGCAAGGGTC	ATATCTTGAT	TTTGTTCCTT	ACCTAATT	TATTTGTTT	780
GGGATTTTG	TTTTTATTC	TTTTATGAA	TTGAGAGATA	TTTCAAACGG	CATTCAAGATT	840
AACTAGGTT	TTGAAATACAT	GGCATTTGTT	GGGGGGACAT	TATTCAAAAT	GGCGATGGTC	900
TCTTTTATCG	CCTATGCAGG	TTTGGTTAT	CTTTATAAAA	TCTCTTATTC	TATTTTATTT	960
GGTTTACGAG	GTGCTTTG	GCTGAAATCAA	GTCTTTTTT	GGGCTTTAGA	TTTGTGCTG	1020
AATTACACTG	TTAATTCAAT	TTTACCTCGG	GTAAGAGCTG	TTTTTTCTAA	TGTTGGCAAC	1080
AACGCTCCTA	GTGGTTACA	AGGCTGCAA	GTGGCAGGTA	TTTCTTTATT	CGCTATT	1140
ATGCAAGTAA	CTATCATTAT	GAGAATAAGC	ACTGGTGTG	TGAAACCTT	GATAGCGGG	1200
GCTTTTACCG	GTATTGTTTT	CCCTATTGCA	GTATGTTGA	TCGTGCTAGA	TTGGTTCAA	1260
GATTCTATGA	AAAACATATT	GATATGCTT	TTTAAATAATC	TGTTTATCTT	GGTTCTAGCT	1320
ATTCCCTATT	TGCTCTTGG	TTTTTTGGCA	TTATTGGCAT	TCAATTGAC	CATAACGCC	1380
TCTGTTGCTA	TACAAAACAT	CAATCAAGGG	GGATTGGGTA	TCGATTCAAC	TATTGCGAGT	1440
TTGATCACTC	TATTTTATTT	AAAAGTTTC	ATAGAGACGA	TTATTGAGAG	CGTCAATGCG	1500
ATCGTTAACCA	CCATTTTCAG	CTCTGTCCT	ATGGATGGTA	GCAGAAATGGA	TAGAGAAAGA	1560
GATGCCCTAA	TGGTGGGAAG	AGTTGGTGG	TCTATGTTA	AAGGA		1605

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196

ATGGCGTTT GGCAGGCTAT CCGGTGGTGG ATTTAAAGT TACCCTTAT GATGGGAGCT	60
ACCATGATGT GGATTCTTC AGAAATGGCG TTTAAATCG CTGGYTYTAT GGCGTTAAA	120
GAACCGAGTC GTGCGGCTAA CCCGGTTTA CTAGACCTA TGATGAAAGT GGAAGTGGAA	180
GTCCTGAAG AATACATGGG CGATGTGATT CCCGATTTAA ACAGAAGAAG AGGGCAAATC	240
AATTCTATGG AGCATAGATT AGGTTTGAAA ATCGTGAATG CTTTCGTGCC GTTAGTGGAA	300
ATGTTTGGTT ATTCTACGGA TTTCGCATCA GCCACTCAAG GGCGTGGGAC TTACTCTATG	360
GAGTTTGACC ACTATGGCGA AGTGCCTAGC AATATCGCTA AGGAAATCGT GGAAAAACGC	420
AAAGGC	426

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 459 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197

ATGCAGAATT TGCCGGGTAT GGCGAGAGCG GCGATGCTAA CCACATCATC AGCCCCAGCC	60
CCTGAGGGTG AAGGGGCTT TAGAGCCATG AAAATGGCTT CAGAAATGGC GAAAGTGGAA	120
GTAGGCTATG TGAACGGCCA TGGGACAAGC ACGCATTATA ACGATTGGTA TGAAAGCATT	180
GGCTTAAAAA ATGTGTTGGC TCTAAAGAAA AAGTCCCCTCC TGTTAGCTCC ACTAAAGGGC	240
AGATGGGCT TGCTTGGGTG CTGCGGGGTT AGAAGCCGTT ATTCTATCAT GGCCATGAAY	300
CAAGGGATCT TACCTCCTAC CATTAATCAA GAAACGCCCTG ACCCAGAATG CGAYCTGGAT	360
TATATCCCTA ATACAGCCAG AGAAAAGCAA GTGAATGGGG TGATGAGTAA CTCATTGGT	420
TTTGGTGGCA CTAATGGTGT TGTGATTTC AAAAAAGCC	459

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 279 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

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- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...279
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198

ATGACTAA AAAATTGAT TTTGTTATT TTAGCAAAGA GAAAACTTAT TTTCATAGAA	60
GCTAATTTT ATACCATTAG TGGGAGCAAG CTTAATGAAG TCGCAAGATC CTATCAAGAC	120
TTAGCTTAA AATTGAAAG ATTTCTTAAT TACGAAATTAA TTGGATAAC TGATGGCATA	180
GGTGGCTAG ACGCTAAAG CAAGCTCCAA GAAGCTTACA AATCTGTAGA AATCTATAAAC	240
TTCAGCTATG TGAATGATT TATATCAAAG GTGCAAAAA	279

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...264
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199

ATGGAATCAC AACTCATGAA ACTGCCATT GAAACTTATA AAATCACTTT GATGATTCT	60
TTACCGGTAT TATTAGCGGG CTTAGTGGTG GGGCTGTTAG TCAGTATTTT TCAAGCGACC	120
ACCCAAATCA ATGAAATGAC TTTGTCTTTT GTGCTTAAGA TTTTACCCGT GATTGGGTG	180
CTGATTAA CCATGCCGTG GATGCCAAC ATGCTTTAG ATTACACCAA AACCTTAATC	240
AAGCTCATTC CTAAAATCAT AGGC	264

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200

ATGAAATTTT TTACAAGAAC CACTGACAGC TACAAGAAAAG TTGTAGTAAC	60
GTGGTAACAA CCAATCCTT AATGGCGGTC ACCAGTCTG CAACAGGGGT TACTGAGACT	120
AAAAGTTGG TTATTTCAGAT CATTCTGTT CTAGCGATCG TAGGTGGTTG CGCTTTAGGG	180
GTCAAAGGCAGA TAGCAGATAT TTGGAAAATC TCTGATGACA TCAAAAGAGG TCAGGGCACT	240
GTTTTTGCTT ACGCGCAACC CATAGCTATG TTACCGGTGG CAGGTGGCAT TATCTATTG	300
AGCACTAAGT TTGGCTTCAA TATTGGCGAG ACTGGAGGAG CTAGC	345

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201

ATGAAAAATTC CCCAAGCTAA TGTTTTAAAA CTCTTTTAA ATCAAGTGGC TGACCAAAAA	60
TACATAGATA TGAATGATGA AAAAAGCTAT GACCCAAGAG AACCTGAACC CCCTTATGGA	120
ACAAAAGGGG CGTTAGATGA GATTATAAGG ACAGATGCTA GGAGTTGGGC AAACACTCCT	180
GATGATGAAT TTGGGAGCAT TATGTCTTCT TTTAAGCGTT TTATGTATGT CTATAAAGAC	240
CCAAAAGTGC GTGAAGCTAC TTCTAAAATG AGCTTTGATT ATGAAGAATT AAGAACGGGC	300
AATATCAGTA TTTACATTGT AATCGCTCAA ATTGATATAG GCACACTTTC TTCTTTAGTA	360
AGAGCCCTTT TAGAGAGTAT TGCTAAAAC CTTATGGTCA AAGAAAGCTC TAAACCTGAA	420
GAGCGTATTT TTATCATTGC TGATGAATTG GTTAGATTTG GTAAGTTGCC TTTCTTGTAA	480
GAAATGCCAG CACTTTGTGCT CTCTTATAAT GTTGTCCCCT TATTTCATCAC GCAAGATTAT	540
GCTATGATTA GAAATACTAT AGCGATGATG ATT	573

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1053 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202

ATGATAAGTC AGATTATTA	60
TTGAATAAAA CTTTAAAC	120
AAGCTTATTA GCTGGGTTT	180
TAAATGCCAA AGCCTTATT	240
AAGCGATGAA GACTTATTGA	300
ATCAAAGAAC ATACGCTGAC	360
TAGCTGTAAT GCTAAGGTGG	420
ACGGCTCTCA ATACTTGAA	480
AGTGGTTGGA ATTTATCTAA	540
AGAATTCCG CAAGAATATA	600
GAGAAAAGAT TTTGAATGC	660
GTAGAAGAAC AAAAACATAA	720
ACAAGCCCTT AATTAAATCA	780
ATAAGAAGAAC	840
TTGCAAAAAA AATCAAAGAA	900
ATTAAGAAA AAGCTAAAGT	960
AAATTATGG CTTTGAAT	1020
GAAAGAACAC TCTAAAGAAT	1053
CTCCAAATAA AAAGCAACTT	
CAAACCATGC TTGAGAACGC	
TTTGATAAT GGAGCTGAAA	
GTTTATTGA TGATTGGCAC	
GAACGCTTTC GGGGTATAAG	
TAGAGAACAT ACTTATAAG	
ACCTTGGCAT TAAAGAATAT	
AGTGTGAAG GAAAGATATT	
AGCCTTGGC GAAAGAAGIT	
ATATTAGACA ATATAAAAAA	
GATTGTGAAG AAAGCACTTA	
TGATACTAGA CAAACCTTAT	
CTGCTATGGC TAATATGAGT	
GGCGAAAACG ATTATAAAAT	
TACTTGGTA AAACCCAAT	
ATCAGCTCCA TAGTTCAAAT	
AATATTAAAC CCTTAATGTC	
AAACACAGAG TTGTTAAATA	
TGATAGAGCT AACCAATATC	
AAAAAGAACAT ATGTTATGGG	
CTGTAATATG GAAATAGATG	
GTCTAAATA TCCCATTCA	
AAAGATTGGG GATTTTTG	
TAAGGCAAAA GTCCCAGAAA	
CTTGGAGAAA TAAGATTG	
GAATGTATTA AGAATAAGT	
AAAGTCTTAT GACAACACTA	
CCGCTGAAAT AGGAATAGTT	
TGGAAAAAAA ATACTTATTTC	
TATCTCTCAT CAC	

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1053 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203

ATGGCTGATA TTTTAAGCCA	60
AGAAGAAATT GATGCGCTTT	120
TAGAAGTCGT TGATGAGAAT	180
GTGGATATTC AAAATGTCCA	240
AAAAAAAGAT ATTATCCCCC	300
AAACGAGCGT AACCCCTCAT	360
GATTICAAGC GCCCTAATCG	420
TGTGAGTAAG GAGCAATTGC	480
CCTCTTTTAG GAGCATCCAT	540
GATAAAATGG CTAGGAATCT	600
TTCCAGTCAA GTCTCTTCTA	660
TCATGCGTT TATTGTAGAA	720
ATCCAGCTTC ATAGCGTGG	780
TCAAATGACT TATGGCGAAT	840
TTTTGATGAG TTGCGCTAGC	900
CCTACGGAGT TTAATGTCTT	
TTCCATGAG CCTATGGGG	
GAACGGGGGT TTTAGAGATT	
AATCCTAGCA TCGCTTTCCC	
TATGATTGAC AGACTATTAG	
CGGGTAAGGG GAGCGCGTAT	
GATCAAAACA GGGAGTTAG	
CGATATTGAA TTGAATTAT	
TGGATACGAT TTACGCCAG	
GTGATGAAA TTTTAAAGA	
AGTGTGGTCG CCTGTGGTGG	
AGATGTATCC TACCATTGAC	
GCTAAAGAAC CCAGCGCGA	
TGTGGTCAA ATCGTCGCTC	
AAAATGAAAT TTCTATCATG	
GTGCTTTAG AGATTATCAT	
TGGGCATAGC CGTGGGATGA	
TGAATATTG TTACCCGGTG	
ATTCCATTG AGAGCAATTCT	
TTCTAAAATG GGGAGTAGGG	
ATTCATGCT TGACGATGCT	
TTTCAGAAACG	
AACTCCAAA AGAGCGTAA	
TAAGGATTG CAAGCACTAT	
TGAGCGGGGT GAGCGTGGAT	
ATGATGGTGT TTTGGGCGC	
GGTGGAAATTG AGTTGAAAG	
AAATGTTGGA TTAGATGTG	
GGGGATACTA TCCGGTTGAA	
AAAAGTCGCT AACGATGAG	
TGAGCGTGTAA TGTACATAAG	

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AAAAAGCGTT ATTTAGCGAG CGTGGGGTTT CAAGGGTATA GGAAAACCAT TCAAATTAAA	960
GAAGTGGTTT ATAGCGAAAA AGAACGCACT AAAGAAATT TAGAAWTGCT WGAAGAACAG	1020
CGCAGGAGGC AAAGTTGGGC GRTGTTATGG AGC	1053

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 570 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...570
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204

ATGCCCACGA TGTTAGCGGT TGGTTTTTGG GTGTTGGTTT TTTTATCCAC GAGCAATGCG	60
GTGAATTAA CCGACGGGTT AGACGGATTA GCGAGGTGTGC CTAGCATTTT CACCCCTCTTA	120
AGCCTTTCTA TCTTTCTGTA TGTGGCAGGG AATGCGGAAT TTCTAAATA CTTGCTCTAT	180
CCTAAAGTCAGA TAGATCTGGG GGAATTGTTT GTGATTTCGC TAGCATTAGT GGGATCGCTC	240
TTTGGCTTTT TGTGCTATAA CTGCAACCCG GCAAGCGTGT TTATGGGCGA TAGCGGGAGT	300
TTGGCAATAG GAGGGTTTAT CGCTTATAAC GCTATTGTTT CGCATAATGA AATCTTGCTC	360
GTTTTAATGG GGTCTATTTT TGTAATAGAA ACTCTGTCTG TGATCTTGCA AGTAGGGAGC	420
TATAAAACCC GTAAAAAACG CCTTTTTTA ATGCCACCCA TCCATCATCA TTTTGAACAA	480
AAGGGTTGGG CAGAAAATAA GGTGATCGTG CGTTTTGGG TCATTCTAT GCTGAGTAAT	540
TTAGTCGCTC TTTTGAGCTT GAAGGTGTGT	570

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1467 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1467
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:205

GTGCGTTTG AAAATTCAT CAACCGCCTA GCCTTTACA TGGCCACAGG GAGCGGTAAA	60
ACGATCGTCA TTATCAAACG GGTAGAGCTT TTAAGCGTGG CTATGGGAAT GGGTTTGATC	120

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CCTAAGAAAA ATATCATGTT TTTTAGCGCG AACGAGCATT TAATCAAGCA ATTTGAAAAA	180
GAAATTGAAA AATAAACCG CAATAAGGAC TATTCAAAC AAATTGATT CAAAAACCTT	240
AAAAGCGTTA AGAATAAGGA TTTTATCGT GCTCCAAAAG ATTCTTTAAT GAAAGAAC	300
GCTCTTTT ATTACCGCGC AGATTTAATG AGCGATGAAG AAACCAAGGA AAACCTTTA	360
AATTATAAGG ATTGTTGGGA TAATGGGAA AATTATGTGA TTTTAGATGA AGCGCATAAG	420
GGGAATAAGA CTGAAAGCAA AAGACAGCGG ATTTTAGCC TGCTGTCTTT AAAAGGGTTT	480
TTATTCAATT TCAGGCCAC TTTCACTGAA GAAAGCGATC TCATCACTGC GGTGTATAAT	540
TTGAGCGTGG CGAGTGGGT GAAACTTGGC TATGTTAAAG ATCTGTTT ATTGAAGAAA	600
AACAACCTTAA ACGCTTTAA GGAATTGAAA GATTAAACG ACAGGGAAAA AGAAATCGCT	660
CTTTTAAAGG CGTTATTGCT TTAGGCATG CAAAACGCT ATAAAGTAGA AGGCTATT	720
CATGACCCTT TAATGCTCGT GTTCACCGAT TCTGTGAACA TGGAAAACAG CGATGCRRAA	780
ATCTTTTTTA AAACTTTACG GCGCGTGATT GAAAATGATG ATGAGAGCGA TTTTCAAAA	840
GCTAAAGACG ATTTATTAGA GGAATTAAAG AATCCGGAAT TCCTTTTAG CGATGGCAA	900
GATAAAGAAA AAGACTATAA AATTGAGGTC TTTAAAGAGA GTTTAAAGGG CATGGATT	960
AAAGGCTTAA AAGAACAGT TTTTATGCC AGTAATGGC ATATTGAAGT CATCATTAAAC	1020
CCTAAAAACA ACCAAGAAAT CGCTTTCAAG CTCAACACGA GCGATAAAAGT CTTTGCTG	1080
ATTAGAATAG CGCATATTAC AGAACGATC CGTAAAAAAT TAAAGAGCGT GAAGGTGGTG	1140
AGTAAGAATT TGAGCTTCAA AGAACGAGAC TATTTCAGCC AGATTGATAA GAGCAGTATC	1200
AATATCTTAG TGGGTCTCG TGCTTTGAC ACTGGGTGGG ATAGCACAAAG GCCTAGCGT	1260
ATTTTATTTT TAAATATAGG GCTTGATGAT GACGCTAAA AGCTGGTGA ACAATCTTT	1320
GGCAGGGGCC TAAGGATTGA AAGCGTAAA AACCAACGCC AAAGGTTAGC GTATTTAGAG	1380
ATAGATGAAG CCATTAAAGA ACAAGCTGAA ACCAACGCT GCAATGCTGG AAATGTTT	1440
TGTGATACCT ACCAACCATG CAAGCCT	1467

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206

GTGTTTAAAA AITCCCTCTT TGGTATATCA ATCTCCATGC TTATCACTTG GGTTTTAAC	60
GCTGTATTT TGATTTTAT CCTTTTGTC CGAATTAAAC CCCTTACGCA TCCCAATT	120
CATTTCACTC CGTTTGGAAA AACCTATTAA CAAATTCTAG GACTTGTTGG TATTGTAAGT	180
TCTATTATTTC TCACCGGGTT TTTGGCTGAT AAAATCAAAC CGCACAAAGT TTGCA	240
TTTACGSCGA CCTTTGGGTT TTTGGCTTT TTATCTTTA AGGAATTAA TTCTAACGCG	300
CCAAGTTAG TCAATACTAT AATTATAC TTTTACGCTT CCTTTGGCC GGGCATTATG	360
AATTTCATGCC CCATTTTCAT GAGCGATGTC TTAGCGCTA RAATCCGTT TAGCGGGATT	420
TCCTTGCTT ATAACATAGC CTATGCTATA ACCGCTGGCT TTACCCCTCA ACTTCAAGC	480
TGGTAAAGC CAAAAGCTA AGCAGTGCCT GAAAGTTATGC AAAGTTATGC TTTAAGCTT	540
TATATCCTTA TAGTTCTTT AATTGCTTT ATTACATCGC TTTAATGGC GCCAATTAT	600
CACAAATCTA ATACCAACA CGAAGTGTGCG CCCACGGCA	639

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs

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(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207

ATGAAAAGCG ATAAACCCCTT TTTAGAACGC TATTTCATG ACCCCACTCT TTTGCAAAAG	60
GGGTGATTT TCGCGCTCTA TCCTTTTCTCT TTAATCTATC AATGTATTGC CACAATTAAA	120
CGAAAAACCG CTAAAAACCA TGATTTTAAA ATCCCCATT TAAGCATAGG CAACTTGATC	180
GCTGGGGGAA GCGGTAAAC CGCCCTTCATT TTAGAAATCG CTCCAAGATA CCAAGAAGTG	240
GCGGTGTTT CTAGAGGGTA TCAACGGGAT TCTAAAGGTT TAGTGGTGGT GAGCGTTAAA	300
GGAAACATT TAGTTCTCA AAAAACAGCG GGCATGAAG CCTATCTTT AGCCTTAAAT	360
CTAAAACAAG CGAGCGTGTAT TGTGAGCGAA AAAAGGGAGC TAGGCGTTTT AAAAGCCCTT	420
GAATAGGAT CAAAGATCGT GTTTTAGAC GATGGTTTTA GGTTTAATTTC CAACCAATT	480
AATGCGCTTT TAAAACCCAA AGTCCCCCCC TACTACCCCTT TTGTTTGCC TAGCGGGTTG	540
TATAGAGAAA ATATTTAAAG CTATAAGAA GCCCATTTAG TCATTACAGA AGATAAGGAT	600
TATCAAAGAA TCACCTCTAT CACTAACCCC ACCAACGC TGCCTTTAGT AACGGCTATC	660
GCTAACCTA GCAGGCTGTA TCGGTTTTA CCCAAGAAG TGCTTAAAAA ATTGTATT	720
AGAGACCATG CCCCTTTGTA TTGAAGCTT TTAGAAAAAG AGTTTATCA AAATAACGCC	780
ACCTCCTTAT TGGTTACTTC AAAAGATCTC GTCAAATTAC AGATTGCAA ATTGCCTTTA	840
AGCGTATTGG ATTAAAAGT AGAAATTGC CCTAAAGTTT TAGAGGAGAT TGATCGTTAT	900
ATCCTTCTT ATCCTTGTAA TATAAAAGAA CATCTA	936

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208

ATGCTTTAG GGGCAGTGAT CAGGCTTATT TTTGTTATA AGTTAGAGGG GGTAATATTA	60
GATTTAAAGC GCATCAATTTC CAAATCCTAT TACCCAAATA ATAAAAATGC ATTATTTATC	120
AACAATAAGA AAAATCCATT ATCTAGTRCT TCAAAGTTCA TATIGCTT	168

230

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 684 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...684
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:209

ATGCTAGAAA	CCACTATTGA	TTTTTCTCGT	TACAGCAGCG	TGAAATCGG	TGGCCCTTA	60
AAAGTGAGCG	TTTAGAAAAA	CGATAATGAA	ATCTCTCAAG	AACACCAGAT	CATAGGATTA	120
GCGAACAAACC	TTTAATCGC	TCCTGACGTG	AAAAATCTCG	CTTTATTAGG	AAAAAACTAC	180
GATTATATTT	GCGATAAGGG	TGAGTGGGTG	GAGGTAGCGG	GAGCGGCCAA	TGGCTCTAAA	240
ATTTTAATT	ATTTTGGGC	GAATGATTTA	GAGGTTTAG	AGTTTTAGG	GCAATTGCCT	300
GGCACTTTAG	GGCGTTAGT	AAAATGAAT	GCTGGCATGA	AAGAATTGAA	AATAAAAAT	360
GTTTTAGAAA	GCGCTTGCCT	TAATGGCGAA	TGGCTAGAAA	AAGAAGCTTT	CGGGCTAGAT	420
TATCCAGCA	GGGGTTTAA	TGGCGTTGTT	TTGAGGGCTA	GGTTAAAAAA	GACGCATGGT	480
TTTAGAGAAG	GGGTTTTAAA	AGCGTGTAAA	AGCATCGCVA	AAAGCCACCC	CAAATTGCCT	540
AATTGGGA	GCTGTTCAA	AAACCGCCT	AACGATTATG	CGGGCAGGCT	TTTAGAGGGC	600
GTGGGCTTAA	GGGGTTATTG	TCTAAAGAG	TGGGCTTGC	CAAAGAACAT	CCGAATTTT	660
GGTGAATTTC	GGGGGCGCAG	AATT				684

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...267
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210

ATGCTAAAAA	ATGGCGATAA	GATTCCGGAC	GCTATTTAG	TGGATATTGA	GATGCCCTAAA	60
ATGGATGGCT	ACACTTTCGC	CTCTGAAGTG	CGTAAATACA	ATAAATTCAA	AAACCTGCC	120
TTGATCGCCG	TTACCAACTCG	GGTAACTAAA	ACGGACAGAA	TGCGCGCGT	TGAATCCGGC	180
ATGACTGAAT	ACATCACCAA	ACCTTATAGC	GGTGAATATT	TAACCACCGT	AGTGAAGCGC	240
AGCATTAAAT	TAGAAGGAGA	CCAATCG				267

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...333
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211

GTGTTTGAGC CGGTTATCGT TTACAAGCTT TTCCATTCTT TTGTGATTTT AGGGTGCACG	60
ATTGAAACTT TAACGACTAA ATGCCGTGAA GGCATCACGG CTAATGAAAA GATTTGCCAC	120
GATTATGTTT TTAACAGCAT TGGCATTGTT ACCGGCCTCA ACCCTCATAT CGGCTATGAA	180
AAATCCGCTA TGATCGCCAA AGAACGCTTA AAAAGCGATC GCTCTATCTA TGATATCGCT	240
TTAGAAAAGA AAATCTTAAAC CAAAGAGCAA CTGGACGATA TTTTCAAGCC AGAAAACATG	300
CTAAGYYCTC ACGCTTTCAA AAAGCATAAA GAC	333

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...195
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:212

ATGTTGCGTT TATTAGCCCA AAAAAGCGCT ATTAAACTCA TTCTTATCCC CCCAAGCGCG	60
AACGCTTTAG GCATCGCTTC TATTGCGAA TTGAGCGAAG AAGTTTTTGA ACATGAAAAA	120
ATCGTAGGCA TTCGCGCTCA AGGGGATTTC ACTATCAATA GCGACGATAG GGGTTTTGG	180
GAAAGACGCT GTCAG	195

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:

232

(A) LENGTH: 804 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213

ATGAAAAAAAC TTCTTTTACT CTTAGAGCAT AAGATCGTAA AAATTGGCTT AATTATTGTG	60
ATTGTGTTAG TGGGTTTTT TCTTTTTTAT GAACAGAAA TCAAAGAAA AGCTGTTAAT	120
GTTCTCAAG GTAAATTCCC CACTTCATCT TATTGTTTC AAGCTTACGA AGGCATTAAG	180
AATAAAATAG ATACTATCAA TCAAGTGAGG CCAAACGATG AAACAAAAAG CGTTAATGAG	240
AATATAGAAA AACACACAAA AGATITAGAT GATTAAATG CGCTAGTGCA AAAGTTACCA	300
AATTGCTTA AGGACTTTAA TAAAACACTT ATAAACCAC AAAGTCATT TTTCAACTAC	360
AATACCGCTA ACGAAGATGA AAAAACCGC CTGGTGATTT TAGCGTCTCG TATTAGCAGC	420
CAAAAAGAAA CGAACCTCC CATTCTATA AAAAATAGCG TTTCTCACAT AAAATCCAAA	480
GAAAACGAG AACTTGAGAA AGAATGGCA AAACCTAGTG TTTCTTTTGG TTCTTTTCC	540
TTGCTTCCA GTCTTCTTC TTTTCTCTCT TTTGAGTTT CTTTTTTATC AAGGGGAATA	600
GGATTTGATT GTGAGAAGCT CAAATCCCTT TAAAAGCTT TTCAAGTTC GCTATTTC	660
TTATTTATCTT CATTGTTTG CCATCCACTT TCTCTTTTT GCTCTCTAAT AGGATTAATC	720
TTTGTGTTT CTAAGTTTC TAGAGACCTA GTGAATGCGT CTAACAATTG GCTTGAGTTT	780
TCATCATTGT CAAGGCTAGG ATCA	804

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214

ATGGGAGCGA TAGCGAGTTG TTACGCGCAT CAAATCATCT TAACTTCAGA CAATCCTAGA	60
AGCGAAAACG AAGAAGACAT CATTAAGGAT ATTAAAAG GCATCAATAA TTCTCTCTAAA	120
GTCATTGTTAG AAAAAGACCG AAAAAGGCC ATTAAAAGC CTTAGAAAA TTTAAAAGAC	180
GATGAGGTGT TGTGATTAA AGGCAAGGGC GATGAAAACA TTCAAATCTT TAAAGACAAA	240
ACGATTTTT TTAGCGACCA GGAAGTCGTT AAAGATTATT ATCTCAATT AAAACAAGGA	300

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...240
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215

GTGATGGACA AACTCACTAA AAGCTTGCAA ACGCAAAAAA ACTTCGCTTA TTTAGGC	60
ATCAAGCCCC ACAAACTCGC TGATTTCATC ATTAACGAAC ACCCTCAAAAC CATCGCCTTG	120
ATTITGGCCC ACATGGAARC CCCTAATGCG GCTGAAACTT TGAGCTATTI CCCTGATGAA	180
ATGAAAGCCG AGATTTCCAT TAGAATGGCG AATTTAGGC GAAATATCGC CCCAAGTGTT	240

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 615 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...615
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216

ATGCCGTATT TTAGAACGCG TTTTTTATTA TTTTCATGA CGCTTTTTTT TGTTCCTTGC	60
TCTAACGACC CTTTTTCTAA GCAAACCCCT AAGACTAAGG AGCGGATCCG ACAAGAAGAA	120
GCCAATAAAA AAAGAGAAGA GACTTTGAAT GCCTTGCGCC AATTCAAGACT CATTTCACATT	180
AACACGCCGG TTTTCGCTT TTATGATTAC GGCACGATCA AAACCGATAA AGACCACAAAT	240
ACTGAAGTAA CCCTTTATAA GCTCAGCCAA AAAGTGGCG ATATTTACAT GACTAAACGG	300
AGCATTTGTT TTAGCCAAAA ATGTTGCGCC AAATGGATTG CTGCAAGGGA TTGTTTGGC	360
AAGGTGAGCT ATGGGGATTT GTTGTGATGAT ATTGTTTAG GGAGGGATAT TTTTAAAGGT	420
TTAGGGAAAC GCCACCTAAC CCCTGAATAT GTGATCCAAA GGTTTCAAAA AAGCGGGGAA	480
ATTATCCTTT ATGAAAGAAA AAATGGCTG ATTTCTTCC AAAACTTGAC TCAAAAAATT	540
GCTATTAGGA TTGAACCTA TGAGCCTTCT TTGCAAGATT TAGAAGACAA TGAAAACGCT	600
GATAGCGAGC TTCAA	615

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...372
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:217

ATGCGCATTG AAGAAAATGG CGTGATTCT CTAGCCTTA GTAACGGGT GGTAGAGCCG	60
GTCGCTCGCA TCGGTATTW AGCTTCACT AACGATCAAG GCTTAAGGAA AATCGGGGT	120
AACCTCTATG AAATGCAAGA AGGCACCATT AATGGCGAAA ACAGACCCCT AAGSGGTAAAC	180
CCCATTITAG GGTGGGACGA AGAGGGCAAG CTCAGTTG GGAAAATCAG GCACAAATAT	240
TTAGAACGA GCAACGTGAA TGCGGGAAC GCCCTAACCA ATCTCATTAA AATGCAAAGA	300
GGCTATTCTA TGAACGCTAG AGCCTTGGC GCGGCCGATG ACATGATCAA AGAAGCCATT	360
AGCTTGAAAA AA	372

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...279
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:218

GTGGAAGCGC GTTATTATTA TGGGGACACT TCATACTTTT ATTIGCATGT GGGAGTTTA	60
CAAAGAGTTCG CTCACTTTGG ATCGAATGAT GTGGCGTCTT TAAACACCTT TAAAATCAAT	120
GCCGCTCGCA GTCCCTTAAG CACCTATGCA AGAGCGATGA TGGGTGGGGA ATTGCAATTG	180
GCTAAAGAAG TGTTTTTGAA TTGGGGCGTG GTTTATTGAC ACAATTGAT TTCCAACGCA	240
AGCCATTTCG CTTCCAATTG AGGAATGAGG TATAGTTTC	279

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 642 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...642
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:219

GTGAGGGAGC TAGCTAAATT GATCAACAAT AATAATAACA ATAAAAAAACT GAGAGGCTTT	60
TTTTTGAAG TTCTCTTAAG TCTCGTTGTT TTCAGTTCTGT ATGGGTCAAG AAATGACGAT	120
AAAGAAGCCA AAAAGAAGC GCTAGAAAAA GAAAAAAACCA CTCCAATGG GCTTGTTTAT	180
ACGAATTCTAG ATTTTGATAG TTTTAAAGCG ACTATCAAAA ATTGAAAGA CAAGAAAGTA	240
ACTTTCAAAG AAGTCAATCC CGATATTATC AAAGATGAAG TTTTGACTT CGTGATTGTC	300
AATAGACTCC TTAAAAAAAT AAAGGATTTG AACCATTAACG ATCCAGTTAT TGAAAAAATC	360
TTTGATGAAA AGGGTAAAGA AATGGGATTG AATGTAGAAT TACAGATCAA TCCTGAAGTG	420
AAAGACTTTT TTACTTTCAA AAGCATCAGC ACGCCAACAA ACAACGCTG CTTTCTATCA	480
TTGCACGGAG AAACAAGAGA AATTITATGC GATGATAAGC TATATAATGT TTTATTGGCC	540
GTATTCAATT TTATGATCTT TAATGATCTT TTGAAACACA TTAGCACCAT AGAGTCTCTC	600
AAAAAAATCT TTTATACGAT TACATGTGAA GCGGTATATC TA	642

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...234
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220

GTGGGGGGCA TTGTGGCAAA CATGAACGAT CTTTCAACTT ACATGGTTGA GAATTACTC	60
ATGGGTTTGT ATCTTTTTC TAGCGTTTA GATTTGGCG TGAAAAAAAGC CATTAACTCA	120
GCGAGCTCTT GCGCTTATCC TAAATACGCC CCTAACCCCTT TAAAAGAGAG CGATTATTCG	180
AACGGCTCTT TAGAACCAAC GAATGAAGGC TACGCTTGC CAAACTCTCT GTRR	234

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 531 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...531
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221

ATGAAGAAAA GAAAACATGT ATCCAAGAAA GTGTTTAATG TCATTATCTT GTTTGTGGCA	60
GTATTCACTC TTTAGTCGT CATTACACAA ACCCTTCAA ACGGCATTCA CATAACAAAT	120
TTAAAAATTG GAAAACATTG CATTCTGAA TTATACCTAA AACTCAATAA CAAGCTTCT	180
TTGGAAGTTG AGCGGGGTTGA TCTCTCTCT TTCTCCATC AAAAACCCAC TAAAAGCGT	240
TTAGAAGTTT CTGATTTGAT TAAAATATC CGTTATGGCA TTTGGCGGT GTCTTATTT	300
GAAAACCTTA AAGTCAAAGA AATCATTTTA GACGATAAAA ATAAGCCAA TATCTTTTT	360
GATGGGATA AATACGAGTT WAGAATTCC AGGAATCAA GGGGAATTTC CCCTAGAAGA	420
CGATTAAGGG TATCAAGCTT AAAATCATCA ATTTGCTTTT TAAAGATGTT AAAGTCCAAG	480
TGGATGGCAA CGCCCCACTAT TCRCACAAAG CCAGAAAAT GGCGTTCAAT T	531

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 774 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...774
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:222

GTGTCATGTT GGGGAGCGTC AAAAACCGGG TTTTAGGGT TTTGTGTTTG GGGGCGTTGT	60
GTTTATGCGG GGGGGTTAAT GGCAGAGCAA GATCTAAAG AGCTTATATT TTCAGGTATA	120
ACTATTTACA CGGATAAAAAA TTTCAGTAGA GCTAAGAAAT ATTTGAAAAA AGCTTGCAA	180
TCAAACGATG CTGATGGCTG TGCAATCTT AGAGAGGTTT ATTCTAGTGG TAAAGCCATA	240
GCGAGAGAAA ACGCAAGAGA GAGCATTGAA AAAGCTTGT AACACACCCG TACTGCTAAA	300
GTTCGTAAAT TAAACGATGC TGAAAAATGC AAGGACTTAG CAGAGTTTA TTTTAATGTA	360
AACGATCTTA AAAATGCTT AGAATATTAC TCTAAATCTT GTAAGTTAAA TAATGTTGAA	420
GGGTGTATGC TGTCAAGCAAC TTTTATAAC GATATGATAA AGGGTTTGAA AAAAGATAAA	480
AAAGATCTAG AATATTATTC TAAAGCTTGC GAGTTAAATA ACGGTGGAGG GTGTTCTAAA	540
TTAGGAGGGG ATTATTTTT TGGTGAAGGC GTAACAAAAG ATTTCAAAAA AGCTTTGAA	600

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TATTCTGCCA AAGCTTGTGA GTTGAACGAT GCTAAAGGGT GTTACGCTCT AGCAGCGTTT	660
TATAATGAGG CTAAAGGCCTG GGCAAAAGGAT GAAAAGCAAA CGACAGAAAAA CCTTGAAAAG	720
AGTGCAAGC TAGGATTAAGA AGAACATGC GATATTCTCA AGAACACAAA ACAA	774

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...225
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223

GTGGCTCTCA CTTTGGGGGC TAGAGGGGGG GTGTATTTGT GTGGGGGGAT TATCCCACGA	60
TTCATTGATT ATTTTAAAC TTGCCCCTT AGAGCGCGTT TTGAAACGAA AGGGCGCATG	120
GGAGCGTTTC TCGCTTCCAT CCCTGTGCAT GTCGTGATGA AAAAAGCTCC CGGACTTGAT	180
GGGGCGGGCA TTGCGTTAGA AAATTATTTA CTGCATGATA GAATA	225

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1263 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1263
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

ATGAAAGGTT TAACAATGAA AAAATTAGTT TTAGCATGC TTTTATGTTG TAAAAGCGTG	60
TTTGCAGAGG GGGAAACTCC TTGATTGTC AATGACCCAG AAACCCATGT AAGTCAAGCC	120
ACTATCATAG GCAAAATGGT AGATAGTATC AAAAGATAAG AAGAGATTAT TTCTAAGGCT	180
CAAGCTCAAG TCAATCAGTT AAAAAAGTC AATAACATGA TAAATACGAC TAATTCTTG	240
ATTAGTAGTA GTGCTATCAC TTAGCCAAT CCTATGCAAG TTTTACAAAAA CGCTCAGTAT	300
CAAATAGAGA GCATTAGATA CAACTATGAG AATTAAAGC AAAGCATAGA AAATTGGAAC	360
GCACAAAATT TGTTAAGAAA CAAATACTTA CAGCAACAAT GCCCTTGGCT TAATGTCAAT	420
GCTCTTACTA ACAATAAGAT TGTCAATCTT AAAGATCTCA ATAACCTAAT CACCAAAAT	480

GGCGAACAAA	CCCAAACCGC	AAGAGATGTG	CAAAATCTCA	TTCAGTCCAT	TAGTGGCAGT	540
GGCTATGGAA	ACATGCAATC	ACTTGCTGGG	GAATTGAGTG	GTAGAGCGTG	GGGGAAATG	600
TTGTGTAAAA	TGGTAAACGA	TAGTAATTAT	GAAAGCGAGC	AAGCTCTTT	ACCAACAGGC	660
AATAACCCAG	AAGAGCAAAA	ACGAAGATTT	TTGCTTAGAG	TAAGAAAAAA	GGTTAATGAT	720
AATAAGCAGT	AAAAAGATAA	ACTTGACCCA	TTTCTAAAAA	GACTTGATGT	CCTACAAAAT	780
GAGTTGGTG	TAACTGACCC	TACAGCTAAC	CATAATAAGC	AAGGGATACA	TTATTGCACA	840
GAAAATAAAG	AGACAGGTAA	ATGCGACCT	ATTAAAAATG	TATTTAGGAC	AACTCGCTTA	900
GATAACGAAT	TAGAAACAAGA	AATCCAACAG	CTCACACTTG	ATTAATCAA	AGCCCTCCAAT	960
AAAGACGCTC	AAAGCCAAGC	CTACGCAAAT	TTCAATCAAA	GGATTTAAATT	ACTTACTCTA	1020
AAATATTTAA	AAAGAATTAC	CAATCAAATG	CTCTTTTAA	ATCAAACAAAT	GGCAATGCAA	1080
AGCGAGATTA	TGACAGATGA	TTATTTTAGG	CAAATAATG	ATGGCTTTGG	GGAAAAGAA	1140
AACCATAATAG	ACGAACAATT	AACGCAAAA	AGAATAAACG	AAAGAGAAG	AGCTAGAATA	1200
TACTTCAAA	ACCCCTAATGT	TAAATTGAC	CAATTGGCT	TTCCCATTTT	TAGTATATGG	1260
GAT						1263

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...330
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:225

ATGAGCGTGA	ATTTATGGA	ATTGTTAAAA	CTCGCTGTGC	CTTITAGCGGT	TATTTTGAGC	60
GTTCAAGTGG	CGGTTATGAT	CCTTTATGTG	GTGCTTGAA	CCTTTAGGGT	ATGCCGGAAAG	120
GATTATGATG	CGGCGGTGTT	GTGCGCGGGG	CATTGCGGTT	TTGGGCTTG	AGCGACCCCA	180
ACGGCTATGG	TGAATATGCA	AACCATCACC	AACCACTATG	GGCCATCGCA	TGTGGCGTTT	240
ATCGCTGTGC	CTTTAGTGGG	AGCGTTTTT	GTTGATATTA	TTAACGCTTT	AGCGATTAAA	300
GGCTTTTGC	TTTGCGCTTT	TTTCCCTAGT				330

(2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:

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- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226

ATGCAACTAA GCCCCTTACA AAGCGCGCTG TTATATTTCG GTTACTTTAT TTATCCGGAA	60
AAAAAAACAA GGAGCTTTGA TTTAACGGAT TTAATTITTA TTGTCATGGT TTTTTTAGTC	120
CTAGCTTGG GGCTGTTGAT GACCGAAGAA ATTTCTATCA GCTACAATGA AGCGAAAGAC	180
TTTTTTATA GCGATGCGTG GTTTGTCAAATCGCTAAA AAAGCGTAGC CATTAAAGG	240
CCAAACGAT TTGGCTTTAA GATTGCCTTT TTGATCGCT CACGTCATCA ACATGTTTT	300
ATTCTACCTC ATAGGGCGAA AGATTTAAA AAAGCC	336

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227

GTGTATGC CG TCATGGTGGC GTTTTTGCT TACATGAGTT ATTGCTTGGG GTATCAATTG	60
TCCAAATTGCG TTTCTAAAAA CAACATTCTA TCGCTCTCAT CGCTTTATC AAGCTGTGTG	120
CGCGTGGTCT CTGTGCTAAT CTTGTCGCTC AGTAGCCTAG AGTTGCGTTA CTTCTCACCC	180
CTAACTATCA TAACCATGCA TTTTGCCCTA ACCCTTATCA TCCTCTTTT CTTTTTGTAT	240
AAGGCTAACG CGTTTGATGA G	261

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228

ATGAGGTCTT GGATGAAGAA AAAATACTTC ACGCTTTAT TGCAAAGTAG TGTGGTATTA	60
GCGGTTTTTA TAGGGTGTTC TTCTACCAAG AATCATACTT TTTCAGCCCT TAGTAATCAA	120
GAAAATACAG ACGATAAGCT CCCAGTGGTC CATTCCATTA AAACGATTA CGATGTGAGT	180
TCAGTGGGCT TTGAATGGTC TAAAGTCGCT GACACTTATG ACATTGACGG GTTGTGTTG	240
TATCGTTMGA AAAAGACTC CAAGCTTAAA AGAACGCCA CCATTAAAAA CCCTTATGCG	300
ACCCACTATT ATGATGAGGG GTTAGAAACA GAGAGTCCT ACACCTACCA ATTAGCCACC	360
TACAAGGGCG ATAAAATTC CAAACTITCA GAACCCATT TAGTAAAAAC CTCCCTTATC	420
AATCCTGTAG AAAGCGTGT TGCAAGCCTT GAATACCCCTA AAAGCGTGA AGTCTTTTGG	480
AGCCCGCAC CAAATCCCAG CGTTTCTAAA TACATCATTC AAAGGCAGAA TAAAGACGGC	540
AAATTTTAA ATGTGGGGC TGTAACAAAC CGCTTATTG TGAGTTTTTG TGATAAAAGAT	600
TTAGAAGATG GCGCAAAATA CCGCTACCAA ATCATCGCCG AAAATTTCAT GGGGGATAAA	660
TCCAGGCCTA CGCTGATAGT GGAGGGAAA ACCAAAGACT TGCCCAAAGA AATCGCTAAT	720
GTAGAGTGA GTCAAAACCT CACACGACAA ATTGAATTGA GTGGGATAAA ATCCCCAGAA	780
GAAGATGTGA TAGCTTATCG CATITACGCT TCCAATAACC GCAACGATAAA ATACAAATTC	840
ATCGCTCAA CCACCAACAC TTCCTATGTG GATAAGATAG AAAAGACAA TCTCACTCGT	900
TATTATAAAG TCGTCGCCGT AGATAAAACG CATCTTGAAG GGGCGTTACC CAAAGAGCCT	960
GCCATGGGTG AGACCTCTGA TAGGCCTGAA GCCCCTATCA TCACTAAAGG GACTATTCAA	1020
GACTCTTCGG CCTTGATCCA ATGGGAAAAC AACCCAAGCC CTAAATAGC CACTTATGCG	1080
GTGTATCGTT TTGAAGCCAA CTCCAAAACC CCTTGCCTTG TTGGGATAT CACACAAAC	1140
CAGTTCTGG ATAAGGACAT GAAAGTGGC GTGGCTTATC GCTATCAGGT GGTGAGCGTG	1200
GATAAAGATG GTTGTAGACTC GCACCCAAGC AAAGAAGTGC GTTGTGTTT AGAGCGC	1257

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...378
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:229

ATGCTTCCTA CTAAACACG CATTAGAGAT CCGAACAAAGC AAGAACTTAC ACAACCAAAA	60
ATAAAAGGAT TGAGTATGGG AAAAATTITA GCTTCTTGT TGGGTGGCGG AACAAATCTT	120
TTTACAGGTT TATCCAGTGA TTGTTTCT ATGATATTAA ATTTTTGTT CTTCTGATG	180
TTAATGATGG GACTTAATGA AGCATTAGGG AAAAATTITA ACTTGCCTAT GGACAATATC	240
AAGAATTITA TGGCAGAACT GCTGAAGAAT GGATTCGATA GTATCAAAA CATGGGATCT	300
GCTTGGTTG GTAATGGTTT TGGTAGCAGC AAATCAGACA AAACCACTAA TAAAATGAGT	360
GTCCCACAAG TAAGACTC	378

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...216
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:230

ATGGCGAACAA TGATGATGGC AGCGGCCATG TTAGGGATTG ATTCTTGCCC GATTGAAGGG	60
TATGATCAAG AAAAAGTGGAA GGCTTATTAA GAGGAAAAAG GCTATCTAAA CACGGCAGAA	120
TTTGGCGTGT CGGTAATGGC CAGTTTGTT TATCTAAACC AAGAGATTAC CCCTAAAACC	180
CGCTGGAAGA CAGAAGTTAT TTATGAAGTC ATTGAA	216

(2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...333
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:231

ATGGCCGGGC TTGTTTTGAT GGTGCTGCTC GCCAGTTATG AAAGCTTGT TTCTAAATTAA	60
GACAAGGTGG ATGCTAGCGA AATCACTTGG CTAAACACA CAGATTTAA CGCTTTAAAA	120
TTAAAGGTTT CCCTCTCCAT TGTAGCCATT TCGGGCATTT TCTTGCTCAA ACGCTACATG	180
AGTTTAGAAG ACGTTTTATC CAGTATTCTT AAAGACACGC CCCTATCGCA TAACCCTATT	240
TTTTGGCAAG TGGTGTACCA TTGGTGTGTT GTGTTGTCAG CGCTGTTAAC CGCTGTTACC	300
AATAACATCG CTTTTTCGCA GAAAGAAAGG CAT	333

(2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232

ATGATTACGA TCGTTATTGC AAAAGCCGGG AATATAGTCA AAGYCGATAT TTTTACGCAC	60
ATTAGCGATA TTAAAATGGG GCTTATTAAA GGAGGTCAAT GGGGGGTTAT TGGTTTAGGC	120
AATATCGGTA AAAGAGTCGC CAAGCTCGCT CAAGCTTTCG GGGCAAAGGT GGTGTATT	180
TCCCCCTAAAG ATAAAAAAGA AGAATACGAG CGCTTGAGTT TAGAGGAATT GCTTAAAACA	240
AGGGTATTTC TCAGCATTCA TGCCCCCTTA AATGAAAGCA CGCGCGATT AATCGCTCTG	300
AAAGAATTGC AAAGCTTAAA AGATGGCGG ATTAAATCA ATGTGGGGCG TGGGGGCATT	360
GTGAATGAAA AGGRTTGGC TTTRRTTTA GAAACCACAG ATTGTATTAA CGCGAGCGAT	420
GTTT	426

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 189 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233

GTGAATTTCACGCTAAAAA TATTCATTGATAATTGG TAGAAATCAA TAATCGTGTG	60
CGTTCTGGAG CCGGGAGAAA AGCCAGCTCT ACGGTTTGATCTTGCAAGC TTCAGAAGGG	120
ATCACTAGYA GTAAAAATGCGAATTCTCTTATGATG GCGCCACGYC AATTGGCTT	180
CAAACAGMG	189

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 930 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234

ATGCGAACGC TCATTCTGTC GCTTCTAAAA CATCGCATTT TAATGGGCAT GCTTTTAAAA	60
GAATGCCAAG AAAAGTTAA GCGTTCTTAA AATTGAGTG CTAATCATTC CGCTCTIGAGC	120
CGGGGGTATG GGGCGAGITC AGCGATTAAG AAATTCAAG AAATTITAGG GGTGTGTATC	180
CCTTCAAAAA CGAAGAAAAA TTAGAGCCG TATTGAAAG ATATGGCTTT AAAGCGTGTG	240
ATTGTAGGGC CTTATGAGCA TCATTCTAAT GAAGTTAGCT GGCGTGAAGG CTTGTGTGAA	300
GTGGTGCCTA TCCCTTAA TGAACATGGT TTATTGGATT TAGAAATTT AGAGCAAAT	360
TTAAAAAAA CCCCTAACAG CTTGGTTCT GTGAGCGCGG CTTCTAATGT AACGGAAATT	420
CTTACGCCTT TAAAAGAAGT TTCACTATTG TGTAGGAAT ATAGGGCTAT TTTAGCTTG	480
GATTAGCGA ATTTAGCGC GCATGCTAAC CCTAAAGATT GCGAATACCA AACCGTTTT	540
TATGCGCTC ATAAGCTTT AGGGGGCGTT GGAGGGTGCG GTCTTTAGG CATTCTAA	600
GATTGATTG ACACGCAAAT YCCTYCGAGT TTTAGCGCAG GGGCGTGTGAT TAAATACGCT	660
AATCGCACAC GGCATGAATT TATTGATGAA TTGCTTTAA GAGAAGAATT TGGCACGCCA	720
GGATTGTTGC AATTTACAG GAGCGCTCTA GCGTATCAAT TAAGAGATGA ATCCGTTTG	780
GATTATC ATAAGAAAGA AAACAACCTT TTAAGGGTGC TTGTGTATGG CTTAAAAGAC	840
TTGCCGCTA TTAATATTTA TGGGAATTAA ACGGCGAGTC GTGTGGGGGT AGTGRCTTT	900
AATATTGGAG GGATTTCRCC CTATGATTAA	930

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235

GTGGCATGCA ACACCGCGAG CGCTCTGGCT TTAGAAGAGA TGCAGAAAGTA TTCTAAAATC	60
CCTATTGTGG CGGTGATTGA GCCAAGCATT TTAGGGATCA AGCGGCAAGT GGAAGATAAA	120
AACGCCCTA TTTAGTGCT AGGGACAAAA GCGACGATT AATCCAACGC CTATGACAAC	180
GCCCTGAAAC ACAAGGCTA TTTGAACATT TCGCATTTAG CTACTCTCT TTTGTGCCT	240
TTGATTGAG AAGTATTIT AGAGGGCGAA TTGTTAGAAA CTTGCATGCA TTATTATTC	300
ACTCCCTTAG AGATTTACG CGAAGTGATC ATTTCAGTTT GCACGCATT TCCCTTAATC	360
GCTAAAAAA TTGAGGGCTA TTTCATGGG CAATTGCCC TTCCAACGCC CCCCTACTC	420
ATCCATTGG GCGATGCTAT TGTAGAATAT TTGCAACAAA AATACGCCCT TAAAAACAT	480
GCATGCACAT TCCCTAAAGT GGAATTTCAT GCGAGCGCG GATGTGATCTG GCTAGAAAGA	540
CAAGCTAAAG AATGGCTCAA ATTG	564

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

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(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236

GTGTTTGTGG	TGCTATATTT	TTTAACCAAGT	TTATTTATTT	GCTCTTGAT	TGTTTTGTGG	60
TCTAAAAAAT	CCATGCTCTT	TGTGGATAAC	GCTAATAAAA	TCCAAGGCTT	CCATCATGCA	120
AGAACCCCCAC	GAGCCGGGGG	GCTTGGGATC	TTTCTTTCTT	TTGCCGTGTC	TTGTTATCTT	180
GAACCTTTG	AGATGCCTTT	TAAGGGCCT	TTTGTGTTCT	TAGGGCTATC	GCTAGTGTTC	240
TTGAGCGGTT	TTTTAGAAGA	CATTAACCTT	TCATTAAGCC	CCAAAATACG	CCTTATTTCG	300
CAAGCTGTAG	GGGTCGTTTG	CATCATTC	TCAACGCCCT	TAGTGGTGAG	CGATTTTCG	360
CCCCTTTTA	GCTTGCCTTA	TTTCATCGCT	TTTTATTTCG	CTATTTTTA	TGCTGGTGGG	420
TATCAG						426

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237

ATGGCGGTGA	AATTTTGC	CC TAAGATCAGA	AAAACAGATT	GGATTTTAT	TTTAATGCC	60
GCTTTAGGCT	TTTATTCA	GTGTAAGCTA	GGGTATGCGC	CCAAATTCAA	TACCCCCACT	120
CCAAAATCTT	CACGCCCTCT	TTCAACCCCT	ATTGAAAAGC	CTAACAAATAT	GACTGAAGAA	180
GAAAGGAAAA	AGCGTTTTAT	AGAGTTGCAA	AAAGCATGCT	TACTTCATAA	AGACAAAAAG	240
GCATGCGAAG	AGGTTTTT					258

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

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- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...363
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:238

GTGGATTCCA	TTTTAATTGA	TGAAGCGAGA	SCTCCTTTAA	TCATTTCA	GGCTGTGGAT	60
AGGCGCATGG	AAAATTACAA	CAAGGCTGAT	GAAGTCGCTA	AAAGCATGCA	AGTGGAACTG	120
GATTTCACCA	TAGACGAAAA	AAACCGCGCG	ATTTTAATCA	CTGAAGAGGG	GATTAAAAAA	180
GCCGAAAATC	TCTTTGGCGT	GGATAATTAA	TACAAAATTG	AAAACGCCGC	CCTATCGCAC	240
CATTAGACC	AAGCCTTGAA	AGCGAATTAC	CTCTTTTTTA	TTGRTAAAGA	TTATATTGTAA	300
GCCAATAATG	AAGTGGTGT	TGTAGATRRA	TTTACCGRCC	GTGTYYTGA	AGGGGAGGCG	360
CTT						363

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...177
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:239

ATGACGATCA	CCACCCATTC	TTTTTATTC	ACAACGCCAG	AAGTGTGTTGT	CAATCAGGAT	60
TTCCCATGGC	TTTCTGGGC	TGGAACCTA	GTGGTTAAAG	ACTTGGCGTT	ATTTGCTGGA	120
GGCTTGTTG	TGGCCGGATT	TGATCCAAC	GCTATTGGA	GGGTAAAGGG	TTTGCT	177

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240

GTGTTTCTG GCAATAAAAG GGCTATAAT TATCGCACGA TTGTCAGCGC CTTTGTGATT	60
CAAGTGGCTT TAGGGGCGTT GGCTTATAT GTGCCCTTGG GCAGAGAAAT ACTGCAGGGT	120
TTAGCTAGCG GCATACAAAG CGTGATTGGT TACGGCTATG AGGGGGTACG CTTTTTATTT	180
GGCAATCTCG CTCCAAACGC TAAGGGCGAT CAAGGGATAG GAGGCTTTAT CTTTGCGATC	240
AACGTTTAG CGATCATTAT CTTTTTGCT AGCTGATTT CACTTCTATA TTATTTAAAAA	300
ATCATGCCCT TAGTAATCAA CCTCATCGGS GGGCGTTGC AAAAATGCTT AGGCACTTCT	360
AAAGCAGAAA GCATGAGCGC AGGGCTAAT AYTYYTGTGG CGCACACCGA AGACRCCCTT	420
AGTCAT	426

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241

ATGCTGGTGG GTATCACTAA CGCTATTAAAT ATCATTGACG GGTTAACGG GCTTGCATCT	60
GGGATTTGCG CGATCGCGCT TTTAGTCATT CATTATATAG ACCSTAGCAG TTTGTCTTGT	120
TTGCTCGCTT ACATGGTGT GGGGTTAT GGTGTTAAW TTCCCTTCAG GAAAGATT	180
TTAGGWCAGT CGGGGGGGCG TATTTTTGG GTTGGTGTWR CGGRATTCT CTCTTGCATT	240

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242

ATGCTACATA AAAAATATCG TCCTAATGTT GCGGCCATT A	TCATGTCGCC AGACTACCC	60
AACACATGCG AAGTTTTAT CGCTGAGCGC ATAGACATTG AAGGGGCGTG GCAGTTCCCC		120
CAAGGAGGCA TTGATGAGGG AGAGACCCCT TTAGAAGCAC TCTATAGAGA ATTACTAGAA		180
GAAATTGGCA CGAATGAAAT AGAGATTTG GCGCAATACC CTAGA		225

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243

GTGATGCTAA TGGCAATTTT TACCCCTTAT ATTCTTATTT TGAAAATGAT GAAAAAGTCT	60
ATGAGTTTAT TCGCCAATAT GGGGTTGGAG CAAATTTTT GCAACAGAGA CATTAAAGAT	120
TTAAATGATT TTGTTTTGG TATAGAAGTG GGGCTTGATA GCAATGCGAG AAAAAATCGT	180
AGCAGAAAGG CTATGGAAA TCATCTTATC GGTCTTTTG TCCAAGCTCA ATTTAATT	240
AAAGAACAAAG TAGATATTAG AGAATTGAG GATITACGCC AGGCTTTGG AAATGATACT	300
AAAAAATTG ATTTTGTAT TTTTAGCAAA GAGAAAACCTT ATTTTCATAG AAGC	354

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...627

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244

ATGATCCGTC TAGCCGCGTT	TTTTTAGCT CTCGCTTGC	CGATTACGCC	AAAAAGCCGC	60
CTTCCTTAA AAAATGTCTT	GCTCAACCCC	ACTCGCATAG	AAGCTTTGA	120
AAAATGGCG CTCATATAGA	ATAIGTTATC	CAATCCAAG	ATTTAGAAGT	180
ATTACATAG AGCATGGCCC	TTTAAAGCG	ATCAGTATTG	ATCAGAATAT	240
ATTGATGAAA TCCCCGCTT	AAGCATCGCT	ATGCTTTTG	CAAAGGCCAA	300
AGAACGCTA AAGATTTAG	AGCCAAGAA	AGCGATAGGA	TAAAGCCGT	360
TTCAAACCTT TAGGGATTGA	GTGCGAAGAA	TTTGAAGACG	GGTTTTATAT	420
GGAGATGCGA GTCAATTAA	GCAGCATTT	TCTAAGATTA	AACCCCTAT	480
TTCAATGATC ACAGGATTGC	GATGAGTTTC	GCTGTTTAA	CTTAGCGTT	540
ATTGATAATT TAGAATGCGC	GAACATTCT	TTCCAACCT	TTCAGTTG	600
TTCAAAAAAA GGAGTCTCAA	TGGAAAT			627

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245

GTGGGGAGTT TGAAATTTTT	AAACGCTATG GGGGTTGATT	TAAAGGTTAA	AGAGAGCGCT	60
AATATCATGG TAGGCTTTC	AAAAATAAG ACCTTATGCC	CGTTATTCA	TTTAGAAGAG	120
CGTTGAAAG CTAACGCTAA	AGAAGTCATT CAGGCTTAC	AAAATCAAGG	CTTGAATTAA	180
GAAATTTAA GCGGGATAA	TGAAAGCTCG	GTTAAGGAGT	GCGCG	225

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...363

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246

ATGGAGGCTT	TAAACGCTTT	GAACGGCAA	AGTGATGAGC	AAATTTATG	CGAGGGTTAT	60
TTTGTGTTGT	TGCAATCTT	AGAGCCTATG	ATCCGCACA	CGGCATGGGA	ATTGAGCGAG	120
AGGCTTTTA	AAAGAGAGAA	TTTCAAGCCT	ATAGAAGTAG	ATGAAAGCGC	TTTGATAGAA	180
GACTTTATGA	CTTTAGGGCT	TACCATTAAT	GGCAAAAGGC	GCGCGGAATT	GAAAGTCAAT	240
ATTAACGCTA	GCAAAAGAAGA	GATTATTATT	TTGGCTAAAA	AAGAATTAGA	GAAATATTAA	300
GAAAACGCGA	CGCTTAAAAAA	AGAAATTAT	GTGCCATAA	AACTTGTAA	TTTTGTIACC	360
GCA						363

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247

ATGAAAAGAAA	GTATTAATAATA	CITGCTAGAA	AGCGTGGGGC	TAGTGCTTT	AATGAGCGTG	60
AATCCGGGCT	TTGGCGGCA	GAAGTTTTA	GATCTAGTGC	TAGAAAAGTG	CTTGAAAGTT	120
AAAGAACTGA	TCAAACGCTA	CAACCCTAGC	TGTCCTTGTAG	AAGTGGATGG	GGGCGTGAAT	180
GATAAAAATA	TCTTTGAACT	CCAACAAGCG	GGCGTGGATG	TGGTGGTTTC	AGGGAGTTAT	240
ATTTTGAAAT	CCAAAGATYG	TAAGCTGGCT	ATTGAAGGCT	TACAGAATGT	CAGACAACCT	300
CTTGCA						306

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248

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GTCATGACCG CGGTGCTTGG GTGGGTAGGC TTCACTTGA TTGCGAGCAT GTATCACATG	60
ACCCCTAGGC TTTCAAAAG AGAGATCTAT TCAGGAAGAC TTGTGGATT CCAATTGG	120
ATCATGACTT TAGGGATTGT GCTTACTTT TCGTCCATGT GGATTGCAGG GATCACGCAA	180
GGGATGATGT GGAGGGATGT GGATCAATAC GGGATCTCA CTTACCAATT CATTGACACG	240
GTAAAGGCGC TAATCCCTTA TTACAATATT AGAGGCCTG GGGGTCTTAT GTATTTTATT	300
GGATTTATTA TTTTGCTTA CAATATCTT ATGACAATCA CGGCAGGCAA AAAATTAGAG	360
CGTGAGCCC ATTACGCCAC SCCTATGGCA RRA	393

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249

ATGATAACGC TCTTTAGTTT TGGAGCGTTC GCTTACTTATT TCGTGTCTTC TCAAATCAGT	60
CACGAAAATC ATCAAAACGA AATGCCCAT TACCAAGTTG TTACCACTAT CAATGAAATT	120
TTAAATAACT ACTCTGATTA TAGAGCCATA GAAGATTACC TCTATAAAAT TGGCTTAAAGA	180
GAAACCACAA TAGAAAATT AGAAAAGGTT TTACCCAAAA GACGCCACCA CTGACCCAC	240
AGAAATATTT GGTATGCTGA AGTGTTTAAA TTCAGCGATA TGGTTTTAT CTTTTAAAAA	300
AAGGATGAGC ATTTTGTGCT TTATAAAAGAT TTGCATTGCG TTTCTTATAG GAATTATTC	360
TTAGCCATTA CGGTGGTTT ATTATTGATT TTATTCTCT TTTTATTGTT TTTGCAGAGT	420
TTATTGCCCT TAAGAGAGT AAGATCTAA GTGAAACGCT TCGCTCAAGG CGATAAAAGC	480
GTGAGTTGTA AAAGCAAGCA AAAAGATGAA ATAGGGATT TGGCTAACGA ATTTGACAAT	540
TGCATCCAAA AAATCAATGC GATGAATGAA TCTCGGGTTT TATTGGCG CTCTATCATG	600
CATGAATTAC GCACCCCTAT CACTAAGGGC AAGACTAA GCTCTATGCT CAAAGAAGAG	660
CTGCTTGCA AACGCTTTTC ATCTATATT GATCACTTGA ACATGTGAT TGAGCAATT	720
GCCCCGATTTG AGCAGCTCGC TTCCAAAAAT TATGGGAGCA ATAAAAGAAA ATTTTTAATG	780
AGCGATTGTA TAGATAAGAT TGAAAAAATG CTTTAAATTG ATGAAGATAA AAAAGCCCT	840
ATCCATGTAT CCTCTTCATA TTACATCATT GAAGCGGATT TGAATTGTT TGCTATAGCG	900
TTAAAAAAACA TGATAGACAA TGCGATCAA TACACCGATG ACAAACAGGT GTTTGGAT	960
TTCATAGGGA ATAATTAGT GGTGTCCAAT AAAAGCAAAC CTTAAAAGA AGATTTGAA	1020
AAGTATTGCA AACCTACTT TAAATCTCT ACCCCAGCC AAGCCCATGG GTTTGGGTTA	1080
GGCATGTATA TCATTTAAA CGCTTTAGAG GCTATGGAT TGAATTGAG CTATCATTAT	1140
AGCAATGGAA GAATCTGTT CACTATCCAT GATTGCGTT TAAATAGTT TTACGATT	1200
GAAGCGATA ATGAAGAGCT ACCCCCCCCC GAAAATTGA GAGAGGTGAA GGGATGAAG	1260
GGAAACAGAAA AAGCCAATTG TGGGGTTAAA GAAAACAAA AAGAGAGAAC ATGTTCAAAC	1320
GAT	1323

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

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- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...381
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:250

GTGCTTCTCC	TTTCTCGTAT	GGGTATCGCT	TTTCCCCACT	CTATTTTTTG	GTCCATCACG	60
GCTTCTTTAG	TCATTCGTGT	CGCGCCAAGA	AACAAAAAAC	ACAGGCCTT	AGGGCTGTTA	120
GCGTTAGGGA	GTTCGTTAGC	GATGATTITA	GGGTGCGC	TTGGGAGGAT	CATTGGCAA	180
ATTTTGGATT	GGCGATCCAC	TTTTGGCGTG	ATTGGGGGCG	TTGCGACTCT	TATAATGCTG	240
CTTATGTGGA	AATTGCTCCC	GCATCTACCG	AGTAGAAACG	CCGGCACGCT	CCCAAGTGT	300
CCTATATTAA	TGAAACGCC	GCTTTTAGTG	GGGATTATTATT	TGCYTGTGAA	TCATGGTTAT	360
TTCTGGGCAT	TTCACCACTT	A				381

(2) INFORMATION FOR SEQ ID NO:251:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...345
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:251

ATGCGCATTA	TCATAAGGTT	ACTTTCATTT	AAAATGAACG	CTTTTTTAAA	ACTCGCGCTC	60
GCTTCTTTGA	TGGGGGGGCT	TTGGTATGCT	TTCAATGGCG	AAGGCTCTGA	GATTGTCGCT	120
ATAGGGATT	TTGTGTTGAT	CTTGTTGTT	TTTTTATCC	GCCCTGTGAG	TTTCCAAGAC	180
CCAGAAAAAC	GAGAAGAATA	CATAGAACGG	CTTAAAAAAA	ACCATGAGAG	GAAAATGATC	240
TTACAAGACA	AGCAAAAAGA	AGAGCAAATG	CGCCTCTATC	AAGCCAAAAA	AGAGCGAGAG	300
AGCAGGCAAA	AACAAGACCT	TAAAGAACAA	ATGAAAAAT	ACTCA		345

(2) INFORMATION FOR SEQ ID NO:252:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

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- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...258
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:252

GTGCGATCTT GCAACAGAT TTTTGATAAG GGTAAAGC CCTATTATAA ACATTCTGTT	60
TGCTAAAGC CTTTTTTAG GTTTTGTCTT CTCAAATTC ATGCCTATCA ACAGCGTTAT	120
AGAGCGTTTG CTCTAACGCT CTTTCTTGT AAGTTTTTA ACGCTTGAA GATTTTTATT	180
CCCATATAATTG ATTAAAAAT CGTTTTATC CCTATTCTAA AACACCAAGC CAAGCTAAAA	240
AGAGTCTCTA ATGCCTAT	258

(2) INFORMATION FOR SEQ ID NO:253:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...132
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:253

ATGTGTGGAA TGGGGTTTAT TGGCTTCAAA ACAAAACTTA CTCAAACAAA GGCATTTATT	60
ATATTGATCC CAATCTTCA GGACAGAGCG GTCAAAGCGG CAACACGCTC AGCACCTATA	120
CAGCTAATTG GT	132

(2) INFORMATION FOR SEQ ID NO:254:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1680 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254

ATGGGAAATT TTAATAGCTA TGGCGATTG GTGTTAAC	TCAGTCATTC AGTTAGTCAT	60
GCTATTATCA ATACTCAAGG CACAGCGACG ATCATGCCA	ATAATAACCC TTTGATCAA	120
TTCACGCTT CTTCAAAAGA AGTGGGTACT TACACGCTGA	TTGATAGCGC TAAAGCCATT	180
TATTAACGGGT ATAACAACCA AATCACAGGA GGCAGTAGCC	TGGATAATTAA CCTTAAGCTT	240
TATGCCGCTCA TTGATATTAA TGGCAAGCAC ATGGTGATGA	CTGACAACGG CCTTAACCTAT	300
AACGGGCAAG CGGTGAGCGT TAAAGATGGC CGTTTAGTTG	TAGGCTTTAA GGACTCTCAA	360
AATCAATACA TTACACTTC CATTACCTTAT AATAAGTGA AAATCGCTGT	TTCTAATGAT	420
CCTATCAATA ACCCACAAGC CCCCACCTTA AAACAATATA	TCGCTCAAAT TCAGGGCGTT	480
CAAAGCGTGG ATAGCATCRA TCAAGCTGGG GGAAATCAAG CGATTAATTG	GCTCAATAAA CCACCTCCACA	540
ATCTTGAAA CTAAAGGAAG CCCTTATTC GCTCCCTATT ATCTAGAGAG	TGGAGATATT GCTAACACTT TAGAAGTCAT	600
AAAGATTTAA CCACGATCGC TGGAGATATT GCTAACACTT TAGAAGTCAT	CGCTAACCC CGCTAACCC	660
AATTTTAAAA ATGACGCCAC TAATATTTA CAGATCAACA CCTACACGCA	GCCTAACCGT	720
CGTTTAGCCA AGCTCTCTGA CACTTCAACT TTGCCCCGTT CTGATTTCTT	AGAACGCTTA	780
GAAGCCCTTA AAAACAAGCG ATTCGCTGAT GCGATCCCTA ACCTATGGG	TGTGATTTA	840
AAATACTCTC AAAGGAATAG AGTTAAAAAT AATGTGTGGG CGACAGGAGT	TGGAGGGCT	900
AGTTTCATTA TTGGAGGTAC TGRAACTTATCA ATGWAGGGTA	TGATAGGTTT	960
ATTAAGGGCG TGATTGTGGG AGGTTATGCC GCTTATGGGT ATAGCGGGTT	CCATGCAAAC	1020
ATCACTCAAT CAGGCTCTAG CAATGTCAAT GTGGCGTTT ATAGCCGAGC	GTTTATCAA	1080
AGAACGAGC TAACCATGAG CTTGAATGAG ACTTGGGGAT ACAATAAAAC	TTTCATCAAC	1140
TCCTATGACC CCCTACTCTC AATCATCAAT CAGTCTTACA GATACGACAC	TGGACGACT	1200
GACGCTAAAA TCAATTATGG CTATGATTTC ATGTTAAAG ATAAAAGCGT	TATTTTAA	1260
CCCCAAGTAG GCTTAAGCTA TTATTACATT GGTTTGTCTG GTTTAAGGGG	CATTATGGAT	1320
GATCCTATT ACAACCAATT CAGAGCCAAT GCTGACCCCTA ATAAAAAATC	CGTTCTAACG	1380
ATCAATTITG CCCTAGAAGG TCGGCATTAT TTCATAAAA ACTCTTATT	TTTTGTGATT	1440
GCGGATGTGG GCAGAGACTT ATTCAATTATCTATGGGG ATAAAATGGT	GGCTTTCATC	1500
GGTAATAACA CCCTAAGCTA TAGAGATGGT GGCAGATACA ACACTTTG	TAGCATTATC	1560
ACAGGGGGGG AGATAAGATT GTTCAAAACC TTATATGTGA ATGCCGCAT	AGGGGCTAGG	1620
TTTGGGCTTG ATTATAAAGA TATTAATATT ACCGAAATA TTGGTATGCW	SYATRCTTT	1680

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255

ATGGAGTCGA ATCAWTCACT CCCCATGGCA TTAATATCAT GCTCACCTAA CGCTAAAGGG	60
GCGGACATTA AAGGCTATAA CGGCTTAGTG GGGGAATTGA TTGAAGGAA TTTCCAACGC	120
TATGGCGTGC CGTTACTGCT TTCTACGCTC ACTAACGGCC TATTGATTGG GATCACTTCG	180
GCTTAAACA ACAGAGGAA TAAAGAAGAG GTGACTAATT TCTTGGGG AATATCTTTA	240
TTGCAATTGA TGAGGCAAAG CGGCATGGGG ATCAATCAAG TGGTCAATCA AATTTTAAGA	300
GACAAGAGCA AGATCGCCCC CATTGTGGTG ATTAGAGAGG GGAGTAGGGT CTTCATTTCG	360

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CCCAATACTG ACATCTTCTT CCCTATAACCC AGAGAGAATG AAGTCATCGC TGAGTTTTG	420
AAG	423

(2) INFORMATION FOR SEQ ID NO:256:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 153 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...153

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:256

GTGAATTTC ACCTTCGCC CAAAGATTAC CACCACTACC ACGCCCCTTG CGATTTAGAA	60
ATTTTAGAGG CTCGTTATT TGCGGGAAA TTACTACCAG TCAATAAGCC CTCATTACAC	120
AAAAAACAAA ATCTGTTGT GGGCAATGAA AGG	153

(2) INFORMATION FOR SEQ ID NO:257:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 699 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...699

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:257

ATGGATATTT TAAAAGCAGA GCATTTAAC AAACAGATTA AAAAACCAA AATCGTTCA	60
GATGTTCTT TAGAAGTGAA AAGCGGGCAA GTGGTGGGC TTTTAGGGCC TAATGGGGCG	120
GGTAAAACCA CCACCTTTA CATGATATGC GGGCTTTAG AGCCTAGTGG GGGGAGCGTT	180
TATTTAAACG ATGTGGATT AGCTAAATAC CCCTTACACA AGCGTTCTAA CTGGGGCATA	240
GGCTACTTGC CCCAAGAAC CAGTATTCTT AAAGAATTGA GCGTGGAAAGA GAATTGGCC	300
CTAGCAGGGG AGAGCACTT TAAAAACTCT AAAGAGAGCG AAGAAAAAT GGAAAGCTTG	360
CTTGATGCTT TTAATATCCA AGCCATAAGA GAGCCAAAGG GCATGAGCTT GAGTGGGGGA	420
GAAAGAAGGC GCGTAGAAAT CGCTAGGGCT TTAATGAAAA ACCCTAAATT CGTGCTGTTA	480
GATGAGCCCTT TTGCGGGCGT GGATCCGATT GCGGTGATTG ACATTCAAAG AATCATTGAA	540
AGCTTGATTG GATTAAACAT TGGCGTGTG ATTACTGATC ACAATGTGCG AGAGACCTTG	600

AGCGTGTGCC ATAGGGCGTA TGTGATCAA AGCGGCACGC TTTTAGCGGC GGGAACGCTA	660
ATGAAATTAA TGAAAACGCT TTGGTGCCTA AGTATTATT	699

(2) INFORMATION FOR SEQ ID NO:258:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 474 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...474
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:258

ATGAAAGAAA TCGTTACAAT AGAGAAATGTG TCTTTTAACT ACCACAATCG CGCTATTTTT	60
AAGGATTTTA ATTTAACGAT TCAAGAAAGGG GATTTTTTAT GGTTTTAGG GGAGAGGGGG	120
AGCGTAAAAA GCACGCTTTT AGGCTTGATT TTAGGGCTTT TAAAACCCAG TCTGGGGAGC	180
GTTAAATCT TTAAATGAGAC CCTTTCAAC AACGCTTTT TAGGCCAAAA AATAGGTAT	240
ATCGCTCAGG GCAATTCCCTT ATTCCCTCAT TTAAACGCTT TACAAAACAT GACTTTTGC	300
CTTAATTAC AAGGCATAAAA CAAACAAGCC GCTCAAAAG AAGCCAAAGC CTTAGCGTTA	360
AAAATGGGGT TAGACGAGAG CCTTATGGAT AAATTCCCTA ATGAATTGAG TGGGGGGCAA	420
GCCAAAGACT GGGCATTATT AGGGGGATTA TCCACAGGCC AGAACTCATT TTAT	474

(2) INFORMATION FOR SEQ ID NO:259:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 573 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...573
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:259

ATGATTTTCC CCGAGCGCTT TCAAAACGCC TTTTAAAGGT TAAGCGAATT GTTTTACTAC	60
GCTTCAGCT TGAGTTTTA TACGATTTG TCTTTATCGC CTATTTGTT GTTCGTGTT	120
AGTCTTTTG TGTCTCATTA CTTGCAAGCG CACAGCGGTG AAATGGAAGC TTGATTTTC	180
CCTAACGCTC CTAAACTCAT TGGCGCGATT AAGGATTTTT TAGAAAATT TAAAAAAACA	240
GACATGACCT TAGGCACGCT TGAAGAGGTG TCTATGTGG TGGCGTTGGT GCTTTTTGT	300

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GAAAAC TACC GCTCCATCGC GTCAAAAATT TTTGACGCAA AGCCCAGAGA TTATGC GCGAT	360
TTTAAGGGTA AAGAAATCTT TTTATTTTCG GGGTTTGGCA CGACTTTAGT GTTTTTATTG	420
GCTTTGCCTT TGGTGGTGT TTTTGATATT AAGATCCAAG TGTTTTTGA AGATAAAAGAT	480
TCAAGCTTGT TGCATGTTT AAGATGGATA GGCACTTACG CGTTTTTTT GATCCTTTT	540
ACCATTCCCA CGAATAAGGT GTTTAACTA YYA	573

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260

ATGGTTTTGA TGATTTTAC AACCATCTTG AAGATAGCGT TAAAAGTTT ATCAGAGCGA	60
AAAAAAATC GTTATGGTTT TCCTAGAATC TTGATGTTG CAGACATAGA ACAAGAACAG	120
AGGGAACTCA TTGAATGGCG AGAAAAAAAG AAACCGTCAA AACAAAGCTA TAAACAAAAC	180
CTTCAAATCA ATAAAATCGC TAACGATTTA AAGCGTATA AGATAGTGGA TAAAAGAACG	240
ATTTTAAGCG TGATAGACGC TGATATAGAG CGTGGTTTTA TCCCGCTAA AGATTTGTTA	300
AAACAATTAG AAAAATTAG CGCTTCTCTT TCTAAAGACA TCGTAATAAC GATAAAGCAA	360
GTAGAAAAAT TAGAGCTTAA CTATGCGCTA ATAGACAATA TCCAACATAA CACGCTTGAT	420
GACACGCTTG ATTTTACCTT TATTGTTGGG GATTCTTTGA CGCTTCAGTC GCCTTATGTT	480
ACCTTAATC TTGTGATTGA TATTGATAGA CCCATGAGCC AGCAGTTCT CAACCWTATT	540
GGGAATTGG GGAGTTTTGA ATCTAGAGAG CAACCGTTAG AGTGGGTGCC ATTATGCCAA	600
ACTAAACTGA TCATTGAAAC CCCTAAAGAA GCGTAAAAA ATGCGGAATT ATCACAAATT	660
GAAGAAATAT TGACCGGCTG TATTTTAAT GGCGCTTACC CCCTCAAAA CGATCTTAAG	720
AAAGGGCGA	729

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...708

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261

GTGAGTGAGG TCGCGAGGGT	GGGGGGCTTT GTGAAGGATT	ATGAAGTAAC GCTTCAAAAC	60
GATTCTTGA TCCGTTATAA	CTTGAGTTA GAACAAGTCG	CTAACCGCGAT TAAAATTCC	120
AATAACGATA CCGGTGGGG CGTTATTATA	GAAAACGGGT TTGAAAAAAT	TATAAGATCG	180
CATGGCTATA TCCAATCTTT	AAACGATTAA GAGAAATTG	TGGTTAAAAA AGAAGGGCT	240
ATCCCCTTAA AAATCAAAGA	TATAGCGAGC GTTAGGCTAG	CGCCCAACC CGCGAGAGG	300
GCGGCTAATC TCAACGGCGA	TAAGGAAGTG GTGGCGGGGA	TTGTTATGGT CGCTATCAC	360
GCTGACACTT ATAAGGTGCT	AAAGCCATT AAAGAAAAAA	TCGCCACCTT ACAAGCGAGT	420
AACCTGATG TGAAAATCAC	CAGCGTGTAT GACAGGAGCG	AATTGATTGA AAAAGGCATT	480
GACAATTGTA TTCACACGCT	CATAGAAAGAA AGCGTCATTG	TGCTAGTCAT TATTGCGATT	540
TTCTTACTGC ATTTCAAGGAG CGCTTIACTG	GTGATTATCA CTCTGCCTTT	AAGYGTGTGC	600
ATCAGTTTCT TGCTCATGSG TTATTTCRAT	ATTGAAGCGA GCATCATGAG	TTGGGGGGC	660
ATTGCAATCG CTATAGGGGC	GATGGTGAAT CGGGCGATTG	TGATGGTG	708

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262

GTGAAACTT TTCTTAAAT TTTTGAAAAA	GATATTTTA ACACGCCCTA	TAAATTAGAA	60
GTCATTAACG CTACTGAGG GGGGGCTAGG	ATTAAGGGA CAAAGAAAT	GCCCTTTAAA	120
GAAGTGTGCG AAAAWTAGA	CAAATCCAAG CAAAGCCTC	CTATCAATCT	180
ACCCATATCG AACAGGCTAA	AAATTTAAAG ATCGCCAAGA	AAAAATGCGA	240
AAATACGCCA ATGAGAAAAA	AACCGAAGTT GAAGAACGCT	TTTTAAAGGT GGCAGAGTTT	300
TTAGAAAAAG TGAAAAGCT	TCATGAAAAA AACAAATTAG	AAGACTTGGA TTTTGAAGAA	360
TTAGAAAATT TGAGCGCTGA	AATTGATAAC GTTAAAGAGC	TTTTGATGA CAAACGATTC	420
AATTGCTATT TTATGGATGC	GATACAATCT TACATTTCC	ACCAGGAATT GCATATCGCT	480
GAAATCGTGT	GAGTAATGAA GACGGGATTAA	AGGGC	525

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263

ATGAAAACGC	CTTGCAACGC	CTATTTCTC	AAAAGCCAC	CCAAAAACAA	AAAAAGAAGA	60
GTATTATGTTA	ATTTAGCGGT	GTTCCTTTT	TTATTGCTAG	CGAGCGCTTT	ATGGCTCATT	120
CCTAGAACGTG	CCATAGAACR	AAAGCCCTTA	GTCGTGGCGA	CAAAACCTAG	CAGCGAGCAG	180
TATATTTTGG	GGCAAATTIT	AAGCCTTTTG	TTAGAAAAAC	ACCATATCCC	TATCAAGCGA	240
GCGTTTGGCA	TTGGTGGGGG	GACGATGAAT	ATCCATCCGG	CATTGATTAG	GGGCGATTIT	300
GATTGTATC	TGGAATATAC	CGGCACCCCT	TGGGTGAACA	CGCTCAAAAA	CCCTTTGACT	360
CAAAAGTGG	ATTTGAAAC	GATTAAGAAG	CGTTATGAGA	AGGAATTAA	TCTTTGTGG	420
GTGGGACTTT	TGGGCTTAA	TAACACCTAT	TCTTGTACCGA	TTTCTAAAGA	AGACGCTCAA	480
AAATAACGCAA	TTGAAACTTT	CAGCGATTAA	GCCTTCATA	GCCCGAATT	TGATTTGGA	540
GCGGAGYTTG	ATTTTTTGA	AAGAGAGGAC	GCTTTAAGG	GCTTAATCAA	AGCTTATCGC	600
TTTCATTAA	GAAGTTGCA	TGAAATGGAY	ATTAATTGCG	GTTATAAAAG	TTTGAATCC	660
CTCATAAGAT	YAACGCTT					678

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 237 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264

GTGATGGTTT	ATAAACTCCC	CAAACACCAAG	CAAAATAAGG	TCATGATTTT	AGGCTTGGGC	60
TTAGCGATGA	TCACTCGTAT	AGGGCTTTA	GGGAGCTTGT	TTTCATCG	CCATTGCAA	120
AAGCCTTAT	TCGCTATAGC	GGGCATGAGC	TTTCATGCC	GTGATGTGGT	GCTGCTTTA	180
GGGGGGCGT	TTTGGCTTT	TAAGGCCTTA	GTGGAATTAA	AAAGAGCAGA	TCTATCC	237

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 630 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265

ATGTTGTGG	TTTTTATAGA	AGGTTTGTT	TTAGCGATT	CTTGTGC	GGCGGTGGG	60
GCGCAATCCT	TGTTTATTGT	GGAAAGGGGG	ATGGCTAGGA	ATTATGTGTT	TTTGATTTC	120
GCCTTGTGTT	TTATGTGCGA	TATTGCTTA	ATGACCATGG	GGTGTGTTGG	CGTGGGGGCT	180
TATTCGCTA	AAAACCTTTA	TTTGAGCTTG	TTTTGAATT	TATTTGGGGC	AGTTTTTACC	240
GGATTTTACG	CTTGTGGC	TTTAAACCC	CTTTTCAA	CCTTAAAAAA	AAAGCAAGTC	300
CAAACCCCTA	AAAAATTATC	CTTAAAAAAG	ACCTTATTAT	TCACTTTAGG	CGTTACCTTA	360
CTCAATCCTC	AAGTGTATT	GGAAATGGTG	TTTTTAATTG	GGCCGAGCGC	TATGTCTTT	420
AACCTAGTGC	AAAAATTCTGT	CTTCTAGCT	GGCACTTTAT	CGGCTGCCTT	TTCTTGGCTT	480
TTATTGTTAT	GCACCATGTC	CTTACGCTAT	GGCTCTAAC	TTTGAAACAA	CCAAAAAAATC	540
TTTATGGCG	TGAATCTCTT	TGTAACCGCT	ATCATGGAA	CGCTCAGCGT	TACTTTATTC	600
AGGGATTTT	TAGCGTTATT	GAGCAAAACC				630

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 888 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266

GTGAAGCCAA	AGAGCATGAA	AGAGAAGCTA	AGAGGCC	TGGTGAATAT	CTTAAGGATA	60
AAAATGATTG	AAATAAGCGA	ATGGTTGCAA	AAACTAGACG	ATGCC	TAAAGTTGTT	120
GCTAAAAAG	AGCCAGAGAG	TTTCTCAAG	CCGATCATT	CACCAATAGA	GGACTACCAA	180
AAGAGTGTCA	GGCAAAATCA	AGCGCAATT	ACAGACCGC	CGAAGTTCA	TGAAGAGGGT	240
GCTTACCCCTC	AATTTTAAG	CTGTGGTTTA	TTGCAAGTTA	GGGGCAAAA	TGGTGCTAAC	300
ATGGAATTIT	TATTGCTAA	AGTTTATCCT	TTCCCCCTA	AAACCTTGT	TATAGAGCAT	360
GAAAAAGACG	GGCAGTTTT	GAGAGAAATG	CTCATGCGCT	TACTCTCCAG	CGCGCCTTTA	420
GTGAATTGG	AAGTGTATT	AATTGATGCG	TTGAGCTTGG	GGGGCATTTT	CAATCTGGCC	480
AGAAGGCTT	TAGATAAAA	CAATGACTTT	ATTTACCA	AAAGGATT	TTTACCGC	540
AAGGAATAG	AAGAAGCCCT	AAAGCATTG	CATGAATATT	TAAGGTTAA	TTTGCAGAA	600
AAATTAGCCG	GTTTTAGAGA	TTTGTGCA	TATAATGAAA	ACGCCAAAGA	CTCCCTTGCCT	660
TTAAAAGCGC	TTTTTTAAG	CGGGGTGGAT	GCTTTGAGTA	AAGACCGC	TTATTATCTA	720
GAAAAGATCA	TGCGTTTIGG	CTCTAAAAAT	GGGGTTTGA	GCTTGTCAA	TTGGAGAGC	780
GAAAAAAACA	ATCAATCCGC	AGAAGATTG	AAACGCTATG	CGGAGTTTT	TAAAGACAGG	840
ACAAGTTTG	AGTGSTAAA	ATACCTTAAT	GTAGAAATCA	TCAGCGAT		888

(2) INFORMATION FOR SEQ ID NO:267:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...282
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:267

GTCCTTATAA CCCTGATGAT AGGCCAAAT CAAGCTTAG GCTTATAGG GACTAATTTC	60
AAGCAAGAAT TAGTCGTGGA TTTCATTGTC CCAAGCGCTG AAATCAACAT AGGCRRTCAA	120
GTGYTAACGA CGGGCTAGA TGGGATTTTG GGAGCGGGGG TGTTTGTGGG TGAAGTTCA	180
AGCGTTGAAG ATCATTACAC TTATAAAAGC GCGGTGTTGA AAAACGCTTT TTTAACCGAA	240
GCCAAACTTT TAAGGCATGT GTTTTAAGC GGTGTGAAAA AC	282

(2) INFORMATION FOR SEQ ID NO:268:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...249
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:268

ATGGAAGGCC AATTACGATT TACGGGTTT GGAGGGCAAG CGGTGTTGTT AGCGGGAGAG	60
ATTTTAGCTG AGGCTAACAGT CGTGAGGGG GGCTATGGCA CTAAGACTTC CACCTACACT	120
TCCGAAGTGC GTGGAGGTCC CACTAAGTGTGATTTGT TAGATAAAAGA TGAAATTATT	180
TTCCCTTATG CTAAAGAGGG CGAGATTGT TTCATGCTTT CAGTCGCTCA AATCAGCTAC	240
AACCAGTTT	249

(2) INFORMATION FOR SEQ ID NO:269:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 609 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

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- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...609
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:269

ATGCAAGCTT	GGGTGGATAA	GCCGGTATTG	TTAGAGCCAG	ATAGTAACGC	CCAATACGCC	60
GCTGTCATTG	AAATTGATGT	GGCAGAACATC	ACGGAGCCTA	TTTGGCATG	CCCTAATGAC	120
CCTGATGACG	TGCTACTTT	GAGCGAAGTT	TTAGCGGATA	CGACCGGCAA	AAGACCCCAC	180
GCTATTGATG	AAGTGTATAT	TGGCTCTTGC	ATGACGAATA	TTGGGCATTT	CAGAGCCTTT	240
GGTAAAATCG	TTAAAAAACGC	CCCTCCCAGT	CAAGCACGCC	TTGGGTAGT	GCCACCCAGT	300
AAAATGGACG	AACAAGAGCT	TATTAATGAG	GGCTATTATG	CGATTTTGG	GGCTGCCCCGG	360
GCAAGGACTG	AAGTACCAAGG	CTGTAGCTTG	TCCATGGCA	ATCAAGCGAG	GGTTAGGGAT	420
AATGCGTCG	TTTTTCTAC	TTCCACACGG	AATTITGATA	ATCGTATGGG	TAGAGGGCT	480
AAAGTGTATT	TGGGCAGTGC	GGAGCTTGGG	GCGCGTGC	CTTACTAGG	GAGGATCCCC	540
ACTAAAGAAG	AATACATGAA	TTTAGTGAGT	AAAAAGCTAG	AGAGCCAAA	AGACAAGATC	600
TATCGCTMC						609

(2) INFORMATION FOR SEQ ID NO:270:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 660 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...660
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:270

GTGGCCAATG	CCGGGGTGGC	TTTAGCGGGT	TTGATGAGCG	ATGAAATTAA	TTTGTGCGCT	60
TTAGATTGGC	CTTATATCAA	AGGGTTAAA	AAGCACGCTC	AAAATTCTA	TTATGGAGAT	120
GAAAAAGAGA	TTGACACCTC	ATCTTTAAC	ACCGTAGAGG	GTAATGTTGA	AGGTTATGAA	180
ACTTTTAGCG	ACTCGTTTT	TTTGCTCTCT	AAAGAAAGGA	TTGAAGAAGC	CCTTCAATTAT	240
TACCAGCTA	AAAAGTCTA	TAATTTAAC	TATGGGGCGA	AAATCAAGCA	CGCCGTTAGC	300
CTCAATCACT	CTCAAGTGA	ATTGAAACAA	ATCAACAAAC	AAGACGCTAT	CGTTCCGATT	360
AAAAGCATGT	TTAGCCCTAG	AAGTAATCAT	GCTAAGGATT	AAAAAAATTT	ACAAAAAAAT	420
CTGATTGTT	TTAAAGAGGA	TTTTTCACG	CATTTAAC	CGCCTTGAA	AACCAAGCAA	480
GAAGCATTG	AATGGGTGGA	TAGCTTGAGT	GGATTTGCC	AAACAGCCAG	CCCTAAAACC	540
CCCACTATAG	GCATTTTATT	TGAAGGGAGT	GTCGCCATA	TCTTACAAAG	CGTTCTAATC	600
GTTTCATTGC	ATCTTAAAGA	AAATGAGCTG	ACGCTTTAT	CAAATTCTCT	AAAAACGCCCT	660

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(2) INFORMATION FOR SEQ ID NO:271:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 744 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...744
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:271

ATGCAAAAAA GTATATTCAA	AATAACTCTG	TTGTTGGTTT	TCCTCTTTT	AAGGAATGCT	60
GTTGGTTTAG	ACGATAAAAA	AGCAGCTCC	AAAAGCGTC	AAAATACCCC	120
CCCCCTATCC	AGTTAAGGCT	CGATCAAGCC	TATGAAGACC	TTATCAAAT	180
ATGGGAAAAA	GCACGCAGTA	TGAGTTCCCT	AAAATTAAAG	AAATCCTAGA	240
GAGGAATGGC	TAGGAGTCGC	CCATGAAGAA	TGTGTGGCGT	TAGTCATGTT	300
AAGGCTTCTA	TTGAAAACAG	CCCGATTAT	AAGAATTGCT	ATGAAGCTTA	360
AGAATCCATG	ATTATATATGA	TTTTATATA	GAGGCCAAA	AAGTGAAAAG	420
AAAGCCCCATG	AGCATGAAAT	GGCCCTCAAC	AAATCCCAAC	CCTTAAAAAA	480
AAAAGCGAGA	ATAAAAAGGG	CTTAACAAAA	CCTAGCTTGA	AGAACGCAAA	540
GGGTATTACT	TCCAATTGG	GGCTTTTTA	AATTCGCCCA	GTAAGGATTT	600
CTCAAAACTT	TCCCCTCACCA	AATGGAGGAA	AAAGACTCCC	TCACGCATTA	660
CCTTATAAAA	CCAAAGAAGA	AGCCCTAAAA	CAGCTGAAA	ATGCGGCTAA	720
AATAAGCCTG	CCTTGGTAGA	GAAG			744

(2) INFORMATION FOR SEQ ID NO:272:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...450
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:272

ATGCAAGAAA TCTTAATCCC	TTTAAAGAA	AAAAGCTATA	AAGTGTGTTT	GGGGGAAC TG	60
CCTGAAATAA	ATTGAAACA	AAAAGCGCTC	ATCATTAGCG	ATAGCATCGT	120
CATTGCCCC	ATTGTTAGA	GCGCTTGAAC	GCCTTAGAAG	TCAGAGTGTG	180
TCCGGGGAAA	AATACAAAAA	TTTCATTCA	TTAGAGCGGA	CGCCTTGAA	240

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ATGCAATTAA ACCGCCATTTC	TTTAATGATA GCCCTTGGTG	GGGGACTGAT AAGCGATATG	300
GTGGGGTTTG CGAGCAGTAT	TTATTTCAAGG GGGATTGATT	TTATTAATAT TCCCTACGAC	360
TTTACTCGCT CAAGTGGATG	CGAGCGTGGG GGGGAAAACA	GGGATCAACA CGCCTTATGG	420
CAAGAACCTA ATCGGATCGT	TCCACCAGCC		450

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273

ATGCGAATAC TTCAATTATGG AGGTGAGCTC CCATGCGATT GTCCAAAACG	CATCGCTGGG	60
CTTGATTTCG CTCTTAAAAT TCTCACCAAT ATCACAGCG ATCATTTAGA	TTTCCATCAA	120
AATATAGAAA ATTACAGGGA CGCTAAAAAC AGCTTTTTA AAGATGAGGG	CTTAAAAGTC	180
ATCAACAGAG ATGAAACAAA CGCCCTTTT AACCCATTAA CGCGCGCAC	TTACGCACTG	240
GATAAAAAG CGCAATTGAA TGTTCAAGCC TTTCGCTCA ACCCTTCAT	TAGCGCGTCT	300
TTATGCTACC AACACGATTAA AAGAGATCCC AATCTAAAG AAACCGCCCT	GATCCATTCC	360
CCCCCTTTAG GGCGTTACAA CCTTTATAAT ATTTTAGCGG GCGTTTTAGG	GGTTAAATTG	420
CTCACTCAAT TGCCCTTAA AACGATCGCA CGGTATTGAA AAACTTTTA	TGGGGTTAAG	480
GGGCGTTGG AAAATTGTACA TTCTAAACCT TTAGTGGTCG TGGATTTCG	CCACACAACA	540
GACGGCATGC ACAAACTTTT		561

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274

GTGAGCATTAA AAGAAGAGAG CCAAACCTTA GCCGATATTA CTITCCAAAA TTATTTCAAGG		60
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ATGTTTCAGT AACTTCAGG CATGACAGGC ACGGCTAAA CCGAAGCCAC AGAATTTTTA	120
GAAATCTACA ATTTAGAAGT GGTGTCCATC CCTACTAATC TAGCGATCAA GCGAAAAGAT	180
TTGAACGATC TGATCTATAA GAGTAAAAAA GAAAAATTG ACGCTGTGAT CCTTAAAATT	240
AAAGAATTAC ACGATAAGGG TCAGCCCGTT TTAGTCGGCA CGGCTAGCAT TGAAAAGAGT	300
GAAACCTTGC ACGCTTTACT CAAAAAAGAG CGCACCCCTC ACACCGTTT AAACGCCAAG	360
CAACACACTA AAGAAGCTGA AATCATCAAA GACGCCGGGC TTAAAGGGGC GGTTACGATT	420
GCGCAACACA GGGCAGGCG ATTAAAGCTCA CTGATGAAGT TAAAGAACTT	480
GGGGGGCTGT ATATCATTGG CACTGAAAGG CATGAGAGCC GTAGGATTGA CAATCAATTA	540
AGGGGGCGAA GCGGGCGTCA AGGCGATCCG GGAGTGAGTC AGTTTTATTG GAGC	594

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275

GTGGTGGCTG ATGAGGTGAG AAAGCTCGCT GAAAAAACCC AAAAGCCAC TAAAGAAATC	60
GCTGTGCTGG TTAAAAGCAT GCAACAAGAA GCGAACGATA TTCAAACCAA CACCCACGAT	120
ATTAATTCTA TTGTAGGCTC TATTAAGGGT GATGTGGAAG AGCTTAAATC CACCCCTAAA	180
AATAACATGA TTGTCGCGCA AGCGCaaaa TACACCATCT ACAATATCAA TAACCGGGTG	240
TTTGGGTY TGGCTAAACT CGATCATGTG GTCTTTAAAA ACAATCTTTA TGGCATGGTG	300
CSTTGGTCT CAATTCCITT GACATTACCA GCCCATAAGA GTTSCCGTTT AGGCAAATGG	360
TATTATGAGG GTGCGGGTAA AGAAAACTTT GCTAACACTT CAGGCTATAG AGCTTTAGAA	420
AGCCACCATG CGAGCGTGCA TGCTGAAGCT AATGATTGG TTAAAGCCGT TCAAGAAGAT	480
CACGTACCG ATTCAAATA CCTAGAACAT AAAGTGCATT TAATGGAAGA TAGCGCTAAG	540
CATGTCAAAG AAAATATTGA TAAGATGTTT TATGAAAAC AAGATGAACT CAATAAAATC	600
ATTGAAAAAA TTCAAAAAGG CGAA	624

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

265

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276

ATGAATACAT CAAAAAAATT AGGTAACCCC TTGCTTTTT TGCATGATAA TAAAATTTTG	60
TGGTGTGCG TAGGGGTGAG CATGGGCGGG TGGCCACTT CTAAAATCTA TCAATTGAA	120
AGCGCTTAG AGCCGATTCA TTTAACGTTT GCGGAAAC TCTCTTAAG CCCTTTTTA	180
AATTGAGCC ATTTAGTAAG GAATAAGCCT TAAACACCA CTGATGGCGG GTTTATGCTA	240
CCACTCTATC ACGAATTAGC CACCCAAATAC CCCTGTTGT TGAAATTGAA CCAACAAAT	300
AACCAAGAG AGCTTTTAAG GCCTAAATACC TTAAACCCAC AGCTCCAACC AAGCTTAACC	360
CCCTTAAAG ACTGCGCTGT CATGGCTTT AGAAACCAT CTTTAAAGA TAGCCTCATG	420
CTAGAACCT GTAAAACCCC CACTGATIGG CAAAAACCCA TTTCTACAAA TCTTAAAC	480
TTAGATGATT CTTAAATTCT ACTCAATTAA AATGGAATAT TGTATTGAT CCACAACCT	540
AGCGATTTAT CACTGCGTCG TAAAGAACCT TGGCTTCTA ATTAGAAAA CCYYCAACTC	600
RTT	603

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 381 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277

ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT TTGCTTCCT	60
GTTTTGCTC ACCAGAAC GCTGGTAAA GTAAAGATG CTGAAGATCA GTGGGTGCA	120
CGAGTGGTT ACATCGAACT GGATCTAAC AGCGGTAAGA TCCCTGAGAG TTTTCGCCCC	180
GAAGAACGTT TTCAATGAT GAGCACTTT AAAGTCTGCG TATGTGGCGC GGTATTATCC	240
CGTATTGACG CGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG	300
GTTGAGTACT CACCAAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT AAGAGAATTA	360
YGCWGGTGGT GCCATAACCA T	381

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 237 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278

GTGAAACGTGG CGGTGCCTTT TAGCTATCAA GTGAGCGCGA CCTTTCAAAA CTCACGCCCT	60
TCTAGTTGC TAGAAACTTT AAAAAGAGT TTTTAGAAA AGCCCTTAAT TGAGAGCAGC	120
GCGAATAAAA TCGCGGATAT TTTTCTAAA GCGGTGTTGT TTTTGCCTT TGTGAGCTTT	180
TTATITGTGGC AATTGGTTT GGGGCTAAT TTGAAAAAS GCTTTAATGG TGTGTAT	237

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279

ATGCTAATGG TTAATGGCTA TCAAATCACG ATGCATAAGG GTTATAAGGT AGGGTTTTTT	60
ACAAGCGTT ACAACCCCTGA TTTCGCTCAA ACCATTCAA ATAGAAGCTA TTTGATGAGC	120
TCTTATGAGT TATCGTTTT AAGAAAT	147

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280

ATGGTGAAT TTCAAAACAC GCTTATAAAA TTCCATGCC TATCCTTTAA AAACGCAAAT	60
TTAATTATA ATGCAAAATT AAACAAAACA TGCTATAAAG AAAATTCAAA TACTATCATT	120
TTAAGGATTA AAATGCTCAC CCAAGAAGAT GTCTAAACG CGTTAAAAAC GATCATCTAC	180
CCTAATTITG AAAAGGATAT TGTAGCTTT GGTTTTGTTA AAAACATCAC CTTGCATGAC	240
AACCAATTAG GGCTTTTAAT AGAACATCCC TCAAGCTCG AGGAAACGAG TCGGATTAA	300
AGGGAAAATA TCTCCAAGC GATGCAAGAA AAAGGGTGA AGCTTTGAA TTGGATATT	360
AAAACCCCGC CTAAACCGCA AGCTCCAAG CCCACCACTA AAAATCTGGC TAAAACATC	420
AAGCATGTGG TCATGATAAG CTCAGGCAAG GGCGGTGTGG GTAAAGCAC CACCAGGTG	480
AATTAAAGCA TCGCTTTAGC GAATTAAAC CAAAAAGTGG GGCTACTAGA CGCTGATGTG	540
TATGGCCCTA ATATCCCTAG AATGATGGGC TTGCAAAACG CTGATGTGAT CATGGATCCT	600
AGCGTAAAAA AACTCATTCC TTAAAAGCT TTGGCGTTT CTGTGATGAG CATGGGGCTT	660
TTGTATGATG AGGGGCAGAG TCTCATTGG AGAGGACCCA TGCTCATGCG AGCGATTGAG	720
CAGATGCTAA GCGATATTAT TTGGGGGAT TTAGACGTGC TCGTGGTGGA TATGCCCCA	780
AGGAACAGGC GATCGGCAGC TCACGCAGCC CAAGGGTGC CACTCAGCGC AGGAATCACC	840
GTTACTACGC CTCAAATCGT GAGTTAGAT GACGCTAAAC GGAGTTTGGA CATGTTAAG	900
AAACTACACA TTCCTATTGC GGGCATTTGA GAAAATATGG GGAGTTTGT GTGCGAGCAT	960
TGCAAGAAAG AGAGCGAGAT TTTGGCTCA AATTCCATGAA GTGGATTATT AGAGGCTTAT	1020
AACACGCAGA TTGTAGCCAA GCTCCCTTA GAGCCTAAAG TCGTCTAGG GGGGGATAAG	1080
GGTGAACCGA TTGTGATTT TCATCCCACT AGCGTGAGTG CTAAAATTG TGAAAAATG	1140
GCAAAGGATT TGAGTGCTT TTAGACAAG GTGGAAGGG AAAAACTAGC CGATAATAAG	1200
GACATCCAGC CCACACAAAC GCATGTTAT TCGCAT	1236

(2) INFORMATION FOR SEQ ID NO:281:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...267

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:281

ATGGGTGTGG TGATTGGCGA GACCACAGAG ATTGGAGATG ATGTTACCAT TTATCATGGC	60
GTAACTCTGG GGGTACGGG CAAGTTAAAG GCGAAACGCC ACCCTACTTT AGGCAACCGA	120
GTGGTACTTG GGGCAGGGGC TAAGGTCTTG GGCGCGATTT GCGTGGGCGA TGATGTGAGG	180
ATTGGGGCTA ATGCGGTGGT GCTTTAGAT TTACCCACGG GTTCTACGGC TGTAGGTGCT	240
AAAGCCAAAA CCATCACAAA GGATCGT	267

(2) INFORMATION FOR SEQ ID NO:282:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 576 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282

ATGCTATCTT TTATAAGCGC GTTTGATAAA AGGGCGTTT CAATACGCCT TCTAACAGCC	60
TTGTTACTGC TTGTTAGTTT GGGTTGGCT AAAGATTAG AAATCCAAC TTTGTGGCT	120
AAATACCTT CTAAAATCA AAAAATACAA GCCTACAGG AGCAAATTGA CGCTTTAGAT	180
TCTCAAGAAA AAGTCGTTAG CAAATGGGAT AACCTTATT TGTTATTAGG CTATAACAAAC	240
GCTAACGTGA GCGATTTTT CAGGCTGGAT AGCACCTTAA TGCAAAACAT GAGCTTGGGT	300
TTGTCTCAAA AAGTGGATT AAATGGTAA AAACTCACGC AGTCTAAAAT GATCAATTAA	360
GAAAAACAAA AAAAATATT AGAGCTAAA AAAACCAAGC AGCAATTGGT GATTAATTAA	420
ATGATAAACG GCATTGAAA CTATAAAAAC CAACAAGAAA TAGAGCTTTT AAACACAGCG	480
ATTAAAAATT TAGAAAACAC CCTCTATCAA GCCAACCTT CCAGTCGCC CGATTAAATA	540
GYGATGYCA AGITRGAAW TTTAAAATC GCCAWT	576

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283

GTGCCGGCTG TTGGGGGGGC TTGATTGG ATCYTATAG YGATTTATGA GCTTTATCAT	60
GGGYATGTGA ATGAGGYAT TTTTAYGTT TTGATTCCA TTTTGTAAAT TGGTGTGTTG	120
ATTGATAGCG TGATCAAGCC AATTTAACG GTTTTATCA AAAAAGAACAT CTTTAAAACC	180
ACCCTTAAAA TCAATGAAAT ATTGATTTC TTTCTATGA TTGCTGGGAT TTCTCAATT	240
GGTTTTGGG GGATTATCGT AGGGCCTACC ATCACGGCGT TTTTATCGC GTTACTGCCA	300
TTGTATGAAA ATTACTTTAT TCaaaAGGAG CAAAAACAT GCGAATGT	348

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 489 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...489
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:284

GTGGTTGTCA TTATTTAGT GGTCGTTATC ATTCAAAACA GCTCTTCCTTT AAAAGAAGAG	60
AGAGACCAAG AACCGCCTAT TAAGCCGAC ACCAAAAATA ATTCTTTCAA TGAAACTAAT	120
CCTACAGAACG AAAAAAAAGTT AGAGCCAACG CCTAAATTAG AAGAAAAACAA CAAAGAACAA	180
GACAAGCAAG GCAAAGAACG GATCAAAGAA AATCCTAATA CCATTACAT TATCCCTAAA 240	
CGAGATATTG GGGTAGAAGT GATTGATTG GATGAGAAAA AAAACTCTTT TCAAAAGGTT	300
TTTAAAAAAA GTTATCCCTTT AGAGGCTAA ACCACCGCT TGGTGTACG CTTTGGGCAT	360
GGGCATCTTA TTCTTAAAAA CAACCATCAA GAACAAGATT ATAACGACAG CAAAACCTAGG	420
CGGTTTTAT ACGAGCCAAA TAAAGGTTA ACGCTCATCA ATGAGGCCCA ATACAAAGCG	480
CTCCAGCAA	489

(2) INFORMATION FOR SEQ ID NO:285:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...120
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:285

ATGGATGAAA TCTATCAAAT CGCTAAAAAT AAAACCTAA TCGTTATCGC CCACCGCTTA	60
AGCACCGATTG AACGCTGTGA AGTCATCATT GACATGAGCC AACACAAAGA CAATCTGGC	120

(2) INFORMATION FOR SEQ ID NO:286:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 135 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

270

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286

GTGGCGGGCA GCTTTATTAT TGCTCTTTTG AGCGTTTGTAG CGGATCAATT TGTGAGCGTG	60
TTTCAGCATG AAAACGCCTT GCAACGCCCTA TTTTCTCAAA ACGCCACCCA AAAACAAAAAA	120
AAGAAGAGTT TATGT	135

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287

ATGGTAGCTT TAAGCAACGC TCTTTCAAGG GTTTTGGTT CTGTGGCTGG CTATAAATTC	60
CCTTCTTTTA TCCAAAAAAAG CATCAACGCT CTTTATGTTA AGATCTTTAA AATTGATTTG	120
AGCGAGTTTG AGCCTTTAGA AAATTATAAG AGTTTGAACG CTCTTTCAT GCGCTCTTTA	180
AAAAAAAGAAC GCCCCTTTGA CAAAGCCCC ATATTGTCAT TGCGCTTGC GATGGCTTTA	240
ATCACTGAAT GCGTTTTTT AGACAACGAT AGCGCTTTAC AAATTAAAGG CATGCCCTAT	300
AAAGCGCATG AATTAGTGGG CGAAATCAAC CCCTTAAGCC CTCTTTTTC TATG	354

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288

ATGGCAGTGT TAAAAAAAGAT GATAGGTTTG GTGGCGGTTT TAAGCGTTTT ATTAGCCAGA	60
GACAACCCCTT TTGAGGCCCTGA AATCAATTC C AAGAATTTCG AAGGGGGCTT TAGCGGGATC	120
TATGATGACT ACCTCAAAGA AATCCATGTG GATTGCCCCA CGAGCCCTAG GATCTTAAA	180
AAAATCACGC TCACITTAACCA AGATATTGAT GGCTCTATCC ATTCTAAAGT CGTGGGTATT	240
GATAAAAGCA TTGATTGGCA CTACCCCTTA AAACCTTCCC AACACACCCCT TAATCAAGAC	300
GCCTTGGAAA AACGCTACCA GATCCAAGAT TTTGATTTT TAATGGAAA CAACACGATG	360
ATTTGCGTT CCCCTTATAA AATTTGCGC TCTTTGTTGTT TACTCAATCC TTATAGAATC	420
GTGTTAGACA CGCAAAAAGG CCCTTGGAT ATTTATCAA ACATGGATTAA AACCCAGAAG	480
TTTTTTCTC ACATTTAAAGT CGGCACGCAC AAAGATTATT ACCGCATCAC GCTCATTTA	540
GACGGGAAAT ACCGCTATCT TTTGGAAGAA AAAAACGGGG CGTATGAATT AAAACTGAAA	600

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289

ATGGCCGGAT TCACAAGCAT ATGGCATTGG GTCATTGTTT TATTAGTGAT TGTGTTGTTA	60
TTTGGGCTA AAAAGATCCC AGAATTGGCT AAAGGTTTAG GCAGTGGGAT TAAGAATTTC	120
AAAAAAAGCCG TGAAAGACGA TGAAGAACAG GCTAAAAACG AGCTAAAAAC CCTAGACGCT	180
CAAGCAACAC AAACCAAAGT GCATGAAACT AGCGAAATTA AAAGCAAACA AGAAAGT	237

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290

GTGCGTTTGA ATGCGGGCGGT TGTGGTGGAT GGCAAGTATA AAATCGCGCT CGAAGACGGG	60
GCAAACGCTT TAGAATACGA GCCTTTAACG GATGAATSGS TTAAAAAAAT CAACGYCCTA	120
GTCAAACAAG CCATGGTGA TAACCAAAT AGAGGCCGATG ACGTGGCGGT GAGTAATT	180
GAGTTAACCT CTATGGTGCC TATGATTGAC AACGCCACCT TGAGTGAAA AATCATCTAT	240
AAAACCCAAA AAATTTAGG TTTATTATG TTTTTAATCA AGGTATATTG GGTGTTTATA	300
GTGTTATTCA TTTTCTATAA AAAAGTGATC GTGCCCTTCGA CGAACGCAT GCTGGAAGTG	360
GTGCCTGATG AAGATAAGGA AGTGAATCC ATGTTTGAAG AAATGAACGA AGAAGAAGAT	420
GAGTTGAACA AACTCGGGCGA TTGAGGAAA AAAGTAGAAG ATCAATTAGG CCTTAATGCA	480
AGCTTTAGCG AAGAAGAAGT AAGATATGAA ATTATTTAG AAAAGATTAG AGGAACCCCTT	540
AAAGAGCGTC CTGATGAAAT CGCCACGCTC TTTAAACTCT TAATCAAAGA TGAAATCTCT	600
TCAGACAGCG CGAAAGGT	618

(2) INFORMATION FOR SEQ ID NO:291:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...294

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:291

GTGTGTTTA TATTGCCCTT TTGTTTAGGG GTTTAGGCA CGCAAATCTT TAAACAAGAG	60
ACCCAAGAC AGCTCCCTAT CGTGGTGGTG GATTGGATA AGACCACTAC AAGCCATCAA	120
GTGGCGTTG ATTAGGCGC AACGAGTGCG GTTGAATCA AATACCAAGT GACTAGCCTT	180
TCAGAAGCTA AACGCTTTTT AAACCTCGCT GAAGTGTATG GGGCGTTAAT TTGCTAAAG	240
GATTGGAGA GAAAATCAA ATGGGGCGA AAAGTGSAT TTGCCCTTT ATT	294

(2) INFORMATION FOR SEQ ID NO:292:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 591 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292

ATGAAAGGCT TATGGCTTGT AATCTCTTTA	60
TTCTATGTTT TTAACAATTTC	120
TAAGGGCGGT TTACAGAAA AAAGCGTTGC	180
GGCGTTTCTA AAGAGCTTTA	240
TCTTAAAACC GGCGTGCCTT TTAGGAAATGAG	300
TTTAAAGC AGCTCAAACC CCCTTGTG	360
GTATTCTTT TCTACCATGA CGCTCAAAAAA	420
ATAGAATTAG TGGCTAACCC TAAAGATTTG CTAGACACTG ATAAAATCTT	480
ATCGCTCCCT TACTCCCCAC AAACGCTAAA GAATACACGC CCCAAAGAAAT	540
TTCAGCCATG CTCATTAACG GCTATTGGT CGCAGTAGAT GCTTTAGCGG AAAAATATCA	591
ACGAAAATT TTAGCGCTCC TAAGGGAGTA ACTTTTGAA AGGTGGTTAT TTATATTTG	
TTATTGACGC TTTTGGGCGC GTTTGGGG CTTTATTTT TTAAAAAAATC T	

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293

ATGTGTTCTA AAAAATAAG AAATCTCATT TTATGCTTTG GTTTTATTTT AAGCTTGTGC	60
GCTGAAGAAA ATATCACCAA AGAAAACATG ACTGAAACGA ACACGACTGA AGAAAACACC	120
CCTAAAGACG CTCCCATTCT TTTGGAAAGAA AAACGCGCCC AAACTCTAGA GCTTAAAGAA	180
AAAAATGAAG TGGCAAAAAA GATT	204

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294

GTGCTAAAGA CATTATCCAT ACGATTAGTC ATACTTTAA ATTGCTCCCT AGCGACAAAC	60
GCTTGCAGTG GGGTGCAGAA ATTGCGCGAT GAAAGCCACC GGTATGCGAT AAACCTCCAT	120
AGATCCACTA AACCTAAAAA CATGAAACAA ATCCGCTTT TAAAAGAAAA GGGCATAGGA	180
GAAGGCCAGCG TGAAAAAATT GTTGGATTAT TTGGGAGTT TTGAAGCGAT AGAAAAGCG	240
AGCGATCAGG AAAAAACGC CGTTTAAAA AACGAAAA	279

(2) INFORMATION FOR SEQ ID NO:295:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...219
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:295

GTGGGCATTA TTAGGGGGAT TATCCACAGG CCAGAACTCA TTTTATTAGA TGAGCCTTT	60
AGCGCTTAG ATAGTTGAA TCGTAAGAAT TTACAGGATC TCATCAAAGA AATACACCAA	120
AATTCTTGCG CTACTTTCAT TATGGTAACG CATGATGAAA ACGAGGGCGCA AAAGTTAGCC	180
ACAAAAACCC TAGAAATCAA AGCCCTTAAA CAAGAGCAG	219

(2) INFORMATION FOR SEQ ID NO:296:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 804 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...804
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:296

GTGATTTTA TCGTACCGC TAATAATATT GACAGGATCC CAGCTCCTTT AAGAGACAGA	60
ATGGAATTAA TCAGCGTGTGTC CAGCTACACG CCTAGCGAAA AAGAAGAGAT CGCTAAAAAC	120
TACCTCATCC CCCAAGAATT AGAAAAGCAC GCCTTAAAGC CTAGCGAAGT GGATATTAGC	180
CATGAATGTT TGAAACTCAT TATTGAAAAA TACACCAGAG AAGCGGGCGT TAGGGATTAA	240
CGAAGACAGA TCGCAACGAT TATGCGTAAA GCGGCTTAA AATACCTAGA AGATAACCCG	300

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CACAAAAAAAG GGCGGACCAA AAAAAGCGAA GACAAAGATA AAAAAGGC GG AAATGAAGAA	360
AACGAAAAAA GAGGTGAGAG TAAAGATTT TGCGTCTCTA TCACGCCCTGA TAACCTTAAA	420
GAGTATTTAG AACCGATGGT GTTTGAAATT GRCCCCATAG ATGAAGAAAA TAAAATCGGT	480
ATCGTCAATC CTTGGCATG GACTCCAGTG GGCCTGATG TGCTTAAAT TGAAGCGGTT	540
AAGATTAGAG GCAAGGGGGA ATTGAAACTC ACCGGGAGTT TGGGCGACGT GATGAAAGAA	600
TCCGCCATTA TTGCTTTTC TGTTGTCAAA GTCTTGTGG ATAACGAAAC CTTAAAAGTC	660
CCTAAAATCC CTAGCGAGAC CGATGCAGAG AATWAGAAAA AGAAAAAAAGT GCTGAAAGTT	720
TWWAACGCTT ACGATTIGCA CTTGCATGTC CCTAAAGGGC TACGCCCTAA GACGGCCCCGA	780
GCGCTGGGAT CGCTATGGCG AGCG	804

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297

ATGGGGTGTGTT CGTTTATCTT TAAAAAAAGTT AGGGTTTATT CTAAAATGTT GGTTGCTTTG	60
GGGCTTCAA CGGTGTTGAT CGGTGCGCG ATGAATCCAA GCGCTGAGAC AAAAAAACCA	120
AATGACGCCA AAAACCAACCA ACCAGTCAA ACTCATGAA GAATGACAAC AAGTTCTGAA	180
CATGTTACGC CACTAGATTT TAATTACCGG GTGCATATTG TTCAAGCCCC ACAAAACCAT	240
CATGTTGTAG GTATTTAAT GCCACGCATT CAAGTGAGCG ATAATCTAAA ACCCTATATT	300
GATAAGTTTC AAGACGCTTT AATTAATCAA ATCCAAACTA TTTTTGAAAA AAGAGGCTAT	360
CAAGTGTGCA GTTTCAAGA TGAAAAAGCT TTGAATGTGC AAGATAAGAA AAAGATTTTT	420
TCCGGTTTGG ATTTGAAAGG GTGGGTAGGA ATCTTAGAAG ATTTGAAAT GAATTAAAAA	480
GATTCCCATA GTCCCAT	498

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...432

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298

ATGGATAGAA AACTCTTAAG ATTATACCAAG CCCTTAAACG CTTATTCTTA CAATAGCGAT	60
TCGTTTTTT TATACGATT TTCACGCCCT TTATCAAAA ATAGCGGCC GATTTTAGAC	120
ATAGGCTCG GGTGTGGGGT TCTAGGCTTG CTCTGCCTA GAGACAACCC GCTAGCGAGC	180
GTTCATTTAG TGGAAAAGGA TAGCAAATG CGCTTTGCT CCCAAAAAAA CGCCCTTAAA	240
TTCCCTAACG CTCAAGTGTG TGAGAGGAT TTTTAGATT TTAACCCCTCC GATTTGTAT	300
GATGCGATTG TGTGCAACCC TCCTTTTAT GCTTTAGGAT CTATTAATC TCAAATTAAA	360
GGGCATGCGA GGCACCAGAG CGAATTAGAC TTGCTTCTT TGGTGGCTAA AGTAAAAAA	420
TGCCTGAAAC CC	432

(2) INFORMATION FOR SEQ ID NO:299:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 141 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299

ATGTGAGTG CGTTGGTGT GCTGCCTTT ATGGAGTTT TTATTTTTT CAATTTCCG	60
TGTTGGCTCA ATCTTTCTT AGGGCAAACC ATTGGAGCGG TGATTTTTT CAAGTGGAT	120
AAGTTGATT TTTCTAAAAA A	141

(2) INFORMATION FOR SEQ ID NO:300:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 387 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300

ATGAATACTA TTATAAGATA TGCGAGTTA TGGGGCTTGT GTATTACTCT AACTCTAGCG	60
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CAAACCCCT	CTAAAACCCC	TGATGAAATC	AAGCAAATCC	TTAACAAATTA	TAGCCATAAG	120
AATTAAAGC	TCATTGATYC	GCCGACAAGT	TCTTTRARRAG	CGACACCGGG	TTTTTWCCCC	180
TCGCCTAAAG	AAACAGCGAC	CACGATCAAT	CAAGAGATCG	CTAAATACCA	TGAAAAAAGC	240
GATAAAGCGG	CTTTGGGGCT	TTATGAATTG	CTAAAGGGGG	CTACCACCAA	TCTCAGTTTG	300
CAAGCGAAG	AACTCAGTGT	CAAGCAAGCG	ATGGAAGAAC	CACACCATCG	CCAAAGCGAT	360
GTTCITGCCT	ACTTGAAACG	CGAGTTA				387

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301

ATGGTTTGT	TTCTATCCAT	TTTTAAAAAA	AGCTTTAATG	ATTTTTTAAG	CGCTAGAATG	60
CTTTAATCA	ATCTTGGCCC	TATCCTTTG	AGTTTGGCGT	TTTTGGAGC	TATCTTTAT	120
TACAATGGCG	GGAGTATTGT	GAATTATTC	CAAACTTTAT	TACCGCAATC	TTTGAATGAT	180
TACGCTCATT	CTCAAGGCTT	TTTTGCCGT	GTGTCGCAT	GGGTTTTAA	AGCGTTAGTG	240
TATTTCTTA	TTTTGGAT	CGTAATTCTT	TTGAGTTAG	TCATCAATAT	TTTGCCTCT	300
ATTTTACA	CCCTTTAGT	GGTCTCTTAT	TTGCACAAA	AATATTATCC	CCATGTCGTT	360
TTAGAAGAAT	TTGGCTCTAT	CCTTTTTCT	ATTAATATT	TTTAAATATC	GCTCACTTT	420
ATGCTTTAT	TCTTAGCGGT	TTTAACGCC	CTTATTTCA	TTCCCTTTAT	AGGGGTCTTT	480
GGGGCTTTT	TTCTATAGT	CCCGCATTT	CYCTTTCA	AAAACACCAT	GAGTTGGAT	540
ATAGCCAGCA	TGATTTCAA	CCATCAAAGC	TATCAAATT	TACTCAAACA	GCACCGATTG	600
AAGCATTATC	TTTTTCGTT	TTTTGCTAT	CTTTTTCCCT	TGATTCTTT	TTTAATT	660
TTTGCACCT	TGTTGAAAC	CCTAAYGCTA	ACGCACTACY	TTTTATCTT	AAAGAGAAA	720
					GAATGC	726

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

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(B) LOCATION 1...378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302

ATGCAATACG CTAACGCTTA TCAAGCCTAC CAGCATAACC GAGTGAGTGT GGAATCCCCG	60
GCAAAACTCA TTGAAATGCT TTATGAGGG ATTTTAAGAT TTTCTTCGCA AGCCAAACGC	120
TGTATTGAGA ATGAAGACAT TGAAAAGAAG ATCTTATTATA TTAATAGGGT TACGGATATT	180
TTCACGGAGT TGTGAAATAT TTAGACTAT GAAAAAGGGG GGRAAGTGGC CGTGTATCTT	240
ACAGGCTTAT ACACCCATCA AATCAAAGTT TTAACGCAAG CCAATGTGGA AAATGACCGG	300
AGTAAGATTG ATTTGGTGT GAATGTGGCT AGGGGTTGT TAGAGGCATG GAGGGAAATC	360
CATTCAAGATG AACTCGCC	378

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303

ATGATGTTTG ATAACACGCT TATCAATTAA TTTGAGACAG CGCCTCTTTT AACYTCGCTT	60
TTAGCTGGGA TTTTAACITTT TTTAACCCCT TCGCTGTTGC CTTTGATCCC GGCGTATATG	120
TCTTATATTT CGCAAATTTC TTTAGAGGAT ATTAAGATG GTAAGGCTAA AAGGGTTTCG	180
GTTTTTTAA AATCCTTGAT GTTGTGCTG GGGTTTCGC TCGTGTGTTT GGGCGTGGGC	240
ATGTCATATGG CCAAGCTTAT CCATAGCTTT TCGTTTCCT GGGTGAATTA TATCGCTGGG	300
GGGATTGTGA TCCTTTTGG TTTCGATTT TTAGGGTGT TTCGTTTGC ATTTTGAT	360
AAAACCCAAA GCGTTGGTTT AGCGAGAAA TCTAACAGCA TGCAGCGCTT TACCCCTTTC	420
TTTTGGCA	429

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

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(B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304

GTGCTGGTGG	TGGGCAAACC	CAACGAAAGC	TATGCAGATA	CCCACGCCCG	CATTGAGCAT	60
TTTATCAAGC	TTGTAGATTT	TAAGCCGAA	ATCGTTTTA	TCAATGAAGA	TAATTCTAGC	120
GTAGAACGCTT	ATGAAAATTT	AGAGCATTG	GGTAAGAAAA	ATAAGCGAT	CGCTACCAAA	180
GATGCCGGT	TAGACTCTTT	GAGCGCTTGT	AGGATTTAG	AGCGCTATTG	CCAGCAGTT	240
TTAAAAAAGG	GC					252

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305

ATGCGGATAT	TAATTCTCAA	AAACAAGCCA	CCAACGCTAC	GATCAAAGGC	TTTGACGCC	60
TCTTGGGCTA	TCATTTTTC	TTTGAAAAAC	ACTTTGGCTT	ACGCCCTTTAT	GGGGTTTTTT	120
GAATACCTC	ATGCCAATT	TATTAAGCTT	AAAAACCTA	ACTATAATAG	CGAAGCGCG	180
CAAGTGGCTA	GTCAAATTCT	TGGGAAACAA	GAAATCAATC	GTTTAACAAA	CATTGCCGAT	240
CCCAGAACTT	TTGAGCCGAA	CATGCTCACT	TATGGGGGGG	CTATGGACGT	GATGGTTAAT	300
GTCATCAATA	ACGGCATCAT	GAGTTTGGGG	GCTTTGGCG	GGATACAATT	GGCCGGCAAT	360
TCAATGCC	TGGCGASACC	GAGCTTTGAG	GGCATTTAG	GGGAACAAGC	CCTTGTGAGC	420
AGAAAGCCAC	TTCTTCCAA	TTTTTATTCA	ATGTGGGGC	TCGCM		465

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...513

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306

ATGAATGTCA	AAAAAAAGGA	AAAGCCACAA	AGTGGAAAGA	TTGATAGGGT	GGATTGTTG	60
GAGAAAAC	TTG	GGAAAGAAAA	CACTACTT	TTAACAGTA	TAGCTATGGG	120
CAATTAGCGA	TCCC	CATTCC	TGGAGIT	GTGCTCAT	GGGGCTT	180
ATGAGTAAA	CTTTT	TATGA	TGTCTCG	ACGAT	TTCA	240
CAAAGGC	GTA	TTGAGATT	AAAAGAAT	TCGAGAG	TCAGACAG	300
CAAATCAAT	TTAAT	GAAGT	TTTGAGC	GGACT	ATTTA	360
GAAAGTT	TTG	AGCTG	GAGGC	TATTC	CATG	420
GTCAATAACA	AGATCCAAGA	GGGGATGG	CAAGAGTT	TGTTG	ACAA	480
TGCTGGGAAT	TTATCACT	AG	CCGTAA	AAGAG	GGT	513

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307

ATGTGGCCGT	RAAAGCT	TTT	TCTAAA	ACCC	CTAAAAGAAA	CGAGCCTT	TGC	CCTTGTGG	GA	60
GTGCC	AAAAAA	ATATAA	AGAT	TGTGCG	CTA	AAAGCG	GGCC	TAAAAG	GGC	120
AATAGATC	CCT	TAATCT	TTTT	CCTT	ATCA	CG	TATT	TGATA	AA	180
TTCATTAG	TA	CACTG	CCTT	GT	AGCCT	TT	TTGCGT	GG	CGGTG	240
ATTGTGG	CTA	TGCGAT	CAT	GAAC	GGCAT	AG	TAAGGA	AT	TG	300
ATGAACTACC	CCTT	AAACG	CCT	CTATAC	ACACA	AG	CCCTT	ATG	GGCGA	360
CAAC	CTT	TTAG	AAA	AAAAG	TT	CCCTA	ATT	TG	AGAAGTGG	420
GCC									TT	423

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

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(B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308

ATGGTATCGT TGCTTGGCCG GCTTAAACGC ACCCCTTGCA CTAATCGCTT TTATCTTAAA	60
GCACTACTAT TTGCTATATT CTATCATGCA GTAAATAATT TTCTAACGCA ATGCCGCC	120
CATCAAGTCC GGGAGTTTT TTCATCACGA CATGCACAGG GATGGAAGCG AGAAACGCTC	180
CCATGCGCCC TTTCGTTTCA AAACGCGCTC	210

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309

GTGCATCATT TGYAACGGCT TTTAGACTCA GGCTCTGAAA GGTGTATAGG CTGTGGCTG	60
TGGAAAAAGA TTTGCACGAG CAACTGCATA AGGATCATCA CGCATAAGGG CGAAGACAAC	120
CGCAAAAGA TCGATTCTTA CACGATCAAT TTGGGGCGTT GCATTTATTC CGGGTTGTGT	180
GCGGAAGTTT GCCCAGAAATT GGCATCGTT ATGGGAATC GTTTGAAAA CGCCAGCACC	240
CAACGCTCCC AATACGGCTC TAAAACCGAG TTCTAACGA GCGAACAAAGA CGCTAAAAC	300
TGCTCGCATG CCGAATTTC AGGCTTTGGT GCGGTAAGCC CTAATTATAA CGAACGCATG	360
CAAGCCACCC CTTTAGATTA TGTCCAAGAA CCTTCAAAGA AGAATCCAA AGAAGAGTTT	420
YCCACAAGCC CAGAAAGCCA TAAGGGAGAT GAAAATGTT	459

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310

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ATGGCTATTT GGGGGTGGTG TTTTTTATTT TTATCGTCCT TGATGTGGGG TTCAAGCATG	60
CATGAGTTGG TTTAAGATC CCAAGCTTTA GGGTTTGAAA CGCGCTTAGT CCAGTGGAT	120
TTATCGTTTT CTATGAAAG GTTATTCT AAAACCAAAC GCTCTTAGC GGTGTTAGAA	180
GAATTGATT GGTTAAATTTC TGGCTTTGAT TTTTCACGCT TGAACGTTGA AAATGACACT	240
CTGGAATTAC TCAAAGCGCT GTATTTAAA TTAGAAAAAT TAGAGAGCCT GCTTTTAAAAA	300
GAAAATTAC TTGAATTGGA GCAAAAGGAT CGCATCATCG CTTTAGGGCA TGGGCTAGTT	360
TGCCTAAAAA AACAAAGCCT GATAGCCCT CAAACTTACT ATGGCCGTT CGTGTAGAG	420
GGGAAAATCC TAGCCTTTTT TGGCGTGGCA AGGGATAAAG ATTTTTTAGA AATCACTCGC	480
ATGCACGCCT TAGACATTAA GCGTTATGAT TCCTTCATTG TTGATAGCGA AAGAAAAGGC	540
TTGAAATTA	549

(2) INFORMATION FOR SEQ ID NO:311:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...201
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:311

ATGCCGGAAA ATTCTAAACT ACAACCTGCT AAGTTAGGGA AAAATTTTGA CCCTGTGGAT	60
CATTCTAACAA GGAATTTTTT CTTTCTCTC ATTCTGTCTG TATTGTTACA CTGGTTGATT	120
TATTTTTAT TTGAACACAG AGAAGATTT TTCTTCAA AACCCAAGCT CGTTAAATTA	180
AATCCGAAA ATTATGGT Y	201

(2) INFORMATION FOR SEQ ID NO:312:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 519 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...519
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:312

GTGTTTTAG TTCAATCGTG GGCTTGGC TTGAAAATAG ACAGCCTGTT TTCTCTTTT	60
AGCGTGGTA AAATCCCTAG CGGATCTAA GATCCCTTTG CGTTAAGGCC TTTGAGTTTT	120
GGGCTATTGA AAATCATCGC GCATTACGGG TTAGAATTG ATTTGAAAGC GGATTTAAAA	180
AACCTCTTTG AAAAAGTGGG CGTTTATCAA AGCTTGTGATT TAGAGGTTTT AGAAAAGTTT	240
TTACTGGAGC GTTTTCATAA TTAAATAGAT TGTAACCTCT CTATTATAAG AAGTGTGTTA	300
AACACCAACG AGCGAGACAT TGTTAAAATC ATTCAAAAAG TCAAAGCCTT AAAACGCTTT	360
TTAGACAATC CTAAGAACGC TCAAAAAAAA GAGTGTGCTT TTAGCGCTTT CAAACGATTA	420
GCTAATATCA ATAAAGACAG AAACCTAAC GAATCAAGCG GGTTTTCTAC GAGTCTTTTC	480
AAAGAATTAC AAGAGCATGC CCTTTTGAA GCGTTCAAC	519

(2) INFORMATION FOR SEQ ID NO:313:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 777 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313

ATGAGCTTTG CTCCAAGCGT TATGGCGGGC TTCTTGTTTT GTGCCGGCTC TTGCTCGCTT	60
CGCTTCCTA ATTATTCTAA AATCATTTCC ATAGATGTGG ATACGGTGTGTTTTAGCGCAT	120
GTTGCAAGCG CTTATTTTGC GCTGGATAAT GAACCCACTA AATTGCTTGG CATGGTGAGA	180
GACACTTTTT CCCACCTTCC TTGAGGCC TTTTGTGATT TTTGCGAACG CACATGCAAG	240
AATTTTAAAA TTGATCTTTT GCGCTTTAGC CAAACGAAT TAAAACGCAT CCATCAGGGC	300
TTAACATGG GCTTTTGTT GGCGAATTAA GATTATGGC GCGAAAATGG TTTGAAAAA	360
ATCGCTTTAG AGTTTTGAA AACTAGGGGA AAGGATCTTT TCTACCCCTGA GCAGTGTITA	420
ATCAATATGG TGTTTTAGA GCGTATTTTA GAATTGCGCTA TTCAATTATAA TTGCTATTCT	480
GATTTTTC AAGAGCACTA CCCTAAAGT ATCATCATGC TCCATTTCAT CAAATACAAG	540
CCGTGGCGTT CTGTCAGITC TTGAAACGGG CGTTGATTG CTATGAAGC TGAAGCGAGT	600
TTTGGCTCG CCAACCTTTT TTGCAACCCCT TTTAAAACG ATTTTTTAA AGAACGCCCTT	660
GAAATGGCTA AAGACCAACA AATGCAATCT TTAAACACC ACATCCGATC AAAACGATT	720
AGGGATTATT TTATTTTAG GATAAAAAAT ATTTGAAAA AAGTTTTCCA ACTCTCT	777

(2) INFORMATION FOR SEQ ID NO:314:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 582 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314

GTGATTGTTT GCAGCGCGGC GGGGTTGAGC CATTTCCTTG GGTTTCTAT GTCTTGGGG	60
GCGTTCATTG TGGGCATGGC GATTTCTAAA TCGCGCTATA AAATCAATGT CCAAGAAAGAA	120
TTCGCGCAAT TAAAAAACCT CTTTTTGGCC CTTTTTTCTA TTACGATAGG GATGCAGATT	180
AATGTGAGTT TCTTCATGGA GAAATTCTTT GTCGTCATCT TTTTACTCAT TTTAGTGATG	240
AGTTAAAGA CTTTTATCAT TTATGCGCTA TTGCGTTTT TTAGAGACGC TAAAACGCC	300
ATCAAAACCGC CTCTTCTTT GGCACAAATT GGGGAGTTTT CTTTCGTGAT CTTTTAAAT	360
TCAGGCTCGC ACCAGCTCTT TAATTGCAA GAAAAAAAAG GGATTCTTGG TTTTTACAC	420
CAAAAAAATA TCTTAAATAT TGCTAAATAT GACATCCACC AGCTCCCTAT TCTCATGGTG	480
GTCTTTCTA TGTTAGCAAC CCCTTTATT TTAAAATACC TAGAATCTAT CGCTCAATT	540
ATTTTGCACC AAAAGAGCCA AGAAAACGAG CGGGCTAAAA AA	582

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315

ATGTTCTATC TTATCAATAC AGGAGTCCT CATTAGTGG GATTTGTGAA AAATAAAGGG	60
TTATTAATT CTCTTAACAC ACTGGAATTA AGGGCTTAA GGCATGAATT TAACGCTAAT	120
ATTAACATCG CTTTTATAGA AAATAAAGAG ACGATTTTT TACAAACTTA TGAGAGAGGG	180
GTTGAAGATT TCACGCTAGC TTGCGGGACA GGCATGGCAG CGGTTTTAT CGCCGCGCGC	240
CTTTTCATA ACACCCCTAA AAAAGCCACT CTCATCCCTA AAAGCAACGA ATTTTTAGAG	300
CTTTCTTAA AAAATGATGG AATTTTTAT AAAGGAGTCG CGCGTTATAT CGGCATGAGC	360
GTTTTAGGCA TGGGTGTTT TAAAAATGGG TGTTT	396

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316

ATGATTAAAG CGATTGATAT TTCTCATGST TTTGAAAARC CTCTTTRTRA TGGCGTGAAAT	60
TTGCCCATTA AACCCAAAGA AAGCYTGGY ATTTAGGCG TGAGCGGGAG CGGTAAAAGC	120
ACGCTTYAA GCCATITGGC CACCATGCTA AAACCGGATA GCGGAACAGT CAGTTTGTAA	180
GAACACCAAG ATATTTATGC CCTAAATTC AAAAGCTT TGGAAATTGCG GCGCTTAAAA	240
GTGGGCATCG TTTTCAATC GCATTACCTT TTTAAGGGTT TAGCGCTTT AGAAAACCTG	300
CAAGTCGCTT CAATCCTAGC CAAGCAAGAA ATAATCATT CCCTTTTAGA ACAATTAGGC	360
ATAGCCCACA CCCTAAAACA AGCCGTGGC GAATTGAGCG GCGGCCAGCA ACAACGCTTA	420
AGCATCGCCA GAGTGCTTTC TAAAAAACCC CAAATCATT TCGCTGATGA ACCCACCGGG	480
AATTAGACA CCACTAGCGC TAATCAAGTC ATCAGCATGC TGCAAAATTAA CATTACAGAA	540
AACGAAGGGG CGTTAGTCTT AGCCACGCA GATGAGCATT TAGCCTTCAC TTGCTCTCAA	600
GTCTATCGCC TAGAAAAAGA ATCTTGTATT AAGGAAAAA	639

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317

ATGCITGATA AACGCATTA AACGCTTTTA CTTTTTTTG GTCTTAATAT GGTGTGTTTG	60
AGCGTGAGTT TTACCAATAA GCCTCAATTG TGTTTTGGT TTTTAGTGTGTT AGGTTGTTAT	120
TTAGTTTATG AGTGGCAAAA GAAACAAAAA AAAGATTTTC AAAGCGCTAA AAGTTTGAAA	180
TTTGACAGCG TTAGCGAATT AGAAAAGGAT TTTGAACATG GAAGTAAC	228

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 207 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318

ATGAAAACAA TAAAAATGG TATTATGATC GGCAACTCG GTGCGTTGTT ATTGAGCGGT	60
TGTTCTAGCT TTGATGCTCA GCGTTTCGCT TGTCTCCCTA AAGACCATTG TTCAAAAGAC	120
GCTTCTACCA AAAAGAAGC GCAATACATT CCTAAGGGCT TTTTGACCC TTATTCTTCT	180
AACTTAAACC ATGGGATTG TACATTG	207

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 570 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319

ATGGAGCTTA TTTTAGGCTC TCAATCCAGC GCTAGGGCGA ATCTTTTAAA AGAGCATGGG	60
ATTAAGTTTG AACAAAAAGC GCTCTATTTT CATGAAGAAA GCCTAAAAAC CACAGACCT	120
AGGGAGTTTG TCTATTTGGC GTGCAAGGGG AAATTAGAAA AAGCTAAAGA GTTACTTGCG	180
AATAATTGCG CTATCGTGGT GGCTGATAGC GTGGTGAGCG TGGGTAATCG CATGCAACGA	240
AAAGCTAAAA ACAACCGAGA AGCCCCTGAA TTTTTAAAC GCCAAATGG CAATGAAATA	300
GAGGTTTTAA CTTGCTCTGC ATTGATTTCT CCTGTGTTGG AATGGCTGGA TCTATCGTT	360
TTTAGAGCGC GTTTAAAGGC GTTTGATGTC AGCGAAATAG AAAATATTT AGAGAGCGGT	420
TTATGGCAAG GAAGTGCAGG CTGTGTGCGT TTAGAGGACT TTCATAAGCC TTATATTAAGA	480
AGCTCAAGCA AGAATTTAAG CGTGGGGTTG GGGCTGAATG TGGAAGGGCTT GTTAGGGGCA	540
CTAAAATTAG GGGTTAAACT TTCATTATTA	570

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 405 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320

ATGCTTATTT TAGGACACCC	TTTAATCCCT AGCGCTCGTT	TTGTTTTCAT TAAAAACACC	60
GATGCTATTC ATTCCAGCGC	CAATAACGAT ATAGTGTGTT	TTGAAGCAAA CCCAAAAAAT	120
TTGGAATTAG CCCAATATTG	CTGTGAAAAT GGCCTCCATT	TTAGCGTGAT CTTTTTATCG	180
CACAAGATAG AGACGGACAC	CTTTTTTTTA TTCAACGCTT	TCAAACCGCT CTATTGTATT	240
TTTAAGGATA TTAAGCAAGC	CATACTGCC CAACAAACACG	CCACTAATTAA CTTGTTAGAT	300
AGCAAATCT TGTTTCTAT	GGATTTAAC GATACAGAGT	CATGGGAGAT TTGCGCTAAA	360
AATCAAATAG ATGGTGTCA	TTCTAAAGAT TCACCTCTTT	TGAAA	405

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321

ATGAAAAAAA GATTGAATAT	AGGGCTTGTG GGTTTAGGAGT	CCGTGGGGAG CACGGTCGCT	60
AAAATCTTAC AAGAAAATCA	AGAAATCATT AAAGACAGAG	CCGGCGTGGAA ATTAAAATT	120
AAAAAAGCGG TTGTCGAGA	CGTAAAAAAA CACAAGGCCT	ATGCTTTTGA AATCAGTGAT	180
GATTAGAAA GCGTGATAGA	AGATAAAGGG ATTGATATTG	TCGTGGAGCT TATGGGTGGG	240
GTGGAAGCGC CTTATCTTT	AGCTAAAAAA ACTTTAGCCA	AACAAAARGC CTTCGTTACA	300
GCCAATAAAG CCATGTTAGC	GTACCAACCGC TATGAATTAG	AACAAATCGC TAAAAACACC	360
CCCATAGGCT TTGAAGCGAG	CGTGTGGGG GGTATCCCCA	TTATCAAGGC TTTAAAAGAC	420
GGCTTGAGCG CTAATCACAT	CCTTCTTTT AAAGGGATT	AAACAGGCAC GAGCAATTAC	480
ATTTTAAGCC AGATGTTAA	AAATCAAGCG AGCTTAAAGG	ACGCTTGTAA AGACGCCAG	540
CATTAGGCT ATGCCGAATT	GAACCTGAA TTTGACATTA	AGGGCATTTGA TGCGGCGCAC	600
AAATTATTGA TTGAGCGTC	TTTACGATGATG CGAAATTAGA	AGAAATCTTG	660
ATTGAAGGCA TTGAAAAGAT	AGAGCCAGAT GACATGAAAT	TTGCAAAAGA GTTTGGTTAT	720
AGCATCAAAC TTTAGGCAT	CGCTAAAAAA CACCAGGGAT	TGCAT	765

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

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- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...729
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:322

ATGCAAGAAA AACGACTTAA AGCCATTCAA AACAAAATCG CTTCTTGGAT CAAGGAAATT	60
GAAAGCGGCT TTATAGATGC ATTGTTTCT AAGATGGCC CTTCAAAGAT GCTCGCCTCC	120
AAACTCATGC TCGCTTGTG AGACGAAAAA ACAGACGCTA TTTTATTAGA TAAAGCGCTC	180
AATTGTCG TGATTGAGA AATGATACAG ACCGCTTCTT TATTGCATGA TGATGTGATT	240
GACAAGGCGA CCATGCGCCG AAAGCTCCT AGCATTAAACG CTCTTTTGG GAATTTAAC	300
GCCGTGATGC TTGGGGATGT GTTTTATTCT AAAGCCTTTT TTGAGTTGTC TAAAATGGGC	360
GAATCCATCG CTCAAGCCCT CTCTAATGCG GTTTAAGGC TCTCTAGGGG CGAGATTGAA	420
GACGTGTTTG TGGGGAAATG TTTTAATAGC GACAAACAAA AATACTGGCG TATTTTAGAA	480
GACAAGACCG CCCATTTCAT AGAAGCGAGC TTAAAAGCA TGGCGATTCT TTAAATAAA	540
GACGCCAAA TGTATGCGGA TTGTTGGTTG CATTGGCA TGGCGTTCA AATCATTGAT	600
GATTGTTAG ACATCACTCA AGACGCCAAC ACTCTAGGTA AGCCCAATTIT TAGCGATT	660
AAAGAGGGCA AGACCCTCT ACCCTACTTG CTTTATATG AAAAATTGAA TCAGCATGAA	720
CAGGGCTTT	729

(2) INFORMATION FOR SEQ ID NO:323:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 756 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...756
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:323

ATGTTAGGGA AAAAACGCA AGAACTTTG ATTGATGAAA ATTTGGTTGG GGGTGTGATA	60
GCCCTTGATA GATTGGAAA ACTCAATAAG GCCAATAGGA CTTTCAAAAG GGCTTTTAT	120
CTCTCTATGG TGCTCAATGT CGCGCTGTA ACGAGTATTG TGATGATGAT GCCTTTGAAG	180
AAAACAGATA TATTTGTTA TGGCATTGAT CGATACACAG GAGAATTAA AATCGTCAA	240
CGCTCCGATG CTAGGCAAAAT CGTCAATTCT GAAGCCTTG TGGATAGTGC AACTTCAAA	300
TTTGTCTCAT TGCTGTTGG TTATAGCAAA AATTCTTGA GGGATCGCAA GGATCAACTA	360
ATGCAAGTATT GCGATGTGAG TTTCCAAACC CAAGCAATGA GAATGTCAA TGAAAATATC	420
AGACAATTG TAGATAAAAGT CCGAGCAGAA CCTATCATTG CTCACACAT ACAAAAGAGAA	480
AAAGTCAAAATAGTCCCTT AACGAGATTA ACATTTCA TTACCATCAA AATCACGCC	540
GATACAATGG AAAATTATGA ATATATCACT AAAAACAAAG TAACATTAA TTATGATT	600
GCTAGAGGTA ACTCTCTCA AGAAAATCTT ATCATCAACC CTTTGGCTT CAAAGT	660
GACATTCAAA TCACGGATT ACAAAACGAA CAGACAGTAA CGAATTTT GAGAAAGATT	720
AAAGAAGTGG AATCAAAAAA TAAGGCATTA AATAAA	756

(2) INFORMATION FOR SEQ ID NO:324:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324

ATGAGAGCGA TCGCTATTGT TTTAGCCAGA AGTTCAGTA AAAGGATTAA GAATAAAAAT	60
ATGATTGATT TTTCAATAA ACCCATGCTC GCTTACCTA TTGAAACAGC ACTAAATTCC	120
AAGCTCTTG AAAAGCTTT TATCTCTAGC GATAGCATGG AGTATGTCAA TTTAGCCAAA	180
AATTATGGGG CGAGTTTTT GAATTTACGC CCTAAAAATT TGACAGACGA CAGGCCACG	240
ACTTTAGAAG TGATGGCCTA TCACATGAAA GAATTAGAAT TAAAAGATGA AGACATTGCG	300
TGTTGTTTGT ATGGCGTTTC AGTATTTTA CAAGAAAAGC ATTACAAAA CGCTTTGAA	360
ACTTTAAAC AAAATCAAAA TACGGATTAT GTTTCACAT GCTCTCCCTT TAGCGCTTCG	420
CCTATCGTTTC TTTTACGCTT GAAAACGGCG TTCAAATGGC TTTTAAAGAG CATTCAAACA	480
CGCGCACGCA AGATC	495

(2) INFORMATION FOR SEQ ID NO:325:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325

ATGACTAATC AAGCGAGCCA TTTGGATAAT TTTATGAACG CAAAAAATCC CAAAAGTTT	60
TTTGATAATA AGGGGAATAC CAAATTCATC GCTATCACAA GCGGTAAGGG GGGCGTGGGG	120
AAATCCAACA TTAGCGCTAA TTTAGCTTAC TCTTATACA AGAAAGGTTA TAAGGTAGGG	180
GTATTTGATG CGRATATTGG TTTAGCGAAT TTAGATGTCA TTTTGGGGT GAAAACCCAY	240
AAAATATCT TGCATGYCCTT AAAAGGCGAA GYCAAATTGY AAGAAATCAT TTGCGAGATT	300
GAACCCGGGC TTGCTTAAT CCCTGGGAT ACCGGCGAAG AAATTTAAA ATACATCAGC	360
GSSGCAGGAAG YTTTCGATTC ATTCTTAGAT GAAGAGGGGG TTCTAAGCGC TTTAATTAT	420

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ATTTTAATTA ATACATTTC TAAAAATTG GGTCCACTAT CTCAAACTTT TCTTAATTTC	480
CAGTCATTTC TTTTATTTC TATTCAATCT CCC	513

(2) INFORMATION FOR SEQ ID NO:326:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 186 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...186

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:326

ATGCAGCAATT TAGTCTTAAT CGGTTTTATG GGGAGCGGTAA AAGCTCTCT AGCACAAAGAA	60
TTGGGGCTGG CTTTGAAATT AGAAAGTGTG GATAACGGATA TGATCATTTAG CGAGAGGGTG	120
GGCTTGAGCG TGAGAGGGAT TTTGAAAGAG CTTGGCGAAG ACAATTTCAG GATGTTTGAA	180
AAAATT	186

(2) INFORMATION FOR SEQ ID NO:327:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 654 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...654

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:327

ATGAGCATTAGGAAATTT AGAGCAAGTT AGAACGAAT TTAAAGCGA TGAAAAGCTT	60
TTAGAAGGAG CGTTTAGATT AGAAAAGTTT TTCAACGCT ACAAGTGGGT GTTGTGTTT	120
ATCGTGGTGG CTTTTATCCG TTATTTAGGG GATAACAAAT TAACAGATTA TAAGCATGAG	180
CAAACGAGAG AGCGGATCAC TCAAATTAT AATGAAGTGC TAGAGAGTCC TAATAATATA	240
GCCTTGCAAA AAAGATTGAA AGAAAGTCGCC CCAGAGTTGT ATGACTTGTA TCAGTTGCC	300
AGAGCGAGTG AGAGGAACGA TGCAAACGAG TTAAAGGC TTTCGCAATC TTCTAATGAA	360
ATCGTTAAAG CGTTGCCAA ATATTCTAC GCATCGCTCT CTAGAGATAA AACCTGCCTT	420
GAAAAAAAGCC CCATTCTTAA AGAAATGAGC GCTTACAAG AAGTGAACCTT GTGTATGAA	480
GAAAATTCTA AAGACGCAAT CAAAAAGCG CATCAAAGTT TATCAACTAT CCCTCTAAGT	540

TCTTCACTCT ATGCTATAAT CTCTGTTTA AAACATTATG GAATGTTAGA AGATATTCA	600
CAAAACCCCTT CCAAACCAAC CAATCTAAAG AAAGAAACCA TTCAAGGAAC GCAT	654

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328

GTCGATTTCA ATCAGGTTGT TCTCCAAAAA GGCCTGGCG CGATTTAGT CGCACCAAAA	60
GGGCCCGGGA GCGCTTTAAG AGAAGAAC CTTAAAATA GGGGTTTATA CCATCTAAC	120
GCCATAGAGC AAGAAAGCTC AATTCTAAC GCTAAAGCGG TGGCTTTAAG CTATGCTAAA	180
GCGATGGGTG GGGGGAGAAT GGGGGTTTA GAAACGAGTT TAAAGAAAGA ATGCGAGAGC	240
GATTATTTCG GCGAGCAAGC GGTCTTGTC GGGGGTTAG AAGTCGATCG TAAGAATGGG	300
GT	303

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329

ATGAAAAAAAT TTTTTCTCA ATCTTGTGA GCTCTTATTA TCTCTATGAA TGCCTATCT	60
GGCATGGATG GTAATGGCGT TTTTTAGGG GCGGGTTATT TCGAAGGACA GGCGCAAATG	120
CATGCGGATA TTAATTCTCA AAAACAAGCC ACCAACGCTA CGATCAAAGG CTTTGACGCG	180
CTCTGGGCT ATCAATTCTT CTTTGAAAAA CACTTGGCT TACGCCCTTA TGGGGTTTT	240

(2) INFORMATION FOR SEQ ID NO:330:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1341
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:330

ATGCTAAAAA AGATTTTTTA TGGTTTATTC GTTTTATTTT TGATTATCGT AGGGTTGTTG	60
CCCTTCTTG TCGCTCAAGT TTGGGTAACT ACGGATAAGG ATATTGCTAA AATTAAAGAT	120
TATCGCCCCA GTGTCGCTTC ACAGATTITA GACAGAAAAG GGCCTTGTAT CGCTAATATT	180
TATGATAAGG AATTTCGTTT TTATGCGGT TTTGAAGAAA TCCCCCCACG ATTGTTGAA	240
AGCCTCTAG CGGTAGAAGA CACCCTCTT TTTGAGCATG GGGGGATCAA TTTAGACGCT	300
GTCATGCGCG CTATGATTA AAACGCTAA AGTGGTCGTT ACACTGAAGG GGGTAGCACT	360
CTAACCCAAAC AACTCGTTAA AAACATGGT CTCACACGGG AAAAACCCCT AACAGAGAAA	420
CTCAAGAAG CTATCATCTC CATACTGCATT AAAAAGTCT TAAGCAAAGA AGAAATTITA	480
GAGCGTTATT TGAACCAAAC TTTTTGGG CATGGTATT ATGGCGTGA AACCGCAAGT	540
TTAGGGTATT TTAAAAAACC CCTTGACAAA CTCACGTTA AGAAATCAC CATGTTAGTC	600
GCCTTACCTA GGGCTCCAAG TTTTATGAC CCTACCAAAA ATTAGAATT TTCACCTCT	660
AGGGCTAATG ATATTTAAG GCGGTTGTAT TCTTTAGGY GGATTCTTC TAACGAGCTC	720
AAATCCGCTC TCAATGAAGT GCCAATCGTC TATAACAAA CTCCACGCA AAATATCGCT	780
CCCTATGTCG TGGATGAAGT GTTGAAGCA TTGGATCAAT TAGACGGGTT AAAAATCCTAA	840
GGCTATACCA TAAAATCAC GATAGATTG GATTACCAAC GCTTAGCGTT GGAGTCTTIG	900
CGTTTGGGC ATCAAAAAT CTTAGAAAAA ATCGCTAAAG AGAAGCCAAA AACTAACGCT	960
TCTAATGATA AAGATGAAGA CAACTAAAC GCCACCATGA TAGTTACAGA AACGAGCACC	1020
GGTAAGATTG TAGCCTTAGT GGGGGGATT GATTAAAAA AAAGCGTTT CAATCGCGCC	1080
ACGCAAGCCA AACGGCAGTT TGGAGCGCR ATCAAGCCTT TTGTGTATCA AATCGCTTT	1140
GATAATGGCT ATTCCACCA TTCCAAAATC CCTGATACCG CGCGAAATT TGAAAATGGC	1200
AATTATAGTA AAAACAGCGT GCAAACCCAC GCATGCCACC CTAGCAATT TRCTCGCAA	1260
TTTTAGGGC TTGTAACCTT GCAAGAAGCC TTGAGCCATT CGTTAAATCT GGCTACGATT	1320
AATTAGCGA TCGCTTGCT A	1341

(2) INFORMATION FOR SEQ ID NO:331:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 654 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:

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(A) NAME/KEY: misc_feature
 (B) LOCATION 1...654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331

ATGAAACGATA	CAACAGAGCA	CCATGGATCC	AATCCGCTAA	ACGCCACC	ACCTAGCAAC	60
TCACAGAGCA	ACGATCTCTT	AAATTGCTA	GACTCGTTAT	ATCCTAAAGG	GAGTTAGGG	120
GAACAAAGAT	TTCACGAAGC	TTTAAAGAAT	CAAGAAGAGT	TGAAAAATAT	CCTAATAGAA	180
ATAGAAAAGC	TACCGCAAGA	AAAAAGGTAT	GAACTTCTGA	TGCAGATAGG	ACAAGCAAA	240
CAGAGAATAA	TGGAAGCATA	CGCTCATTCA	TTCTTAGGAT	ATATAGGGGG	ACTAGAGCAT	300
CTGTTAGGAT	TGTGTATGGG	TGGGATATT	GTTTGTTTG	CAATCTATT	TGTATTTTA	360
AGAACTAGCA	AAAACACAGA	GCTAGTGGAA	AGTCTAAAAA	CAAATTAAA	ACTTCAGTAT	420
TTTACTATG	CCTTTGGTGT	GGGTGGGTT	TTGTTTTTG	GATTAGAAC	AATTAGATCG	480
ATTATGAAAC	TATATATCTT	AGGAATTGGT	AGCACTAACG	ACAAGGTGCT	CTTTGTTTG	540
AAAACATT	GCTTCATAGG	TATGGGCTAT	TTGATTATA	AGTTATTAA	AGTTATTGGT	600
ATAAAAAATT	TTATCAATGG	TCTTTCGCT	TCAAAGAAC	AAGGCGGTGC	AGAA	654

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332

ATGATGGATA	AGGTGGGTTT	TAAATCTCAA	GGCATCTTTG	TGATGGACGC	TAGCAAGAGG	60
GATGGCGTT	TGAACGCGTA	TTTIGGAGGC	TTGGTAAAAA	ACAAGCGGGT	GGTGTGTTT	120
GACACTTGA	TCTCTAAAGT	TGGGACAGAA	SGGCTTTAG	CCATTTAGG	GCATGAGTTA	180
GGGCATTTA	AAAATAAGGA	TTTGTGAAA	AATTAGGGA	TTATGGGAGG	CTTGCTCGCT	240
CTTGTGTTTG	CTTGATCGC	TCATTGCG	CCGTGGTTT	TTGAAGGCTT	TAATGTCTCG	300
CAAACGCCAG	CGAGTTTGAT	CACGATTCTA	CTCTGTGTTT	TGCGGGTGT	TCCTTTTAC	360
GCCATGCCCT	TGATTGGGTT	TTTAGCCGC	AAGAACGAAT	ACAATGCCGA	CAAGTTGGG	420
GCGACTTAA	GCTCTAAAGA	GACTTTAGCC	AAAGCGTTAG	TGTCCATTGT	GAATGAAAAT	480
AAACGGTICC	CCTATTGCA	CCCTTTTAT	GTGTTCTGC	ATTTCACGCA	CCCAGCGCTA	540
TTAGAACGCC	AAAAAGCTTT	GGATTATGAA	ATTGAA			576

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

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- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...603
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:333

ATGAATATTT	ATCAAAAAAA	CTTGCAAGCT	CTTTTCAAAA	AAGACCCCTCT	TTTGTTCGCA	60
AAGCTCAAAG	CCATTAAAGA	AAACAAAAAA	TACGAAGTGT	TTTTAGGGAA	TGATAGCGCG	120
AATTCAACC	TCTTAGATAA	AGAAACAAAC	ACGCCCTTAT	TTGAAAAAAG	CCCGCTAGAT	180
TCAAGCTTAG	AGCTATATAA	AAATAGCGAA	ATTACACATGC	TCTATCCTTA	TTTGTATTAT	240
TTTGGCTTGG	GTAATGGGT	TTTTTATCGC	TTGCTTTAG	GCAATGAAA	TTTAAAACGC	300
TTGAGGCTCA	TTGAGGCTCA	AATAGAGGTG	ATTTTCATIG	TGCTGAATCT	TTTGGATTIT	360
TCCACTGAGA	TTTTAGAAA	TCGTTGATT	TTATTCATG	CAAGTTTTG	CAATTACAAC	420
ATGATTGCTT	CATTATTTG	TATGGATAAA	AAAGTCGTT	TATACGCAAG	AATGTATGAT	480
TTAAAACTTT	TTAACGTTA	TTATGAACGA	TACTCTCATC	AAATGATAGA	AATCAACCAG	540
CATTTCACGC	GCGCTTTAGA	GCATGGCGCT	ATTAGCGTAG	GCAATGACGC	TAAGCGCAC	600
TCA						603

(2) INFORMATION FOR SEQ ID NO:334:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334

ATGAAAAAAGA	TTATTCTTGC	ATGCCCTGTG	GCTTTTGTGG	GTGCCAATT	AAGCGCAGAG	60
CCTAAGTGGT	ATAGCAAGGC	CTATAACAAA	ACAAACGCC	AAAAAGGCTA	TCTTTATGGG	120
AGTGGTTCAG	CCACTTCTAA	AGAGGCTTCT	AAACAAAAAG	CGTTAGCGGA	TTTAGTGGCG	180
TCTATTAGCG	TGGTGGTCAA	TTCACAAATC	CACATTCAA	AAAGTCGTGT	GGATAATAAG	240
TTAAAATCCA	GCGATTCAAC	AACGATCAAC	TTAAAACCG	ATGACTTGG	ATTGAATAAT	300
GTAGAAATTG	TCAATCAAGA	AGCGAAAAAA	GGGATCTACT	ACACCAAGT	GAGGAATCAA	360
TCAAAACTTG	TTTTTGCAGG	GT	TTAAGGG			390

(2) INFORMATION FOR SEQ ID NO:335:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...432
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:335

ATGAAAATCC	AAACAATTTC	AACACTTGTC	CTTACAATAA	TAATGGTAAT	ACAAAAAATG	60
ATTGTTGGCA	AAATTTCAACC	CCACAAAACC	GCAGAAGAAC	TCACYAATTTC	AATGTTGAAC	120
ATGATCGCTG	TTTTAGACTC	CCAATCTGG	GGCGATGCGA	TCTTAAACGC	TCCTTTGAG	180
TTCACTAACCA	GCCCCAACAGA	TTGCGATAAT	GATCCTTCAA	AATGCGTAAA	TCCTGGGACA	240
AACGGGTTG	TCAATTCTAA	AGTCGATCAA	AAATATGTGT	AAACAAACAA	AGACATTGTC	300
AATAAAATTAA	AAACAAACAGC	RGATCTTGAT	GTAATTGTTT	AAAGGATTTC	AGGGGTTGTA	360
GGGTTRGSCA	ATGGATATGG	CAATGATGGT	GAATATGGCA	CATTAGGGGT	AGWAGCCTAT	420
GCTTGTAGGAT	CC					432

(2) INFORMATION FOR SEQ ID NO:336:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 927 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...927
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:336

GTGGTAATAA	GGTTAGTCCT	AAACATGCTA	ACATGTCAAA	TTAGCTATAT	AAGGATAAGT	60
TATCTTGTCT	CTGTTAGCGA	TTTTGTGATT	TGCAAGGAAA	GATTATGGA	TGAAATTAAA	120
ACCGCTTGTAG	TGGATTTTTT	CCCGCAGGCA	AAGCATTTTG	GGATAATCTT	AATCAAGGCT	180
ATTGTTGTCT	TTTGTTAGG	TTTTTATTTC	TCGTTTTCT	TACGGAACAA	AACCATGAAA	240
CTCTTATCCA	AAAAGGATGA	GATTTGGCG	AATTGTTGTCG	CGCAGGTTAC	TTTTATCTTA	300
ATCCTTATCA	TTACTACAAT	CATCGCGCTC	AGCACGCTAG	GGCTCCAAAC	CACCTCTATT	360
ATCACCTGTTT	TAGGAACCGGT	GGGGATTGCG	GTGGCGTTGG	CTTAAAGA	TTATCTTICA	420
ACCATTGCTG	GAGGGATAAT	CCTTATTATT	TTACACCCCTT	TCAAAAAAGG	AGACATCATT	480
GAAATCTCTG	GCCTAGAGGG	CAAAGTAGAA	GCGCTTAATT	TTTTAAATAC	TTCTTTACGC	540
TTGCGATGACG	GGCGCTTGGC	GGTTTTGCCT	AATAGAAGTG	TCGCTTAATT	TAATATTATC	600
AATAGCAATA	ACACTGCGTG	TCGGCGCATT	GAATGGGTCT	GTGGGGTAGG	GTATGGGAGC	660
GATATGAAAC	TGGTGCATAA	GACTATAAAA	GATGTTATTG	ACGGGATGGA	AAAAATTGAT	720
AAAAAACATGC	CCACTTTTCAT	TGGAATCACG	GATTTTGGAC	AAAGTTCGCT	GAACATTCACC	780
ATTAGGGTTT	GGGCAAAGAT	TGAAGACGGG	ATCTTAATG	TGAGGACCGA	ACTCATTGAA	840
CGCATCAAAA	ACGCCCTGGA	CGCTAATCGT	ATTGAAATCC	CTTCAACAA	GCTAGATATT	900
TCTATCAACA	AAACAGACTC	TTCTAAG				927

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(2) INFORMATION FOR SEQ ID NO:337:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 491 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...491
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:337

ATGAAAAAACT TTTCCCCACT CTATTGTCTT AAAARGCTCA AAAAACGCCA TTTAATCGCT	60
CTGAGTCTGC CTTGCTTTC TTATGGAAT GGCTTAAAAA TCCAAGAGCA AAGCTTGAAAT	120
GGCACGGCTT TAGGCTCGGC GTATGTCGCT GGGGCTAGGG GTGCTGACGC TTCTTTTAC	180
AACCCGGCTA ACATGGGCTT TACTAACGAT TGGGGCGAAA ACAGAACGCA ATTTGAAATG	240
ACCACCAACG TGATCAATAT CCCGACCTTT AGCTTAAAG TCCCTACGAC CAATCAAGRC	300
TTATATTCCG TAACAAGTTT AGAAATTGAT AAAAGCCAAC AAAATATTTT AGGCATCATC	360
AACACTATAG GTTCTAGGCAA TATCCTTAA GCGCTTGGCA ATACGGCCGC TACCAATGGC	420
TTATCACAAG CTATCAATCG TGTTCAGGG CTTATGAACT TAACCAATCA AAAAGTCGTA	480
ACCCTCGCTT C	491

(2) INFORMATION FOR SEQ ID NO:338:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 162 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...162
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:338

ATGTGTTTAG CGATCCCCTC TAAAGTCATA GCCATTAACG ATAATGTGGC ACTCTTAGAG	60
ACTTTGGGCG TTCAAAGAGA AGCGAGCTTG GATTAAATGG GCGAGTCCGT TAAAGTGGC	120
GATTATGTGC TACTACACAT CGGCTATGTG ATGAGTAAAG AT	162

(2) INFORMATION FOR SEQ ID NO:339:

- (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 606 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339

ATGAAATATT TATGGCTTTT	TTTAATATAC GCTATAGGGC	TTTTTGCAAC AGATAAAACG	60
CTAGATATTA TTAAAACCAT	TCAAAAACTT CCTAAGATTG	AAGTGCCTGA CTCCATAGAT	120
AACGATGCCA ATTACGCTTT	AAAATTGCTAT GAAGTCCTAG	CGAACCGATTT AAAGACTAGC	180
CAGCATTITG ATGTTTCTCA	AAACAAGAG CAAGGTGCTA	TCAATTACGG AGAACTCAAG	240
GATAAAAAG TCCATCTGT	AGCGCTTGTG AGCGTGGCGG	TAGAAAACGG CAATAAAATT	300
TCACGATTAA AACTTTATGA	TGTGGATACA GGAACGCTCA	AAAAGACTTT TGACTACCCC	360
ATTTGAAGTT TAGATCTATA	CCCTTTTGCA GCGCACAAACA	TGGCCATTGTG GGTGAATGAT	420
TATTAAAAG CCCCTTCTAT	CCCTTGGATG AAGGCCCTGA	TTGTTTTTTC TAAATACATT	480
GGACCAGGAA TCACAAACAT	CGCACTAGCG AATTATACGA	TGCGTTATCA AAAAGAAATC	540
ATCAAAAACA ACCGACTCAA	TATTTTCCCC AAATGGCGA	ACCGCTGAGCA AACGGAGTTT	600
TATTAC			606

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 615 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340

GTGGTGAGCG GGGTGGTGAT	CATTATTGTG TTTTTGTGC CGATTCTAAC	CTTACAGGGG	60
TTAGAGGCCA AGATGTTTAG	GCCTTTAGCG CAAAGCATTG	TGTATGCCT	120
TTAGTTCTAT CCATCACTAT	CATTCTGTGA GTGAGCTCTC	TTGCTTAAAGGCCACGCCC	180
CATAGCGAAA CCTTTTAAC	GAGGTTTTTA AACAGAATCT	ACGCCCTTT ATTGGAATT	240
TTTGTGCTATA ACCCTAAAAA	AGTGAATTG GGAGCTTGT	TTTTTTTAAT CGCAAGCCTT	300
TCTTITATTCC CTTTGTGGG	GAAGAATTTC ATGCCCTGCTT	TAGATGAGGG CGATGTGGTT	360
TTGAGCGTGG AAACCACCCC	CTCTATTCC TTAGATCAAT	CTAAAGATCT CATGTTAAC	420
ATTGAAAGCG CGATTAACAA	GAAGTTAAA GCATTGTCGC	CCGCACAGGG	480
ACCGATGAAT TGGGGCTGGA	TTTAGGGGT TTGAATCAA	CCGATACTTT TATTCTTC	540

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ATCCCTAAAA AAGAAATGGAG CGTTAAAACC AAAGATGAAT TGGTTAGAAA AAATCATGGA 600
TTCTTTAAAA GACTT 615

(2) INFORMATION FOR SEQ ID NO:341:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - ii) MOLECULE TYPE: DNA (genomic)
 - iii) HYPOTHETICAL: NO
 - iv) ANTI-SENSE: NO
 - vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
 - ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1 ... 216

GTGGGATATA	TCCCTARGGA	AAAGATTGTA	GGCATTAGCG	CGATCGCTAA	ACTCATTGAA	60
ATTTATAGCA	AACGCTGCA	AATCCAAGAA	AGGCTGACCA	CTCAAATTGC	AGAAACTTTT	120
GATGAAATCA	TAGAGGCCAAG	GGGCGTGATC	GTGGTTTGTG	AAGCCAAGCC	ACTTGTGCAT	180
GACCATGCAA	GGGGTGCAAA	AGCAAAATGC	GATCAT			216

(2) INFORMATION FOR SEQ ID NO:342:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...39
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:341

GTGGGCTCTTG TGTGATAG TTTGATAGAG AACAAAGAAG 39

(2) INFORMATION FOR SEO ID NO:343:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

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(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343

ATGAAAAAAA TTGGTTTGAG CTTGTGTTG GTTGTGAGTT TGGGTTTTTT AAAAGCCCAT	60
GAAGTGAGCG CTGAAGAGAT TCGGGATATT TTCTACAAAC TCAACGCCAA AGAGCCTAAA	120
ATGAAAATCA ACCACACGAA GGGGTTTTGC GCTAAAGGCG TGTTCCCTCCC TAACCCGCAA	180
GCAAGAGAGG ATTTAGAGGT GCCACTACTC AATGAAAAAG AAATCCCTGC GTCTGTAAGG	240
TATTCTTITAG GGGCCGTGGT CGATTGGACG ATAAAAGCAA GGTTAGGGGA ATGGCGT	297

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344

GTGATCAAAC CTCATAGCGT GGGATTGGTA AGGATTGGGA TTTGTTTGTC TTTAGAAGTG	60
GGGTATGAAAC TGCAGGTACG CACCCGTAGC GGCTTGGCTT TGAATCATCA GGTGATGGTG	120
TTAAATTYCC CTGGCACCGT GGATAATGAT TATAGGGGCG AAATTAAGGT CATTITAGCG	180
AATTGAGCG ATAAAGATTT TAAAGTTCAA GTAGGGGATA GGATCGCTCA AGGGGTGGTT	240
AAAAAAACTT ATAAAGCCGA ATTATAGAA TGCGAACAT TAGATGAAAC CTTCAAGGGG	300

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

300

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345

ATGCAAATCA	TTTAAATTAAAT	TGTGCGGGCG	GTTGCTGTGT	TTTATTTTTA	CAACACCCCTC	60
AAAGAATATT	TGAAAACCCC	CCTAAACCCCT	AAAACCAAAA	CCGAAGAATA	CGACTTGAAA	120
AATGACCCCT	ATTTGCTGGT	GCAATCTAGC	CCCTTAGACA	AATTCAAGCA	AACCCAAATA	180
GGCGGTATA	TGCGTCTTTT	AAAATTTTA	GACATTCAAA	AAAACGCCCT	GGATAACGCT	240
TTAAGAACGC	TTTTTATCCA	TGAATTGGAG	CAGCCCTTAA	ACAGCGAACCA	GCAAAATTAA	300
GCCAAAGAGC	TTCTCAATGA	GCCSGTGGAT	AAAAAGAAAA	ATTTGAATC	CTTATGCCAA	360
GAAATCGCCG	ACCACACGCA	TGGAGAATAC	ACCAAACGCC	TGAAATTAGT	GAATTCTT	420
ATGCTATTAG	CCTATGCTGA	TGGGATTTG	GACAGCAAAG	AAAAGAATT	CTTTTTAGAT	480
GTGGGGCGT	TTTGCGAGAT	AGACAATCAA	GATTAAACG	AGCTTATGA	CAATTGAA	540
CACTICAATT	CAATAGAAAT	CCCTATGCT	TTAGAAGAAG	CAAAAAATCT	TTTGAATC	600
CAAACCCACA	CCACCATGCA	AGATTTAGAA	AAAAAGCTT	TGGATTTAAG	CGCCCCCTAT	660
TACCATAAAA	TGAATGACAA	CAAACGCTAC	AGCGAACAG	ATTTTATCTC	TTTGAAAAAA	720
ATCCCCCTCG	CTTCCCAACT	TTTAGAAAAT	GATTAAAAG	ACTCA		765

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346

ATGGAAGTAG	AGCATGGCAA	GATTGAAACC	ACTTTAAGCT	TGGGGCGTC	TCATTTGGAA	60
GTCATTAAAA	TGATGCTTTT	AGAGAGCCTG	CCTTCTTTAG	TGAATAATAT	CACCATCACT	120
TTAATTTCTC	TAATAGGCTA	TTCGGCTAWG	GCYGGAGCGT	TAGGGGCTGG	GGGATTGGGG	180
GATTTAGCCA	TTAGGATTGG	CTATCAAAGT	TATAGGGCG	ATGTGTTTT	TTATGCGGTG	240
GTCGTGATCA	TCGTTTTAGT	GCAAATCATT	CAAAGCGCGG	GGGATTATGT	GGTGAACGC	300
TTGAGAAAAGA	ATAAGTAT					318

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1581 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular**SUBSTITUTE SHEET (RULE 26)**

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1581
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:347

ATGAAACAAA	TTCGACAATC	CGTTTGATATC	GGATTCTTAC	GGATTCTGGA	TGTTTATTA	AAA	60
AAAGTTAAAA	CCCCAAAGGG	TGGTATTGAG	GTTTTAAGGA	CTTTAATTGA	TTTCACGCC	AA	120
AAAATTGAAA	ACGCCCTAAA	TTTAGCGACC	AAAAGCCATA	AGGGGCAATA	CAGAAAGAGC	AA	180
GGTAGAGCCTT	ATATTGTCCA	TCCTATTGTC	GTGGCGAGCG	TGGTGGCGTT	TTGTGGGGC	GG	240
GATGAGGCAGA	TGGTGTGCGC	CGCGCTTTG	CATGATGTGG	TAGAAGACAC	GCCTTGTGAG	GA	300
ATTGAAACGA	TTGAGCGAGA	ATTGGGCAA	GATGTGCTA	ATTAGTGGGA	TGCGCTCAC	AT	360
AAAATCACTG	AAATCAGGAA	AGAAGAGTTA	GGCGTGAGTT	CTCAAGATCC	CAGAATGGTG	AA	420
GTTTCAGCCC	TCACTTTAG	AAAGATCCTT	ATTAGCGCGA	TACAAGAGTCC	AAGAGCCTTA	GT	480
GTGGTAAAGA	TTAGCGACAG	GTTGCACAC	ATGCTCACCT	TAGACGCCCT	GCCTCATGAC	GG	540
AAGCAGGTGC	GTATTCTAA	AGAAACTCTA	GCGGTGTATG	CCCCCATAGC	GAGTCGATTG	AA	600
GGCATGTCCT	CAATCAAAAA	CGAATTAGAA	GACAAGAGCT	TTTATTATAT	TTATCCAGAA	GG	660
GAGTATAAAA	ATATTAAGGA	GTATTTGCAC	AAAACAAAC	AGTCTTTACT	CTTAAACTC	AT	720
AACGCTTTG	CGAGCAGGT	AGAAAAAAAG	CTTTTGACCA	GGGGGTTTAG	CCATTGGAT	AC	780
TTTAAACTCG	TTACAAGGGT	GAAACGCCCT	TATTCTATT	ATCTTAAGAT	GCAACGAAAA	TC	840
GGGGCGGTTA	ATATTGATGA	AATTGGAC	TTGTTAGCCA	TTAGGATT	ATTGAAAAAC	GG	900
CCGATTGATT	GCTACAAGGT	TTTAGGGATT	ATTCTATTGA	ATTTCAAACC	CATTGTTCT	CC	960
CGTTTTAAAG	ATTACATCGC	TTTGCCTAA	GAAAATGGCT	ATAAGACAAT	ACACACGACG	TT	1020
ATTTTTGATG	AATCTCTGT	TTATGAAGTG	CAGATCCGCA	CTTTGATAT	GCACATGGG	TT	1080
GCGGAGATG	GTAAATTCA	CCATTGGAAG	TATAAACCG	GGGGCGTGG	TCATGAAGAA	AC	1140
CATCATGAGG	GCATGCGGTG	GTTGCAAAT	TTTAATACC	ATGACAGCGA	TTTGAAAAAC	AT	1200
GACCTTAAGG	AATTTACGA	ACTCGCTAAG	AACGATTGT	ATCGTGAAGA	TATTGTCGTT	AT	1260
TTTTCGCCCC	ATGGGGACAC	TTACACTTT	CCGGTGGCG	CGATCGCTT	AGATTTCGCT	TT	1320
TACATGGTGC	ATAGTGATT	GGGCATAAA	GCCACGGACG	CTTATATCAA	TAGTAAAAAA	AC	1380
GCCTTACTCA	ATCAAGAATT	AAGGAGTCGG	CATGTTGTTA	AAATCATTAA	AGGGATAAA	TC	1440
GTAATACCTC	GTTCATTTG	GATGGATCAG	CTTAAACTT	CTAAGGCTAA	AAACCATTTG	TT	1500
CGCATCCAAA	GAAGAAACCG	CTTGAAAGAA	ATTGACACTA	AGAGCATGAT	CAATATCTA	CC	1560
GCGACTTTT	TTTGGCGCT	C					1581

(2) INFORMATION FOR SEQ ID NO:348:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...372

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348

GTGGTGGTGG TTGAGAATAT AAAAGACGCT GTGCCCTTAG CGCAAAGCCT RATARAGGGG	60
GGTATTCCAA TCATAGAAGT AACTTTCGCA TCAAACGTG CTTTAGAGGC CATAGAGCTT	120
ATCGCTAACGA ATGTGCCAA AATGCGCGTG GGTGCTGGCA CGATACTCAA TCTCACTCAA	180
TTAGAGCAGG CTCAAAATAG GGGGGCAGAG TTTTTGATTA GCCCGGGGTCT TAGGATAAAG	240
CTTTTAAACAC ACGCAAAGAA AAAAGACATG CCTTTAATAC CTGGGGTTTC TAGCAGCAGT	300
GAAGTCATGC AAGCTTTAGA ATTGGGTTAT AACGCTTTGA AATTTTTCCC GGCGGAGTAT	360
TGCGGGGGCC GT	372

(2) INFORMATION FOR SEQ ID NO:349:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 330 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349

GTGGAAAAAA TCAAACCCCTA TGCCCTAA GATAGCCCTT TAATAGACTA TTCTAGCCA	60
GTTAGAACCG TCCAATCCAC TTTAAAAGGC ACTTCTTTTG AAACGCTTAT CAATGGCGTT	120
TGGGAAAGCT TTGAAACGAA GGTTTTAGGG GAGTTAACG CCTATAATAT CGCTTCAGCG	180
ATTTTAACCG CTAAGCATTG AGGCTTAGAG ACAGAAAGGA TCAAACGGCT TGTTTTGAG	240
CCTAACGCCA TTAACCATCG TTGCAACTG TTGGAAGCGA ATCAAAAAAT CATTATAGAC	300
GATASCTTAA ATGGGAATTAA AAAGGGCATG	330

(2) INFORMATION FOR SEQ ID NO:350:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1791 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350

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ATGTCTAATC AAGAATACAC CTTCCAAACT GAAATCAACC AGCTTTGGA TTTGATGATC	60
CACTCTTGT ATTCTAATAA AGAGATTTT TTAAGGGAGT TGATTTCTAA CGCGAGCGAC	120
GCTTTGGATA AGCTGAATTA TTGATGCTA ACCGATGAGA AATTAAAAGG GCTGAATACC	180
ACGCCTAGCA TCCATTTGAG TTTGATAGC CAAAAAAA CCTAACGAT TAAAGACAAT	240
GGTATAGGCA TGGATAAAAG CGATCTCATC GAGCATTAG GCACGATCGC TAAATCAGGC	300
ACGAAGAGTT TTTAAGCGC TTGAGTGGG GATAAGAAA AAAGATAGCGC CTTAATTGGC	360
CAATTGGCG TGGCTTTA TCGGCGTTC ATGGTAGCGA GTAAGATTGT CGTTCAAACC	420
AAAAAAGTTT CCAGTCATCA AGCTTATGCA TGGGTGACCG ATGGTAAGGG CAAGTTGAA	480
ATCAGCGAAT CGCTCAAAGA GGAGCAAGGC ACAGAAATCA CCCTCTTTT AAAAGAAGAA	540
GATTCCTATT TTGCGAGCCG TTGGGAGATT GATAGCGTTG TAAAAAGTA TTCTGAGCAT	600
ATCCCCTTCC CTATTTTTT AACTTACAC GATACGAAAT TTGAGGGCGA AGGGATAAT	660
AAAAAAGAAG TTAAAGAAGA AAAATCGGAT CAGATCAATC AAGCGAGCGC TTATGGAAA	720
ATGAATAAGA GCGAATTGAA AGAAAAGGAT TACAAAGACT TTACCAATC GTTGTGCGAT	780
GATAACAGCG AGCCTTGAG CTATATCCAT AATAAAGTGG AAGGCTCTT AGAATACACG	840
ACGCTTTTTT ATATCCCTAG CAAAGCGCC TTTGATTTGT TTAGGGTGGA TTATAAAAGC	900
GGGGTCAAAC TTATGTTAA ACGGGTGTT ATCACTGATG ATGACAAAGA ATTGTTGCCG	960
TCTTATTGAG GTTTGTTAA AGGGTGTGATT GACACCGAAG ATTGCCCCCTT GAACGTGAGT	1020
CGTGAATATCT TACAGCAGAA TAAGATTITA GCCAATATCC GTTCGGCTTC AGTGAAGAA	1080
ATTTTAAGCG AGATTGAAAG GCTGAGCAAG GATAACAAGA ATTACCATAA ATTCTATGAG	1140
CCTTTGGGA AAGTGTAAA AGAAGGCTTG TATGGGATT TTGAAAACAA AGAAAAACTT	1200
TTAGAATTGT TGAGATTCTA TTCTAAAGAC AAAGGAGAAAT GGATTTCTT AAAAGAATAC	1260
AAAGAAAATT TAAAAGAAA TCAAAAAGC ATTTACTACC TTTAGGCAGA AAATTTAGAC	1320
TTATTAAAAG CGTCCCCCCT TTTAGAAAAA TACGCTCAAA AAGGCTATGA TGTTTTGTTA	1380
TTGAGCGATG AAATTGATGC TTGAGCTGATG CCAGGCGTGA ATGAATACGA TAAAACGCC	1440
TTTAGAGACG CTAGCCATAG TGAGAGCTTG AAAGAGCTTG GTTGGCAGA AATCCATGAT	1500
GAGGTTAAAG ATCAGTTAA AGATTATAAC AAAGCGTTTG AAGAAAATCT TAAAGATGAG	1560
ATTAAGGGCG TAGAGCTTTC TGGTCATCTC ACTTCAGCGG TGCTTTAAT AGGCATGAA	1620
CCAAATGCGA TGATGGCTAA TTGGATGGCT CAAATGGGC AAAGCGTGCC TGAAAGCAAG	1680
AAAACTTAG AATTAAACCC TAACCATGCC ATTTIGCAAA AACTCTTAAA ATGCGAAGAT	1740
AAAGAGCAGT TGAGCGTTT TATCTGGTTG CTTATGATG GGCGAAGCTT T	1791

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351

GTGAATTTAG GGGCTTACTA CACGCCCT TATTTAGTGG ATTGGCTTA CAAGCTTTA	60
AAAAAGCATG TTGGTATTGA AAACTACACG CTTTCTAGACA CCGCATGTGG TAATAAAGAG	120
TTTTTAAAGC TCCACCCACCC TAAAAAAATA GGAGCGGATA TTGACCTAA GTGTGATGCT	180
TTAATAATAA ACGCTCTAGC CAATCCTAAA AGAGAAAATT ATGGCATTAG CCAAGATGAA	240
CCTTTAATCA TCGTGGCAA TCCCCCTAT AACGATAGAA CTTCCTTTAT CAAACAAGAT	300
ATTAAAAATA AAGATTTCAT TTTTGAGATA GACAACGATT TGAAATCCCG AGATTTAGGG	360
ATAAGTTTTT TAAATCTTT TGCAATTITA AAGCGGGCGT TTATTTGCGT GCTACACCC	420
TTATCTTATC TCATCAAAGA AGCTAATTAA AAGCAATTAA AAGCTATT	468

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352

ATGAAAAGCA	TTTGCTCTT	TATAATTTTT	GTA	GTTC	AGTTAGAAGG	CAAAAAAATT	60
TCACAAGATA	ATTTTAAGGT	GGATTATAAC	TACT	TTG	CACATC	120	
ATTA	AAACGATT	GTCCAA	TG	CTCC	ACACAAA	180	
GAACATTCTT	GGGTGATT	TGCT	CTCCACACAA	AGCCCCCAA	240		
TATTTTTG	CTTTTATCA	TAGTT	CCCATT	TGATGGATT	300		
AACCCCTACY	AACGAA	TACC	ATGGTACCA	CCCTAATATC	360		
CATATTCTT	GGACTAAAGG	CTG	TTAGAGTGC	TGTATTAGG	420		
ATTATAATG	ACCGCTCAATC	CTGGY	TTATA	CCCAA	CTGGTTCAA	471	

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353

ATGGGCTTGA	TGGCGTGT	GCAAGGCTTA	CCAAACACCA	CTAGCAAGTT	TGGTATTGAA	60
TTTGACTCTT	TAGCTGATGT	GGTCGCTTTT	GGAGTCGCC	CAAGCCTTAT	TACTTACTTT	120
TATGTGGGGT	ATAACTTTGG	GCGTATAAGGC	ATGGCGGTGA	GCGCGTTGTT	TGTGATTTTT	180
GGAGCGATAC	GATTAGCGCG	ATTCAATATC	AGCACCAACA	CAAGCGATCC	CTATTCTTC	240
ATCGGTATCC	CCATTCCCTG	GGCGGCGGTA	TTGGTGGTGC	TTGCGGTGTT	ATTAGATAAT	300
AAATACCAATT	TCTTAAAGG	CAATACCGAA	AAGTTATTTT	TAGGCTTTAT	TGTCTTATTA	360
GGGGTGCTTA	TGGTGAGCAA	TATCCGCTAC	CCTAATT	AAAAAGTC	GTGGAAATCTC	420
AAGCTTTCA	TCTTACTGTT	TCGTTAGTGT	TTGTCGCCC	TTTAGAGGCT		480

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TTGAGCGTGT TTATGGGTT GTATTGATC TATGCCATCA TTCGGTGGAT CTTTTTAATG	540
GTAAAAATTA CTTTTAATAA AAATAAAAGC GCA	573

(2) INFORMATION FOR SEQ ID NO:354:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...270
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:354

ATGATAGGAG TTTACCCCAA TTATTCCAAA AAGCAACTAA AACGCCCTT AGTCATATTT	60
GTAAGTAGGG AGTTAGCGCT GGCTAATGGT ATTCTTACAG ACGCTTATGA CATTGAAGCA	120
AATCTTTACA TGAATGCTCG TATCGTTATG AARAATAATA AAAGGAAACCA TTATGAGCAG	180
CGGGTTAATT TACATTTCRT TAGAAGCTTT GGTARCGTGT TTGATCACCG CTCTAATCAT	240
GTATTATGTG ATGAAAAGA TCTATTACGC	270

(2) INFORMATION FOR SEQ ID NO:355:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 831 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...831
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:355

GTGAAAATAA CCATAATGAT TAAAGATTTT AACCACTATT GTAGAAAAAT AACGAGAGGG	60
TTTGAAAAAA TTCCCACCAA AAAACAAGGA GCAAAAAGA TGAAAAAAAGC GGGTTTTCTT	120
TTTTGGCGG CGATGGCTAT CATTGTTGAG AGTTTAAACG CCAAAGATCC GAATGTGTG	180
CGTAAGATTG TTTTGAGAA ATGTTGCTT AATTATGAGA AAAATCAAAA TCCCTCACCA	240
TGCATAGAAG TCAAACCCGA CGCCGGCTAT GTGGTTTAA AGATATTAA CGGTCCGTTG	300
CAATATTGTT TGATGCCAAC GACTCACATT AGTGGCATTG AAAACCCCTTT GTTGCTTGAT	360
CCTTCTACGC CTAACTTTT TTACTTGCA TGGCAAGCGC GCGATTTTAT GACTWAAAAA	420
TACGGAAAAC CCATTCCCTGA TTATGCGATC TCTTTGACGA TCAATTCTAA AAAAGGGCGA	480

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TCGCAAAACC ATTTTCACAT CCATATTCT TGCAATTAGCC TTGATGTGCCG CAAACAGCTG	540
GATAATAATC TAAAAAAATAT CAACAGCCGT TGGTCGCCAT TATCAGGTGG CTTGAACGGG	600
CATAAAATATT TGGCGCGTCG GGTAAACAGAG AGCGAATTAG CGCAAAAAG CCCGTTGTC	660
ATGCTTGCTA AAGAAGTGCC TAACGCCAC AAACGCATGG GAGACTATGG CTTGGCGGTG	720
GTGCAACAGA GCGATAACTC CTTTGCTTIG TTAGGCACAC AATTAAACCC ATTGACTTTA	780
AATCGCGCTT CAGCCGAAGA GATTCAAGAT CATGAATGCC CGATTTGCC T	831

(2) INFORMATION FOR SEQ ID NO:356:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...174
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:356

GTGCTAACGA GTGGGGACAT GATCAATTGT CGGTATTGCCG GGCATTTT RTACGCTGAG	60
AGTACGCATG AAAGTAACGC TCAACCTCCA AAAGAAAGCC AACCAAAAGA AAGCCAAGAA	120
GAAAGCCAAG AAGAAAGCCA AGAAGAAAGC CAAGAAGCCG TCCGTTGAT TGTT	174

(2) INFORMATION FOR SEQ ID NO:357:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 837 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...837
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:357

ATGAAATTGA ATGACCCCTT CACAAGCCCT AATAAGCCA AAAAGAAATT ATCGCCAAAA	60
GGCTTTAGGG GGGGGTTAGA GTCTGAAATT TTATTAGGCT TTGTCCTTGCA AAAAGAAAGG	120
GTTCCTTTGC ACACGCATGA GCATTGGAA TTAAGCCACG AAGAAGAAC ACGCTTTTT	180
GAATTGGTAG GAAAGCGTTT GAATGACTGC CCCATAGAGT ATTTATTAGG AAGCTGTGAT	240
TTTTATGGGC GCTCTTTTCT CGTGAATGAG CATGTTTAA TCCCACGGCC TGAAACCGAG	300
ATTTTAGTCC AAAAGCCCT TAATATTATT TCTCAATACC ATTTAAAAGA AATAGGCAGA	360

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ATCGGCATAG GGAGCGGATG CGTGTCCGTG AGTTGGCTT TAGAAAACCC TAATCTCTCT	420
ATTATGCGA GCGATATTTC ACCAAAAGCT TTAGAAGTGG CGTTAAAAAA TATTGAACGC	480
TTTGTCTAA AAGAGCGTGT TTTTTAAAAA CAAACCGGCC TTTGGGATCA TATGCCAACG	540
ATAGAAATGC TTGTCTCTAA CCCGCCCTAT ATCGCTAGAA ATTATCCTTT CGAAAAATCC	600
GTTCTCAAAG ACCCGCACGA AGCCCCTTTT GGGGGGTTA AAGGCGATGA AATCTTAAA	660
GAAATCGTTT TTTAGCCGC TAAATTTAAA ATCCCCTTTT TGGTTTGCG AATGGGGTAT	720
GACCAAGTTAA AGAGCTTGA AGAATGCTTG GAGTTTGCG GTTATGATGC AGAGTTTAC	780
AAGGATTGAGCGGCCTTGA TAGAGGGTTT GTGGCGTTT TAAAAAGTTT TTAAAGA	837

(2) INFORMATION FOR SEQ ID NO:358:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...108
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:358

ATGATTTCTT TCATTGGTT TGAATGCTCC GCATTAAGG TTTTTTTAAC TTTTGGTTAC	60
ATAGTTTTTA AAAGYGGCA CTATAGCGCT ATAAGACTAA TTGTTATA	108

(2) INFORMATION FOR SEQ ID NO:359:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 387 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...387
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:359

GTGATCCAGT CTCACCCCTAA ACAAACTCTA ATTGAAGATG AAAATTATTT TTATGCTAAC	60
AAGGGCTTTT ATAAAACCAA CAAAGAAGCC TTTTAAGGG TTATATAAAAT CCCAGAGAGC	120
ATGCCCATAG AAAAACGAGA AAGTTTAAGC AAGGTTTCTA AAAATCTTTT AGCGTTGCTT	180
TTTTTCATTT CTAGCATGCT TTTTGGGATC TTTTGGCGTT TGCCCAAACG ATTGGACACT	240
AAAATGAGTT TAGAGAGCGC GCACAAAAAC GAATTAGAAA ATGCATTCCA ACGATACGAT	300

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GGCCTAGGGG TCGTTTGCA AGACATTGCA GGGGTGAATG AAGTCAAAGA AGAATTACTA	360
GAAGTGATRG ATTWTTTWAA AAAACCC	387

(2) INFORMATION FOR SEQ ID NO:360:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...381

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:360

ATGTTTGTAG TTAAATGGT GTTAGGGTTT TTGATCCTTT TAAGCCCTTT GTGCGCTACT	60
GGATTGGATA TTTCACAAAC AGACATTATA GAGCGTTCTT TAAATTTCTT CTGTTTGTG	120
GGGATTTTGT GGTATTCTT GGCTAAAAGA TTGCGTTCAT TTTGCATTC CAAAAGCCTT	180
GAAATCTCCA AACGCTTAGA AGAGATCAA GCCCACTTA AAGTGAGTAA AGAACATAAG	240
AAAAACTCC TTAAAGAATT AGAGCAAGCC AAAGAAAAAG CTGAATTGAT TATTTCGAT	300
GGGAATAAAG AAGCCCTACA CGATCACGCA AAAATACGAA TTACAAACCA AAATGGATGT	360
GGAAAATTG ATCAAAATT C	381

(2) INFORMATION FOR SEQ ID NO:361:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 885 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...885

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:361

ATGAGGGTTT TAGAGTGGAA ATATGGTTA AATACTGATA ACTGGGATAC GCCCACCAAC	60
AAACCGCCTC AAACTTTAA AATACAAATT TTTAAGATAC AAATAGGTAT AATCAATAAC	120
TTCATTCATT TAATCAAAGG GAGTTCTATG AAAAACGCTT TCAAAGCGTT TGCCCTGTTA	180
ATCGTATTTT TCTCAAACGC TCTATTAGCG CAGGATTAA AAATCGCTGC TGCTGCTAAT	240
CTCACGCGCG CCTTAAAGC CCTTGTAAA GAATTCAAA AAGAACACCC AAAAGACGCT	300
ATTAACATTA GCTTTAATTG TTCAGGCAAA CTCTACGCTC AAATCGCTCA AAACGCCCT	360

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TTTGATTTAT TCATTTCAAG GGATATTGCT AGACCCAAAA AACTTTATGA TGAAAAAATA	420
ACCCCTTTTA AAGAAGAAGT CTATGCTAAA GGGGTGTTGG TTTTATGGAG TGAAAATCTA	480
AAAATGGATT CTTTAGAAAT TCTTAAAGAC CCTAAAATTAA AACGTATCGC TATGGCTAAT	540
CCTAAACTAG CCCCTTATGG AAAAGCAGC ATGGAAGTCT TGGATCGTTT AAAACTCACT	600
CCTAGTCCTTA AATCTAAAAT CATTATGGC GCTTCTATTT CTCAAGGCCA TCAATTCATC	660
GCCACCAAAA ACGCTCAAAT AGGCTTGGA GCGTTATCTT TGATCGATAA AAAAGACAAA	720
AACCTCTCTT ATTTCATCAT TGATAAAAACC CTTTATAACC CTATTGAACA AGCCTTAATC	780
ATCACTAAAA ATGGGGCTAA TAACCCCTTA GCCAAAGTTT TTAAAGATT TTATTCAGC	840
CCTAAAGCTA GAGCTATCTT TAAAGAATAC GGCTATATTG TGGAT	885

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362

GTGGCTTTAT TAGAGCCAAG CGTGATGTAT CTTACCGAAA AGTATCAATA CTCTCGTTTT	60
AAGGTTACTT GGGGTCTTGT AGCGTTAATC TTGTTGGTAG CGCTGGTGTGTT GATTTTCTCG	120
CTCCATAAGG ATTATAAAGA CTATCTCACT TTCTTGAAA AAAGTCTTT TGATTTGGTTG	180
GATTTGCAT CAAGCACCAT TATCATSCCT TTAGGCAGGA TGRCAACCTT TATTTTTATG	240
GGCTGGGTTT TGAAAAAGA AAAATTGCGT CTTTGAGCG CGCACTTTT AGGCCCTAAA	300
TTGTTGCCTT CTTGGTATTT CTTGCTTAAA TACATCACCC CTTTAATTGT GTTTTCCATT	360
TGGTTGAGCA AGATTTAT	378

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363

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GTGGGGCTTA	TGAAAATAAG	ATTTATGGGG	CGGAGTGT	TTGTGGGGGA	TTTGGAACGC	60
ATTGAAGAAG	TGGCTAGATT	TGAAGAATT	TGCGTTTAG	GGGGCAAAA	ACCGATCAA	120
GACCGTAGAA	GATTGGTTTT	AGAAATCGCT	TTAAACACC	AGCTCAACAA	GCTTTAAAAA	180
CCCGTTCAAA	AGCATTCAA	AGAAGACGAA	TTAGGAATT	TTAAACAAAT	GCATGACAAA	240
AAAATTCAAA	GCGTCGCCAC	CAATTCCATA	GGCGTTGT	TTGATATAGT	GGCGTTAGT	300
TTGGGGGTGG	TGGGAACGAT	TAGTTTGAA	GCCGAGAGCG	GGCAGGTTT	AGAAAATCTA	360
GCCCTACAAA	GCGATGAGAT	CCCTTTTAC	CCTTTTGAAA	TCAAAAACAG	CGTGGTGCCT	420
TTGAAGGAAT	TTTATCAAGC	GTTTGAAAAG	GATTGGCCG	TTTTAGAAC	CAAACGCCATC	480
GCTAAGGAAAT	TTTTAACAG	CTTAGTAGAA	ATCATTACCG	CTTGATTCG	GCCTTTAAA	540
GGGCATGTCG	TGGTGTGCA	TGGGGCGTG	TTTGCAACC	AATTGTTGTG	CAGAACATTA	600
GCCAAGCGAT	TGAAAAAGCT	TCAAAAGGAG	TATTTTTTCC	ACAAGCATTT	CCCCCTAAT	660
GACAGYAGTA	TCCCTGTCGG	TCAAGCCTTA	ATGGCGTATT	TCAACCCCTAC	AATCATCAAA	720
AAAGGA						726

(2) INFORMATION FOR SEQ ID NO:364:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 453 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...453
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:364

GTGAGCGATT	CTAACGCTTT	AAAGGAAGTG	TTTTTAAACA	TCAGCGCTAA	AGAAGATCAT	60
TGCGACGTTT	TGATCAATT	CGCCCGTTAT	GGGGTGT	GGAGCGT	GGAGACAGCCC	120
ATTGAAGAGG	TTAAAAAGCA	ATTTAGCGTG	ATTTTTTTCG	CCCTTTGTGA	AGTGGTGCAA	180
CTTTGTTG	CCTTATTAAA	AAACAAGCCT	TATTCTAAGA	TTTCAATCT	TTCTTCCATA	240
GCAGGGCGTG	TGAGCATGCT	CTTTTTAGGC	CATTACAGG	CGAGTAAGCA	TGCCCTAGAG	300
GCTTATAGCG	ATGCCTTGCG	TTTAGAGCTT	AAGCCCTTA	ACGTTCAAGT	GTGTTGATT	360
GAGCCAGGCC	CGGTGAAAG	CAATTGGAA	AAAACCGCTT	TTGAAAATGA	TGAGCGGAAA	420
GATAGCGTTT	ATGCTTGTGA	AGTGAATGCG	GCT			453

(2) INFORMATION FOR SEQ ID NO:365:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365

GTGATAGTGG CGTGGCTTT TAGGTTAAA AGCATIGCGT TTTCTATTIT AATCACTCTG	60
TTGGTTATTT TAGTGGATAT TTGGGTGTAT AGCGATGTGC GCCAGTTTTT ATTGGACACT	120
TCTAGCTCTT TTATTTGGCT TTTAACATCGCT TTACTAATCA AGTGGGGCGT GATTGTTATA	180
AGTGCAGCAGCA AATGCTACCA ATTCAAGCCAA AAAATGTTTG CGTTAACATCCA AAGAAAAAAGG	240
CAAATCAGAG AGAATTAAA AAACCGCTCC AATCGCAAAG ATGCTAAAAAA TTTTGAAAAAA	300
CTCTCTAACCA TCGCTGAAGA AATCAATTCA AAAAACAAAG AAGAGTCCTCA CCACAAAGAA	360
GATTCTAATG ATGAAAACCA CAAAGACAAG CTTCTAACCA TTACCGAAGA AATGATTCTC	420
AAAAAACAAAG AGGAACTGAA AGCTAGAAAG GATAAGGGGG AT	462

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...537

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366

ATGAACTTACCA CTAATCTACC TAACAGCGCT TTAGRGATAA GCGAACAGCC AGAAGTGAAA	60
GAAATCACTA ACGAGCTTTT AAAGCAATTAA CAAAACGCTT TAAGGAGCAA CGCGCAATTIT	120
AGCGAGCAAG TGGAATTAAAG CCTTAAATGC ATCGTTAGGA TTTTAGAAGT GCTTTTGAGT	180
TTGGATTTTT TTAAGAAATGC GAATGAGATT GATAGCAGTT TAAGAAATTC CATTGAGTGG	240
CTGACTAACG CCCGCCAGAG CTTGAAATTAA AAAATGAAAG AATACGAGCG CTTTTTITAGC	300
GAGTTTAATA CGAGCATGCA TGCCAACGAG CAGGAAGTAA CCAATACCTT AAACGCTAAC	360
GCCGAGAACAA TTAAAAGCGR AATTAAAARG CTAGAAAATC AATTGATAGA AACCACGACA	420
AGACTTTTAA CGAGCTATCA AATCTTTTA AACCAAGCCA GAGATAACGC TAACAACCAA	480
ATCACAAAAAA ACAAAACCCR AAGCCTTGAA GCGATTACAC AAGCTAAAAAA CAACAGC	537

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367

GTGTTTGCCTA	CTGACAGCAG	TAGCTTTCT	ATGGGGCTTA	CCATGGCGAG	TGCTTATGAY	60
CCCATTTCAG	GATCGCAAAA	ACCCATTGTG	GGCAAGGCC	TTTATTGTT	AGCGATTAA	120
ATTTTATTGG	ATTTATCGTT	CCACCATCAA	ATCATTTAT	TGTGGATCA	CAGCTTAAA	180
GCCGTCCTT	TAGGGCGATT	TGTCTTGAG	CCAGAATTAG	CTAAAAACAT	TGTCAAAGCC	240
TTTTCACACT	TGTTTGTCT	AGGGTTTCT	ATGGCGTTCC	CTATTTATG	CTTGGTGTAA	300
TTGAGCGATA	TTATTTTGG	CATGATCATG	AAAACCCACC	CTCAATTCAA	CCTGCTCGCT	360
ATCGGGTTTC	CGGTTAAAT	TGCGATCGGG	TTTGTGGCA	TTATTTTAAT	CGCTTCGGCT	420
ATCATGGGGC	GTTTAAAGA	AGAAATCAGC	CTGGCCTTTA	GCCTTATRG	AAAAATCTT	480

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 282 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368

ATGTATGGCG	TGAAAGAGAT	AAAGATAAAA	ATTGACAAGC	AACTCCACAA	TAACGATCAT	60
TTGTTTGAAG	GGCTTTTGG	GGAAAAAGAA	GATTGAAAAA	AATTGGTGAG	CATGTTGGG	120
CAGTTGCGTT	TCCAAAAGCG	CTGGAGCCAA	ACCCAAAGAG	TGCCACAAAC	CAGTGTCTA	180
GGGCATACTT	TATGCGTGGC	GATTATGGGG	TATTTATTGA	GTTTTGACTT	GAAAGCTTGT	240
AAAACCATGC	GGATCAATCA	TTTTTGGGC	GGGCTTTTC	CA		282

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 438 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369

ATGACTTTAG ATGACTTATT AGGGGGAGT TTGGACCCGC ATIGTTTTTG CAAACCCITA	60
ATCAAAACCA AAAAAGACCA AGAAAGGCTC TTATCCCTTG CTTAAAAGC CCACCCCTAAA	120
ATCTCTTTG GAWWGACAG TGCCCCGCAT TTCATTTCTA AAAAGCATAG CGCTAACATC	180
CCGGCGGGCA TCTTTCTGC CCCTATTTTG TTGCGCTGCGT TGTGCGAAGT TTTGAAAAAA	240
CACAACGCTT TAGAAAATTG GCAAGCCTT ATCACTGATA ACGCTAAAAA AATCTACGCG	300
CTAGACAATT TACCCAGTAA AAAAGGCAT TTGTCTAAAA AACCCCTTAT AGTCCCTACG	360
CACACGCTTT GCTTGAATGA AAAAATCGCT ATCTTAAGAG GGGCGAAAC GCTATCTTGG	420
AACCTTCAAG AAATCGCC	438

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370

ATGGCGTTT TGGGCATGTT CGCTTTTTT TCATGGTTT TTTTATTCAA GCACAATCTC	60
AGCCATAAAA TCCGCTTATA CCATGAAAAA AAGGATTTG ACAAAATTGCT CAAACAAATC	120
CTATCCAAG ACACCCAAAA GACTTTTTA AAAACAAAAT TTAAAAGCGA TCTCGCTAAA	180
AACCTCTCTC AAATCTTAGC CCGCTATGAT TTAAAAGCTG ATTTAAACAC GCCAAATAGC	240
GGGTGCGAAA AAGTGGATAA CCTTTTTAAA CATTACCACA ATATAGAAAA TAACACCTT	300
GAGCCTAAAG ATCACGCTAA ACATTCCCTA GCTTATGAGC ATGCTTATTT TTCTAAACGC	360
TTGAAGGCTT TCATTCTATA CGATTTGAAA AACCCCTTGT AAGTTTTAAC AAACGCGCAA	420
ATCCCTTTGG AATTACGCCG CTACGCTTAT AGAAATCGCC CAAAAAGGCA GCAAAAAAGA	480
GGTTTAAAG GCTGTGAATG CGATGCAAGA GGATTTGGA	519

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371

GTGAGTGTTC	CTGCAACGAG	TGCGAATTAA	GGCCCCGGTT	TTGATTGCTT	GGGTTTGAGT	60
TTGAATTTAC	GCAATCGTTT	TTTTATTGAG	CCTAGTAATA	TCCATGCGGT	GAAATTGGTT	120
GGGGAGGGTG	AAGGGATCCC	AAATTTTTA	ACCAACAATA	TTTTCACCAA	AGTGTTTTAT	180
GAGATTTAA	AAAAGCATGG	GAATGACGGC	TCGTTTAAAT	TTTTATTGCA	TAATAAAGTC	240
CCTATTACAA	GGGGCATGGG	GTCTAGCTCA	GCGATGATTG	TGGGGCGGT	CGCTTCAGCG	300
TTTGCCTTTT	TAGGGTTTGC	TTTTGATAGA	GAAAACATTC	TCAATACTGC	TCTAATTAT	360
GAAAACCACC	CGGATAATAT	CACCCCGCCG	GTGTTGGGG	GGTATAATGC	AGCGTTGTG	420
GAAAAAAAGA	AACTGATAAG	TTTAAAAACC	AAAATCCCTT	CTTTTTAAA	AGCGGTGATG	480
GTGATCCCTA	ATAGGGTCAT	TTCTACCAAG	CAATCGCGCC	ATCTCTGCC	AAGCGTTACA	540
GGGTGCAAGA	AAGCGTGT	AACTTTCGC	ATGCGAGT			579

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 312 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372

GTGGCTAAAA	ATTTGGTAGC	GAGCGGGGTT	TGCGATAAAAG	CGACCGTGCA	GCTTGCTTAT	60
GCGATTGGGG	TGATAGAGCC	TGTGTCTATT	TATGTGAACA	CGCATAACAC	GAGCAAGCAT	120
TCAAGCGCCG	AGTTGGAAAA	ATGCGTGAAA	TCGGTTTTCA	AACTCACGCC	AAAAGGCATC	180
ATTGAAAGCT	TGGATTGTT	AAGACCCATT	TATTGCTCA	CTTCAGCTTA	TGGGCATTTT	240
GGGCGCGAGT	TAGAAGAATT	CACTTGGGAA	AAGACTAACCA	AGGTTGAAGA	GATTAAGCG	300
TTCTTTAACG	GT					312

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1065 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373

GTGCGTTTGT TTAGATTTGT GGGGTGGTAT TATTCAAAT ACTTTTAAT CGTGCTTTA	60
GCTTGGAAAT TGTTTTTGT AGCCATTGAC AGCCTGAAAT ACGCCGATAA AATGCCTGAT	120
TCTGCGAACCA TGATCATTTC ATTTTTCACC TATGATATTTC TATTGCTCT CAATTACACC	180
TTGCCCATTT CCTTGCTTT AGCGATGGTT TTATTTATA TCACCTTCAT TAAATCCAAC	240
CAATACACCG CCCTGCTCTC TATTGGATT TCCAAATGCC AGATTTTAAG CCCTATTTC	300
TTGATTAGCC TGTTTTTCAC GGCTGTTAT GTGGGGTTGA ACGCCACTCC TTTTGTGTAT	360
ATGGAAGAAA AAACCCAAA TTAAATTAT AAAGACAATT CTTTGAGCGT TTCAGAGCAT	420
TTCTTAGTGA ATACAAACGA TGATTACGTG TATTTGATA AGATTAATCC CTTATTGCAA	480
AAACCCAAA ATATCAAGGT TTTCGCTTA AAAGATAAAA CTTCTAGAATC TTATGCTGAA	540
GCTAAAGAAG CTTTTTTGAG ACACAAATAT TGGATTTCAC ATGACACTAC TATCTATGAG	600
ATGCCCTTGA GTTTTGAACG GGGCGGAAC GCTTAAACA CCACGCATT AGAAACCTTT	660
AAAACGCTCA AAAATTTCGG CCCTAAAGTT TAGACACCA TTATCAAACAA CAAGCCTGCG	720
GTTCTATCA CAGACGCTCT TTATCCTTG CATGCTTGT TGCCCAAAA CGCGGACACG	780
AAAAAAAGTGC GCTCGTTTGT GTATGTGTT GCGATTTCG CTTTTTTGT GCCGTTTTA	840
AGCGTTTAA TCGCTTATTTTTCGCCCCAGT CTCCGGCGCT ATGAAAACCT GGCTTTTTA	900
GGGCTAAAGT TTATCAATTAT CACGCTCGTT GTTGGGGGC TATCTTTGC TTTAGGGAAAG	960
TTCAGCATTTCAGGGATACT CATTCTGAA ATAGGCCTTC TATGCCCTT TTTCGTATTTC	1020
CTAGCTCTCA GTCTTGGTA TTTTAAAAAA CTTAATAAGA GATTG	1065

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 717 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374

ATGATTTATG CGTTTTAGA CGGCTGTTT TTGGCTATT TACAGGCTCA AAATTACCCC	60
TTCCATTGCG TTATTTGTT TGAAGAAAAT TTAGACTTGT TAAATTCAG TTGCTATTTC	120
GCGCGTTATG AAGATTTGAT TAAAAAGGG GCTAAACTTT TTATCAAGG GTTTTTTAAC	180
CCTAATGAAT TGAAAATGGA TTTTTGAAA CGCCCTATCA CGCATTCTT TTTAAAGCTA	240
GAAATCATGC CCTATAAAAG CGCTTTTAAT TTGCGCATGC GAGAAAACAT TCAAAGCTAT	300
TACAAACAAG CCTTAAGGGG TTGGGGAGT TTGAAAGACG AATTGCTAGG GTTAAAGAAC	360
ACGCTTAAAAA ACTTACCCCT ATACCAAACC CTAAAACCA AACCCAAAAA ATTAACGCC	420
CCCATTGCG TGGTGGTAA TGGGCCAAGC CTGGATTAT TTGAGATTT TTTAAAGAA	480
AATGAAGAAA AATTCAATCAT TTTCATGC GGAACCGCTT TAAAGCCTT AAAACCCAT	540
GGCCTTAAAG TGGATTTC AATAGAAGTG GAGCCATAG ACTATCTTAA GGAGGTTTA	600
GAAAGAGCCC CCCTAGAAGA CACCCCTTA ATGGCGCTA ACATGCTCAA TCCTAACGCT	660
TTTGATTAG CCAAAGAAGC GTTGATGTTT ATGCGTGGGG GGAGCGCTTG CGCAGTA	717

(2) INFORMATION FOR SEQ ID NO:375:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 867 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375

ATGCTGGCGT	TTTAAAAAAC	CCCTAGAAC	AGCGCTTTTC	CTTGGGTYT	TTTCGTGGGG	60
GCGTTATTGT	TTTACTGGTG	CGCTTTAAGG	CTTCGCATT	CGGATTTCAC	YTATTATTG	120
CCCTTAATCA	TTGTTTAGT	AGCGTTAGTT	TATGGGGTTT	TATTTTATT	GTIGCTCTAT	180
TTTGAAAACC	CCTACTTCAG	GCTTTGAGT	TTTTAGGCT	CTAGTTTAT	CCACCCCTTT	240
GGATTTGATT	GGTTAGTCCC	GGATAGCTT	TTTCTTATA	GGGTGTTAG	GGTGGATAAA	300
TTATCTTAG	GGCTTATT	TTTAGCTTGC	ATTTTTTGGA	GGGCTCAAAA	TCTTAAAAAA	360
TACAGAATGA	TAGGGGTTT	ATTGCTGCTT	GGCGCGTTGG	ATTTTCATT	TTTTAAAATA	420
AGCGATTTAA	AAGAGGTGG	AAATATTGAA	TTAGTCTCTA	CAAGAACGCC	CCAAGATTG	480
AAATTTGACT	CAAATTACCT	TAATAATT	GAAAACAACA	TTCTTAAAGA	AATCAAATC	540
GCTCAAAGCA	ACCAAAAAC	CTTGATTGTT	TTTCCAGAGA	CCGCTTACCC	TATCGCTTTA	600
GAAAACCTCCC	CTTTTAAAC	CCAACTAGAA	GATTTAAGCG	ACAAGATCGC	CATTAAATA	660
GGGACATTGC	GCGCTCARGG	CTATAGCCTT	TATAACAGCT	CGTTTTATT	TTCTTAAAAAA	720
AGCGTTCAAA	TCGCTGATAA	AGTGATCTTA	GCCCCCTTGT	GCGAGATAAT	GCCTTACCG	780
GAGTTTCTTC	AAAAACCCCT	TGAAAGCTC	TTTTTGCGA	GAGCGTTAT	TTATACCGCA	840
ACGCTCCCCA	TTTCAGCGAT	TTTACAT				867

(2) INFORMATION FOR SEQ ID NO:376:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1308
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:376

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ATGAACGATC	CTAACGCATGT	GGTGTATGTT	TGGCTGGACG	CTTTATTGAA	TTATCCGAGC	60
GGCTTAGGGT	ATTTAACCGG	TTTAGACAAT	AAAATGGCGC	ATTTTAACG	CGCTAGGCAT	120
ATTGTGGGTA	AGGATATTTC	ACGCTTCCAT	CCCATTTATT	GGCCAGCCTT	TTTGATGAGT	180
TTGAATTGTC	CCTTATTCAA	ACAGCTCTGT	GTGCATGGGT	GGTGGACGAT	AGAGGGCGTG	240
AAAATGAGTA	AGAGCTTGGG	TAATGTTTA	GACGCTCAAA	AGCTCGCCAT	GGACTATGGG	300
ATTGAAGAAT	TACGCTATTT	TTTATTGCGT	GAGGTGCCCT	TTGGGCAAGA	TGGGGATTTT	360
TCTAAAAAG	CGTTAGTAGA	ACGGATTAAAT	CGGAATTGAA	ATAACGATT	GGGAAATTG	420
TTGAATCGTT	TGCTAGGCAT	GGCTAAAAAG	TATTCATCAATT	ATTCTCTAAA	AAGCACCAAA	480
ATCACTCGGT	ATTATCCTAA	AGAGCTAGAA	AAAGCACATC	AAATTTTAA	TAACGCTAAT	540
TCTTTTGTC	CTAAAATGCA	ATTGCAATAAG	GCTTTAGAGG	AATTGTTAA	TATTTATGAT	600
TTTTGATAA	AACTCATCGC	TAAGAACAGAG	CCGTGGGTCT	TGCACAAAAAA	CAACGAATCA	660
GAAAAATTAG	AAGCCTTATT	GAGTTGATC	GCAAAACACGC	TACTACAACT	AAGCTTCTTG	720
CTCTATCGGT	TCATGCCAAA	GAGCGCTATG	AAATTAGCGA	GCGCTTTTCG	TGTAGAAATC	780
ACGCCAATA	ATTACGAACG	CTTTTTTAAG	GCTAAAAAAAT	TACAAGATAT	GGTTTTACAA	840
GACACCGAGC	CTTTTATTTTC	CAAAATTGAG	AAAATTGAAA	AGATTGAAAA	GATTGAAAAG	900
ATTGAAAAGA	TTGAAAAGG	GGAGGAAGCC	CTAGCAGAAA	AAGCAGAAAA	AAAAGAAAAA	960
GAAAAGCCC	CACCAACACAA	AGAAAATTAT	ATTAGTATG	AGGATTTCAA	GAAAGTAGAG	1020
ATTAAAGTGG	GGCTTATCAA	AGAACCTCAA	AGGATTGAAA	AATCCAATAA	ATTACTGCGC	1080
TTAAAGTGG	ATTAGGCGA	AAATCGTTTG	AGGCAGATCA	TCTCAGGGAT	CGCTTTGGAT	1140
TATGACCTG	AAAGCTTGGT	GGGTCAAATG	GTGTGCGTGG	TGGCTAATT	AAAACCCGCA	1200
AAGCTTATGG	GTGAAATGAG	TGAGGGCATG	ATTTAGCGG	TGCGAGATAA	TGATAATCTG	1260
GCTTAATCA	GCCCTACCAAG	AGAAAAAATT	GCAGGAAGTT	TGATCAGC		1308

(2) INFORMATION FOR SEQ ID NO:377:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...342
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:377

ATGAAACGAC	CGATCAGCAA	ATTGAAACAA	AACTTTTAC	AATTCAAACA	TTCTTTCAAC	60
AAACATTTAG	ATAAGTACAG	CCTTTATTAT	AGGTGTTCA	ATATCAGCTC	TATCGTTATA	120
GGTTTTTAA	TAGCGTTTT	TTCTTATGGG	GCAGGGGTGA	TTTAGTTTA	TCCAATATTA	180
TTCTTGTGTTG	CTCTTATAAT	AAAACCTAGC	TTTTTTATT	ACACTACTTA	TCTTTGCTA	240
CTCGTTCTC	TCAGCATAAT	AAGCAAATAC	TATCTCTAA	GCCACGCAA	TTTCACAATG	300
AAGCTAATCA	TGCTTATGAC	TCAATGGCAA	AATTGGTCT	TA		342

(2) INFORMATION FOR SEQ ID NO:378:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

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- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...5
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:378

ATGGG

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(2) INFORMATION FOR SEQ ID NO:379:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...381
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:379

GTGTTCACTT ATTCCCTTGGG GCAGGGTTTC TTTTCTCTAA GTATCGGTTT AGGGATCAAT	60
ATCACTTATG CTGCCGTAC GGATAAAACG CAGAATTGCG TTAAAAGCAC GATTTGGGTG	120
GTTTTATCAG GRATTTTAAT TTCTCTTGTG RCAGGGCTTA TGATTTTCAC TTTTGTGTTT	180
GAATATGGGG CTAATGTCTC ACAAGGCACA GGGTTAACCT TCACCTCTTT ACCGGTGTT	240
TTTGGCCAAA TGGGAGGCAT ACGCGTCCCT TGTTCATT CTTTCTTGC TCGCGCTCGC	300
TTTGTGTCGC ATCACTTCATA CGGTGGCTTT ATTAGAGCCA AGCGTGATGT ATCTTACCGA	360
AAAGTATCAA TACTCTCGTT T	381

(2) INFORMATION FOR SEQ ID NO:380:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 537 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...537

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380

ATGAAACCAT	TGCATTTTTC	ACACCTGGAC	AGAGAGCAAT	CAGGCGATGT	GGGTTTTATC	60
ATTAAAAACC	TTATTTTTT	AGGGTTTTT	TCCCTTATTGG	GTGGGTGAA	TACCGAGTAT	120
TTCTATGGC	CTAGCATGCT	GGAATTAAA	AAAATCCTT	TAGAAGAAA	TCGTAAAAAA	180
ACGTTTTAG	AATACGCCA	AAGGCATT	AAAACAGCCC	TAGCAAACTA	CCGCAATCAA	240
AAAGAAACCA	GCGAATCTT	GTAAAGATT	TTAATGATG	AAGAGTCCAG	GCGGATTTTA	300
GAAAAGATCT	AAAAAAATG	TTTGACGCC	TATAAAATCA	AACCTTGCT	CTCTAAAC	360
CCCTCCAAA	AAACCAATT	TTTATCATG	GCTAGAGCGA	GCGAATTGGA	AAAAACTTAT	420
CTTTTTTCA	CCTTAATCAA	CAAGTATT	CCGAGCGCTC	AAAGCCAATT	GCCCTTAAAG	480
ATTCTAAAG	ATAGCGACGG	GTTGTTGGT	CAATTGGCG	TGAGTATTGA	TCTCCAA	537

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381

ATGAATGCCAT	TGAAGCGTGC	GTGTTTAAGA	TTGATGGGCG	AAACCAATAC	CGATGATTTA	60
ASCCCARYGA	GCGACGCTT	CACACGGAGC	GATATTCTT	TACACGCCA	AGCCATGCTA	120
AAAAACCGGA	TTGAAATT	CGAACAAACGC	ATTGAAGCCA	TTAAAACTAA	AGGCCTTCCT	180
GTAGCGTATG	GGGGCGATGT	GGTTGGCAC	CGAACGCTCA	AAAAAAGCGC	GACTAACTCT	240
ATCATGTGCC	ATTTTGGTAA	GGACATTCTT	TTTGTGCCTA	ATAAAAGGAG	TGGAGGCATT	300
GTGATTGGGG	GGGTGATCGC	TCCGATTTC	TTTGCAGCTT	GTGAAGATA	CGGGGCGTTA	360
CCCAATTGTGG	CTGATGTTAA	GGATTGAAA	GAGGGCGATA	TCAATTAAAT	CTACCCCTTAT	420
AAAGGCAGAA	TCACGCTGAA	CGATAAGGTG	GTAGCACCT	TTAAGCTAGA	GCCTGAAACT	480
TTATTAGATG	AAGTCAGGGC	TTCTGGCGT	ATCCCCCTAA	TCATTGGTAG	GGGTTTGACC	540
AATAAAGCGC	GTAAATTTT	GGGCCGGCGA	ATCGGAAGCG	TTCAAAAAAC	CTTCCGCC	600
TCAAGCGCGC	TAAGGCTACA	CTTTGCC				627

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

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- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...702
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:382

ATGCTTTCAG CCCACCAACC	TTTTAAAAAT TACCCCTGATC	TGATTAAAAA AGAGTTGCAA	60
GAGCATAACG CCTATCGGAG	CGTCGCTAGT GGGGTGCCAG	CGATGTTGTA TGTTATCACG	120
CAAGGTTATG AGGGATGGA	ATTGAGCTTG TTTAGTAGAG	ATGTGATCGC ATTAAGCACC	180
SCCGTAGGGT TAAGCCATAA	TGTTTTGAC CGGGCCTTTT	TTTTGGGCCT GTGCGATAAAA	240
ATTGTGCCAG GCTTGCTCAT	AGGAGCGTTA ACCTTTGGGA	ATTTAGCGAG CGTGTGTTG	300
CCAAGGGGGC CTATGGTGA	CGGGATAGAA ATTAAAAA	AAGCCAAAGG GCGCCAAAGAT	360
TTTCAATGG GAAAGATCAA	CAGAGAAGAG CTTTAAAG	TGGAAATGCA AAGCTATCAT	420
GATGTGGGCA TTGCACTTT	TTATGGCAGC GCTAATTCTA	ATCAAATGAT GATGGAGTT	480
ATGGGGTTGC ATGTGCCAA	TTCTAGCTTT ATCAACCCCTA	ACAACCCCTT ACGAAAGGTT	540
TTAGTAGAAG AGAGCGCTAA	AAGATTAGCG AGCGGGAAAG	TCCTGCCTTT AGCCAAACTC	600
ATTGATGAAA AAAGCATTCT	AAACGCTTAA TAGGCTTAA	TGGCAACAGG GGGTTCTACT	660
AACCACACTT TGCATTGAT	CGCTATCGCA GATCTGTGG	GG	702

(2) INFORMATION FOR SEQ ID NO:383:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 795 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...795
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:383

ATGAAATTCTT TAAAATTCTT	TGCCAGTAGC GTAACCTCTAG	ATGAAAAATT TTTAATGTC	60
CTTCCTTGCA ACGCTTTTC	TAACGCTTAC AAAATAGCG	ATTTGTTTTC TTTCTCTAAA	120
GGCCTTTTAG GCGCTTTTTT	AATCGGGTTT GTGGTGTATT	ATGGTTGCCG GCTAATCCCT	180
AAAAAAACGCT	TGAAATATTTC ATTAGAATGG	CTGTTTATAG GAAGCGGTAT TATTTTTAGC	240
GTGGCAGAAA	TTTTTACGCT GTTTATGTTT	AAAATGCCCTT TTCCCAAAGG CTTGATTGAC	300
ACGCTTTAG	CCACAAACAG CTCTGAAACG	ATGGCGTTTA TAAAAGCTA TAAAATTAT	360
TTCGCTTACT	ACGCTTTGAT TTGATCGCT	TTGTTGATCG CCATTAAT CATTCGCTT	420
AGAGCGCTTG	TGCCTGGTGT GATAGCGAGC	GTTTTAGGGC TTCCTATCCT TACAATAGGG	480
AGCGTTCGTA	ACATTAACAA CCTTACAAAG AACGATGCGA	TTTTAAAAG ATCACTCTTT	540
TCTCTTCTT	TAGCTAGGGG GTTTTATTCC	GCTTATTTGA GTTGTGTTGA TCGCCAAACAA	600
GCCTAAAAAT	TTTATAGCTT TTTAAATAAT	CTTTATTTAC CAAGCGATTA TCTTTCTAGC	660
ACGGGCGATA	TTTCAAATGT CGTCTAGTC ATCGCGAAAG	CGCGAGCAGA AATTTCATGC	720
AACTCTATGG	CTATAGCGTT CCTAATAATC	CCTTATSCGA GCGAACTCGC CAACGAGAGA	780
GAGAGAGAGA	GAGAG		795

(2) INFORMATION FOR SEQ ID NO:384:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384

Met	Cys	Ser	Gln	Glu	Ile	Leu	Ser	Ser	Leu	Gln	Thr	Ile	Ile	Ala	Glu
1					5				10					15	
Gln	Phe	Ser	Ile	Asn	Ile	Ile	Thr	Gln	Leu	Ala	Asn	Lys	Leu	Thr	Gln
					20				25					30	
Val	Lys	Asn	Leu	Asn	Phe	Phe	Glu	Asn	Lys	Asp	His	Thr	Ile	Lys	Leu
					35				40					45	
Asn	Thr	Ile	His	Asn	Gly	Leu	His	Ile	Arg	Pro	Leu	Asn	Tyr	Val	Ser
					50				55					60	
Asn	Leu	Phe	Phe	Asn	Leu	Gln	Arg	Ile	Ile	Gly	Leu	Ile	Ser	Leu	Phe
					65				70					80	
Gly	Ile	Leu	Phe	Ser	Ile	Ser	Ile	Tyr	Leu	Pro	Phe	Ile	Met	Ile	Phe
					85				90					95	
Ala	Thr	Val	Pro	Cys	Ile	Leu	Ile	Ser	Asn	His	Ile	Ala	Lys	Lys	His
					100				105					110	
Ser	Ala	Ser	Ile	Asp	Lys	Leu	Gln	Asp	Gln	Lys	Glu	Ser	Met	Gln	Asn
					115				120					125	
Tyr	Leu	Tyr	Ser	Gly	Leu	Asp	Asn	Gln	Lys	Asn	Lys	Asp	Asn	Leu	Leu
					130				135					140	
Phe	Asn	Phe	Met	Leu	Asn	Phe	His	His	Lys	Phe	Ile	Glu	Thr	Lys	Glu
					145				150					160	
Leu	Tyr	Leu	Asn	Asn	Phe	Val	Lys	Val	Ala	Gln	Lys	Asn	Leu	Ile	Phe
					165				170					175	
Thr	Ile	Tyr	Ala	Asp	Val	Leu	Ile	Thr	Thr	Leu	Ser	Ile	Ala	Leu	Phe
					180				185					190	
Phe	Leu	Met	Val	Phe	Ile	Ile	Leu	Ser	Lys	Leu	Ile	Gly	Val	Gly	Ala
					195				200					205	
Ile	Ala	Gly	Tyr	Ile	Gln	Ala	Phe	Ser	Ser	Thr	Gln	Gln	Gln	Leu	Gln
					210				215					220	
Asp	Leu	Ser	Phe	Tyr	Gly	Lys	Trp	Phe	Phe	Ala	Ile	Asn	Lys	Tyr	Phe
					225				230					240	
Glu	Asn	Tyr	Phe	Cys	Ile	Leu	Asp	Tyr	Lys	Ile	Pro	Lys	Pro	Glu	Thr
					245				250					255	
Gln	Ile	Lys	Leu	Glu	Glu	Lys	Ile	His	Ser	Ile	Thr	Phe	Glu	Asn	Ile
					260				265					270	
Ser	Phe	Ser	Tyr	Pro	Asn	Ser	Lys	Leu	Ile	Phe	Glu	Asn	Phe	Asn	Leu
					275				280					285	
Ser	Leu	His	Ser	Asn	Lys	Ile	Tyr	Ala	Leu	Val	Gly	Lys	Asn	Ala	Ser
					290				295					300	
Gly	Lys	Ser	Thr	Leu	Ile	Asn	Leu	Leu	Gly	Phe	Tyr	Thr	Pro	Asn	
					305				310					320	
Ser	Gly	Gln	Ile	Ile	Asn	Asn	Lys	Tyr	Pro	Leu	Gln	Asp	Leu	Glu	
					325				330					335	
Leu	Asn	Ser	Tyr	His	Gln	Gln	Met	Ser	Ala	Ile	Phe	Gln	Asp	Phe	Ser
					340				345					350	
Leu	Tyr	Ala	Gly	Tyr	Ser	Ile	Asp	Asp	Asn	Leu	Phe	Met	Gln	Asn	Asn
					355				360					365	

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Ile Thr Lys Glu Gln Leu Lys Gln Lys Arg Glu Ile Leu Lys Ser Phe
 370 375 380
 Asp Glu Asn Phe Gln Asn Cys Leu Asn Asp Cys Asn Asn Thr Leu Phe
 385 390 395 400
 Gly Ala Gln Tyr Asn Gly Val Asp Phe Ser Leu Gly Gln Lys Gln Arg
 405 410 415
 Ile Ala Thr Met Arg Ala Phe Leu Lys Pro Ser Asn Cys Ile Val Leu
 420 425 430
 Asp Glu Pro Ser Ser Ala Ile Asp Pro Ile Met Glu Lys Glu Phe Leu
 435 440 445
 Asp Phe Ile Phe Lys Lys Ser Gln Ser Lys Met Ala Leu Ile Ile Thr
 450 455 460
 His Arg Met Asn Ser Val Lys Gln Ala Asn Glu Ile Ile Val Leu Asp
 465 470 475 480
 Gln Gly Lys Leu Ile Glu Gln Gly Asn Phe Glu Thr Leu Met Lys Lys
 485 490 495
 Gln Gly Leu Phe Cys Glu Leu Phe Leu Lys Gln Gln Tyr
 500 505

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385

Met Lys Gly Pro Ile Leu Trp Pro Ala Phe Ser Gln Phe Ser Asp Gln
 1 5 10 15
 Asp Leu Ser Asp Ile Val Ala Tyr Leu Thr Ser Ile Leu Pro Lys Asn
 20 25 30
 Leu Ser Asp Lys Glu Val Phe Ala Gln Ser Cys Gln Arg Cys His Ser
 35 40 45
 Leu Asp Tyr Ala Lys Asp Lys Ala Phe Ser Asp Pro Lys Asp Leu Ala
 50 55 60
 Asn Tyr Leu Gly Ser His Ala Pro Asp Leu Ser Met Met Ile Arg Ala
 65 70 75 80
 Lys Gly Glu His Gly Leu Asn Val Phe Ile Asn Asp Pro Gln Lys Leu
 85 90 95
 Leu Pro Gly Thr Ala Met Pro Arg Val Gly Leu Asn Glu Lys Ala Gln
 100 105 110
 Lys Gln Val Ile Ser Tyr Leu Glu Lys Ala Gly Asp Arg Lys Lys His
 115 120 125
 Glu Arg Asn Thr Leu Gly Ile Lys Ile Met Ile Phe Phe Ala Val Leu
 130 135 140
 Ser Phe Leu Ala Tyr Ala Gly Lys Glu Lys Phe Gly Ala Lys Cys Ile
 145 150 155 160
 Lys Phe Lys Lys Gly Gly Thr Trp Phe Tyr Asp Phe
 165 170

(2) INFORMATION FOR SEQ ID NO:385:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 172 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...172
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:385

Met	Lys	Gly	Pro	Ile	Leu	Trp	Pro	Ala	Phe	Ser	Gln	Phe	Ser	Asp	Gln
1															
															10
															15
Asp	Leu	Ser	Asp	Ile	Val	Ala	Tyr	Leu	Thr	Ser	Ile	Leu	Pro	Lys	Asn
															20
															25
															30
Leu	Ser	Asp	Lys	Glu	Val	Phe	Ala	Gln	Ser	Cys	Gln	Arg	Cys	His	Ser
															35
															40
															45
Leu	Asp	Tyr	Ala	Lys	Asp	Lys	Ala	Phe	Ser	Asp	Pro	Lys	Asp	Leu	Ala
															50
															55
															60
Asn	Tyr	Leu	Gly	Ser	His	Ala	Pro	Asp	Leu	Ser	Met	Met	Ile	Arg	Ala
															65
															70
															75
															80
Lys	Gly	Glu	His	Gly	Leu	Asn	Val	Phe	Ile	Asn	Asp	Pro	Gln	Lys	Leu
															85
															90
															95
Leu	Pro	Gly	Thr	Ala	Met	Pro	Arg	Val	Gly	Leu	Asn	Glu	Lys	Ala	Gln
															100
															105
															110
Lys	Gln	Val	Ile	Ser	Tyr	Leu	Glu	Lys	Ala	Gly	Asp	Arg	Lys	Lys	His
															115
															120
															125
Glu	Arg	Asn	Thr	Leu	Gly	Ile	Lys	Ile	Met	Ile	Phe	Phe	Ala	Val	Leu
															130
															135
															140
Ser	Phe	Leu	Ala	Tyr	Ala	Gly	Lys	Glu	Lys	Phe	Gly	Ala	Lys	Cys	Ile
															145
															150
															155
Lys	Phe	Lys	Lys	Gly	Gly	Thr	Trp	Phe	Tyr	Asp	Phe				
															160
															165
															170

(2) INFORMATION FOR SEQ ID NO:386:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...133
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:386

Met	Glu	Arg	Lys	Thr	Leu	Gln	Ser	Ile	Leu	Cys	Leu	Ile	Lys	Lys	Glu
1															
															5
															10
															15

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Met Met Arg Pro Lys Gly Ile Leu Met Asn Cys Cys Arg Thr Trp Lys
 20 25 30
 His Gln Val Leu Lys Gln Ser Thr Thr Gly Leu Val Val Leu Ser Ile
 35 40 45
 Ile Ser Ser Thr Ala Pro Phe Ile Gly Leu Phe Gly Thr Val Val Glu
 50 55 60
 Ile Leu Glu Ala Phe Asn Asn Leu Gly Ala Leu Gly Gln Ala Ser Phe
 65 70 75 80
 Gly Val Ile Ala Pro Ile Ile Ser Lys Ala Leu Ile Ala Thr Ala Ala
 85 90 95
 Gly Ile Leu Ala Ala Ile Pro Ala Tyr Ser Phe Tyr Leu Ile Leu Lys
 100 105 110
 Arg Lys Val Tyr Asp Leu Ser Val Tyr Val Gln Met Gln Val Asp Ile
 115 120 125
 Leu Ser Ser Lys Lys
 130

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387

Met His Glu Arg Ile Glu Arg Gly Ile Unk Asn Asn Glu Cys Lys Glu
 1 5 10 15
 Ile Phe Gly Asn Glu Leu Lys Gln Arg Lys Thr Lys Leu Ile Glu Asp
 20 25 30
 Ile Glu Arg Arg Phe Lys Glu Cys Glu Glu Gln Phe Arg Gly Ser Val
 35 40 45
 Gly Lys Asn Ile Glu Gln Leu Glu Arg Val Lys Asp Ser Leu Ala
 50 55 60
 Ile Ile Lys Arg Ile Asn Asn Leu Gly Leu Asn Pro Asn Ser Asn Phe
 65 70 75 80
 Asn Met Asp Ser Gly Ile Asp Thr Ile Gly Leu Phe Ser Ser Ile Gly
 85 90 95
 Gly Leu Val Leu Leu Leu Thr Pro Val Val Gly Glu Phe Ala Leu
 100 105 110
 Ile Ala Gly Val Gly Leu Ala Leu Val Gly Val Gly Lys Ser Ile Trp
 115 120 125
 Ser Phe Asp Ser Asp Tyr Lys Lys Ser Gln Gln Arg Lys Glu Val
 130 135 140
 Asp Lys Asn Leu His Gln Ile Cys Glu Lys Leu Cys Arg Met
 145 150 155

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388

Met	Pro	Gly	Val	Tyr	Gln	Met	Ser	Ile	Glu	Pro	Leu	Leu	Lys	Glu	Cys
1						5			10					15	
Glu	Glu	Leu	Val	Gly	Leu	Gly	Ile	Lys	Ala	Val	Leu	Leu	Phe	Gly	Ile
						20			25					30	
Pro	Lys	His	Lys	Asp	Ala	Thr	Gly	Ser	His	Ala	Leu	Asn	Lys	Asp	His
						35			40					45	
Ile	Val	Ala	Lys	Ala	Thr	Arg	Glu	Ile	Lys	Arg	Phe	Lys	Asp	Leu	
						50			55					60	
Ile	Val	Ile	Ala	Asp	Leu	Cys	Phe	Cys	Glu	Tyr	Thr	Asp	His	Gly	His
						65			70					80	
Cys	Gly	Ile	Leu	Glu	Asn	Ala	Ser	Val	Ser	Asn	Asp	Lys	Thr	Leu	Lys
						85			90					95	
Ile	Leu	Asn	Leu	Gln	Gly	Leu	Ile	Leu	Leu	Lys	Ala	Val	Trp	Ile	Phe
						100			105					110	

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389

Val	Glu	Asn	Asn	Lys	Ser	Leu	Lys	His	Ala	Asn	Glu	Leu	Arg	Asp	Lys
1								5			10			15	
Arg	Asp	Glu	Leu	Glu	Phe	His	Leu	Arg	Glu	Leu	Phe	Gly	Gly	Asn	Val
						20			25					30	
Phe	Lys	Ser	Ser	Ile	Lys	Thr	His	Ser	Leu	Thr	Asp	Lys	Asp	Ser	Ala
						35			40					45	
Asp	Phe	Asp	Glu	Ser	Tyr	Asn	Leu	Asn	Ile	Gly	His	Gly	Unk	Asn	Unk
						50			55					60	
Ile															
65															

(2) INFORMATION FOR SEQ ID NO:390:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390

Met	Gln	Glu	Phe	Ser	Leu	Trp	Cys	Asp	Phe	Ile	Glu	Arg	Asp	Phe	Leu	
1																
														10	15	
Glu	Asn	Asp	Phe	Leu	Lys	Leu	Ile	Asn	Lys	Gly	Ala	Ile	Cys	Gly	Unk	
														20	25	30
Thr	Ser	Asn	Pro	Ser	Leu	Phe	Cys	Glu	Ala	Ile	Thr	Lys	Ser	Ala	Phe	
														35	40	45
Tyr	Gln	Asp	Glu	Ile	Ala	Lys	Unk	Gln	Arg	Gln	Lys	Ser				
														50	55	60

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390

Met	Gln	Glu	Phe	Ser	Leu	Trp	Cys	Asp	Phe	Ile	Glu	Arg	Asp	Phe	Leu	
1																
Glu	Asn	Asp	Phe	Leu	Lys	Leu	Ile	Asn	Lys	Gly	Ala	Ile	Cys	Gly	Unk	
														20	25	30
Thr	Ser	Asn	Pro	Ser	Leu	Phe	Cys	Glu	Ala	Ile	Thr	Lys	Ser	Ala	Phe	
														35	40	45
Tyr	Gln	Asp	Glu	Ile	Ala	Lys	Unk	Gln	Arg	Gln	Lys	Ser				
														50	55	60

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 619 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391

Val Phe Val Ala Ser Lys Gln Ala Asp Glu Gln Lys Lys Leu Val Ile
 1 5 10 15
 Glu Gln Glu Val Gln Lys Arg Gln Phe Gln Lys Ile Glu Glu Leu Lys
 20 25 30
 Ala Asp Met Gln Lys Gly Val Asn Pro Phe Phe Lys Val Leu Phe Asp
 35 40 45
 Gly Gly Asn Arg Leu Phe Gly Phe Pro Glu Thr Phe Ile Tyr Ser Ser
 50 55 60
 Ile Phe Ile Leu Phe Val Thr Ile Val Leu Ser Val Ile Leu Phe Gln
 65 70 75 80
 Ala Tyr Glu Pro Val Leu Ile Val Ala Ile Val Ile Val Leu Val Ala
 85 90 95
 Leu Gly Phe Lys Lys Asp Tyr Arg Leu Tyr Gln Arg Met Glu Arg Ala
 100 105 110
 Met Lys Phe Lys Lys Pro Phe Leu Phe Lys Gly Val Lys Asn Lys Ala
 115 120 125
 Phe Met Ser Ile Phe Ser Met Lys Pro Ser Lys Glu Met Ala Asn Asp
 130 135 140
 Ile His Leu Asn Pro Asn Arg Glu Asp Arg Leu Val Ser Ala Ala Asn
 145 150 155 160
 Ser Tyr Leu Ala Asn Asn Tyr Glu Cys Phe Leu Asp Asp Gly Val Ile
 165 170 175
 Leu Thr Asn Asn Tyr Ser Leu Leu Gly Thr Ile Lys Leu Gly Gly Ile
 180 185 190
 Asp Phe Leu Thr Thr Ser Lys Lys Asp Leu Ile Glu Leu His Ala Ser
 195 200 205
 Ile Tyr Ser Val Phe Arg Asn Phe Val Thr Pro Glu Phe Lys Phe Tyr
 210 215 220
 Phe His Thr Val Lys Lys Ile Val Ile Asp Glu Thr Asn Arg Asp
 225 230 235 240
 Tyr Gly Leu Ile Phe Ser Asn Asp Phe Met Arg Ala Tyr Asn Glu Lys
 245 250 255
 Gln Lys Arg Glu Ser Phe Tyr Asp Ile Ser Phe Tyr Leu Thr Ile Glu
 260 265 270
 Gln Asp Leu Leu Asp Thr Leu Asn Glu Pro Val Met Asn Lys Lys His
 275 280 285
 Phe Ala Asp Asn Asn Phe Glu Glu Phe Gln Arg Ile Ile Arg Ala Lys
 290 295 300
 Leu Glu Asn Phe Lys Asp Arg Ile Glu Leu Ile Glu Glu Leu Leu Ser
 305 310 315 320
 Lys Tyr His Pro Thr Arg Leu Lys Glu Tyr Thr Lys Asp Gly Ile Ile
 325 330 335
 Tyr Ser Lys Gln Cys Glu Phe Tyr Asn Phe Leu Val Gly Met Asn Glu
 340 345 350
 Ala Pro Phe Ile Cys Asn Arg Lys Asp Leu Tyr Leu Lys Glu Lys Met
 355 360 365
 His Gly Gly Val Lys Glu Val Tyr Phe Ala Asn Lys His Gly Lys Ile
 370 375 380
 Leu Asn Asp Asp Leu Ser Glu Lys Tyr Phe Ser Ala Ile Glu Ile Ser
 385 390 395 400
 Glu Tyr Ala Pro Lys Ser Gln Ser Asp Leu Phe Asp Lys Ile Asn Ala
 405 410 415

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Leu Asp Ser Glu Phe Ile Phe Met His Ala Tyr Ser Pro Lys Asn Ser
 420 425 430
 Gln Val Leu Lys Asp Lys Leu Ala Phe Thr Ser Arg Arg Ile Ile Ile
 435 440 445
 Ser Gly Gly Ser Lys Glu Gln Gly Met Thr Leu Gly Cys Leu Ser Glu
 450 455 460
 Leu Val Gly Asn Gly Asp Ile Thr Leu Gly Ser Tyr Gly Asn Ser Leu
 465 470 475 480
 Val Leu Phe Ala Asp Ser Phe Glu Lys Met Lys Gln Ser Val Lys Glu
 485 490 495
 Cys Val Ser Ser Leu Asn Ala Lys Gly Phe Leu Ala Asn Ala Ala Thr
 500 505 510
 Phe Ser Met Glu Asn Tyr Phe Phe Ala Lys His Cys Ser Phe Ile Thr
 515 520 525
 Leu Pro Phe Ile Phe Asp Val Thr Ser Asn Asn Phe Ala Asp Phe Ile
 530 535 540
 Ala Met Arg Ala Met Ser Phe Asp Gly Lys Glu Asp Asn Asn Ala Trp
 545 550 555 560
 Gly Asn Ser Val Met Thr Leu Lys Ser Glu Ile Asn Ser Pro Phe Tyr
 565 570 575
 Leu Asn Phe His Met Pro Thr Asp Phe Gly Ser Ala Ser Ala Gly His
 580 585 590
 Thr Leu Ile Leu Gly Ser Thr Gly Ser Gly Lys Asn Ser Val Tyr Val
 595 600 605
 His Asp Ser Lys Arg Tyr Gly Ala Ile Cys Leu
 610 615

(2) INFORMATION FOR SEQ ID NO:392:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: amino acid
 - (C) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...110
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:392

Val Lys Thr Ser Cys Leu Val Thr Ile Gly Arg Ile Arg Gly Val Phe
 1 5 10 15
 Ile Ile Lys Ala Gln Leu Leu Leu Arg Glu Gly Gly Phe Met Asn Phe
 20 25 30
 Thr Ala Tyr Asn Thr Lys Thr Pro Gly His Leu His Leu Tyr Val His
 35 40 45
 Lys Gly His Thr Glu Leu Gly Glu Gly Glu Arg Leu Ile Lys Thr Leu
 50 55 60
 Ser Met Lys Leu Ala Gln Gly Leu Pro Lys Glu Trp Arg Val Phe Pro
 65 70 75 80
 Ser Asn Glu Trp Pro Lys Glu Phe Asn Ile Leu Ala Leu Pro Tyr Glu
 85 90 95
 Val Phe Ala Lys Glu Arg Gly Ser Ser Trp Ala Lys His Leu
 100 105 110

(2) INFORMATION FOR SEQ ID NO:393:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...68
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:393

```

Val Ala Lys Asp Ile Ile Ser Glu Ser Gln Asn Leu Cys Ala Arg Lys
1          5           10          15
Phe Arg Arg Leu Tyr Ala Leu Leu Lys Glu Asn Glu Met Leu Ile Arg
20         25           30
Ile Gly Ser Tyr Gln Met Gly Asn Asp Lys Glu Leu Asp Glu Ala Ile
35         40           45
Lys Lys Lys Ala Leu Met Glu Gln Phe Leu Val Gln Asp Glu Asn Ala
50         55           60
Leu Unk Ala Phe
65

```

(2) INFORMATION FOR SEQ ID NO:394:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 446 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...446
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:394

```

Met Lys Ser Arg Pro Ile Leu Ala Gln Ala Tyr Ala Leu Gln Met Met
1          5           10          15
Val Lys Gln Ile Ala Phe Leu Glu Thr Ile Leu Val Glu Asn Glu Gln
20         25           30
Asp Ala Leu Ile Leu Glu Asn Ser Leu Ile Lys Gln Leu Lys Pro Lys
35         40           45
Tyr Asn Ile Leu Leu Arg Asp Asp Lys Thr Tyr Pro Tyr Ile Tyr Met
50         55           60
Asp Phe Ser Ile Asp Phe Pro Ile Pro Leu Ile Thr Arg Lys Ile Leu
65         70           75          80
Lys Gln Pro Gly Val Lys Tyr Phe Gly Pro Phe Thr Ser Gly Ala Lys
85         90           95
Asp Ile Leu Asp Ser Leu Tyr Glu Leu Leu Pro Leu Val Gln Lys Lys
100        105          110

```

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Asn Cys Ile Lys Asp Lys Lys Ala Cys Met Phe Tyr Gln Ile Glu Arg
 115 120 125
 Cys Lys Ala Pro Cys Glu Asp Lys Ile Thr Lys Glu Glu Tyr Leu Lys
 130 135 140
 Ile Ala Lys Glu Cys Leu Glu Met Ile Glu Asn Lys Asp Arg Leu Ile
 145 150 155 160
 Lys Glu Leu Glu Leu Lys Met Glu Arg Leu Ser Ser Asn Leu Arg Phe
 165 170 175
 Glu Glu Ala Leu Ile Tyr Arg Asp Arg Ile Ala Lys Ile Gln Lys Ile
 180 185 190
 Ala Pro Phe Thr Cys Met Asp Leu Ala Lys Leu Tyr Asp Leu Asp Ile
 195 200 205
 Phe Ala Phe Tyr Gly Gly Asn Asn Lys Ala Val Leu Val Lys Met Phe
 210 215 220
 Met Arg Gly Gly Lys Ile Ile Ser Ser Ala Phe Glu Lys Ile His Ser
 225 230 235 240
 Leu Asn Gly Phe Asp Thr Asp Glu Ala Met Lys Gln Ala Ile Ile Asn
 245 250 255
 His Tyr Gln Ser His Leu Pro Leu Met Pro Glu Gln Ile Leu Leu Ser
 260 265 270
 Ala Cys Ser Asn Glu Thr Leu Lys Glu Leu Gln Glu Phe Ile Ser His
 275 280 285
 Gln Tyr Ser Lys Lys Ile Ala Leu Ser Ile Pro Lys Lys Gly Asp Lys
 290 295 300
 Leu Ala Leu Ile Glu Ile Ala Met Lys Asn Ala Gln Glu Ile Phe Ser
 305 310 315 320
 Gln Glu Lys Thr Ser Asn Glu Asp Arg Ile Leu Glu Glu Ala Arg Ser
 325 330 335
 Leu Phe Asn Leu Glu Cys Val Pro Tyr Arg Val Glu Ile Phe Asp Thr
 340 345 350
 Ser His His Ser Asn Ser Gln Cys Val Gly Gly Met Val Val Tyr Glu
 355 360 365
 Asn Asn Ala Phe Gln Lys Asp Ser Tyr Arg Arg Tyr His Leu Lys Gly
 370 375 380
 Ser Asn Glu Tyr Asp Gln Met Ser Glu Leu Leu Thr Arg Arg Ala Leu
 385 390 395 400
 Asp Phe Ala Lys Glu Pro Pro Pro Asn Leu Trp Val Ile Asp Gly Gly
 405 410 415
 Arg Ala Gln Leu Asn Ile Ala Leu Glu Ile Leu Lys Ser Ser Gly Ser
 420 425 430
 Phe Val Glu Val Ile Ala Ile Ser Lys Glu Lys Arg Gly Phe
 435 440 445

(2) INFORMATION FOR SEQ ID NO:395:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...84
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:395

Val Ser Leu Gly Ala Phe Gln Gly Tyr Tyr Gly Gly Leu Val Asp Leu

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1	5	10	15												
Val	Gly	Gln	Arg	Leu	Ser	Glu	Ile	Trp	Ser	Ala	Ile	Pro	Met	Leu	Phe
				20				25					30		
Leu	Leu	Ile	Val	Ile	Ser	Ser	Ala	Phe	Asn	Ser	Asn	Phe	Trp	Ile	Ile
				35				40				45			
Leu	Phe	Leu	Val	Leu	Leu	Phe	Ser	Trp	Met	Gly	Leu	Ser	Gln	Val	Val
				50				55			60				
Arg	Thr	Glu	Phe	Leu	Lys	Ala	Arg	Asn	Met	Asp	Tyr	Thr	Lys	Ala	Ala
				65				70			75			80	
Arg	Ala	Leu	Gly												

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396

Met	Ser	Glu	Ala	Tyr	Phe	Leu	His	His	Lys	Asn	Ala	Ser	Gln	Val	Ser
							5		10				15		
Leu	Asn	Glu	Gln	Val	Leu	Asn	Val	Met	Lys	Gln	Val	Gln	Leu	Asp	Glu
							20		25				30		
Asn	Phe	Trp	Asn	Val	Ser	Leu	Met								
							35								40

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397

Val	Ile	Leu	Ile	Phe	Ile	Ile	Val	Val	Glu	Asp	Gln	Lys	Gly	Ile	Phe
							5		10			15			
Pro	Ile	Ala	Ala	Ser	Lys	Arg	Lys	Ser	Gln	Ser	Ser	Val	Ile	Ile	Glu
							20		25			30			

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Asp Val Cys Phe Ser Lys Glu Asp Phe Val Glu Gly Ala Lys Ala Ile
 35 40 45
 Glu Gly Leu Leu Lys Lys His Gly Phe Lys Asp Asn Gly Ile Ile Phe
 50 55 60
 Gly His Ala Leu Ser Gly Asn Leu His Phe Val Val Thr Pro Ile Leu
 65 70 75 80
 Glu Asn Glu Ala Glu Arg Lys Ala Phe Glu Asn Leu Val Ser Glu Met
 85 90 95
 Phe Leu Met Val Ser Ser Gly Ser Ile Lys Ala Glu His Gly
 100 105 110
 Thr Gly Arg Met Val Ala Pro Phe Val Glu Met Glu Trp Gly Glu Lys
 115 120 125
 Ala Tyr Lys Ile His Lys Gln Ile Lys Glu Leu Phe Asp Pro Asn Gly
 130 135 140
 Leu Leu Asn Pro Asp Val Ile Ile Thr Asn Asp Lys Glu Ile His Thr
 145 150 155 160
 Lys Asn Leu Lys Ser Ile Tyr Pro Ile Glu Glu His Leu Asp Met Cys
 165 170 175
 Met Glu Cys Gly Phe Cys Glu Arg Ile Cys Pro Ser Lys Asp Leu Ser
 180 185 190
 Leu Thr Pro Arg Gln Arg Ile Val Ile His Arg Glu Val Glu Arg Leu
 195 200 205
 Lys Glu Arg Val Ser His Gly His Asp Glu Asp Gln Val Leu Leu Asp
 210 215 220
 Glu Leu Leu Lys Glu Ser Glu Tyr Leu Ala His Ala Thr Cys Ala Val
 225 230 235 240
 Cys His Met Cys Ser Thr Leu Cys Pro Leu Gly Ile Asp Thr Gly Unk
 245 250 255
 Ile Ala Leu Asn His Tyr Gln Lys Asn Pro Lys Gly Glu Lys Ile Ala
 260 265 270
 Ser Lys Ile Leu Lys Ser His Ala Asn Asp His Lys Arg Gly Ser Phe
 275 280 285
 Phe Phe Lys Unk Arg Phe Arg Gly Phe Lys Asn Ser
 290 295 300

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398

Met Lys Glu Lys Asn Phe Trp Pro Leu Gly Ile Met Ser Val Leu Ile
 1 5 10 15
 Phe Gly Leu Gly Ile Val Val Phe Leu Val Val Phe Ala Leu Lys Asn
 20 25 30
 Ser Pro Lys Asn Asp Leu Val Tyr Phe Lys Gly His Asn Glu Val Asp
 35 40 45
 Leu Asn Phe Asn Ala Met Leu Lys Thr Tyr Glu Asn Phe Lys Ser Asn
 50 55 60
 Tyr Arg Phe Ser Val Gly Leu Lys Pro Leu Thr Glu Ser Pro Lys Thr

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65	70	75	80
Pro Ile Leu Pro Tyr Phe Ser Lys Gly Thr His Gly Asp Lys Lys Ile			
85	90	95	
Gln Glu Asn Leu Leu Asn Asn Ala Leu Ile Leu Glu Lys Ser Asn Thr			
100	105	110	
Leu Tyr Ala Gln Leu Gln Pro Leu Lys Pro Ala Leu Asp Ser Pro Asn			
115	120	125	
Ile Gln Val Tyr Leu Ala Phe Tyr Pro Ser Gln Ser Gln Pro Arg Leu			
130	135	140	
Leu Gly Thr Leu Asp Cys Lys Asn Ala Cys Glu Pro Leu Lys Phe Asp			
145	150	155	160
Leu Leu Glu Gly Asp Lys Val Gly Arg Tyr Lys Ile Leu Phe Lys Phe			
165	170	175	
Val Phe Lys Asn Lys Glu Glu Leu Ile Leu Glu Gln Leu Leu Phe Leu			
180	185	190	
Ser Ser Met Ala Cys Met Gly Ile Ser Ile Leu Lys Asn Ala Lys Ala			
195	200	205	
Phe Phe Lys Tyr Lys Ile			
210			

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399

Met Pro Ile Lys Gly Ser Phe Leu Ala Arg Asn Arg Leu Val Ile Ala			
1	5	10	15
Leu Thr Asp Ala Val Ile Ile Pro Gln Ala Asp Leu Lys Ser Gly Ser			
20	25	30	
Met Ser Ser Ala Arg Leu Ala Gln Lys Tyr Gln Lys Pro Leu Phe Val			
35	40	45	
Leu Pro Gln Arg Leu Asn Glu Ser Asp Gly Thr Asn Glu Leu Leu Glu			
50	55	60	
Lys Gly Gln Ala Gln Gly Ile Phe Asn Ile Gln Asn Phe Ile Asn Thr			
65	70	75	80
Leu Leu Lys Asp Tyr His Leu Lys Glu Met Pro Glu Met Lys Asp Glu			
85	90	95	
Phe Leu Glu Tyr Cys Ala Lys Asn Pro Ser Tyr Glu Glu Ala Tyr Leu			
100	105	110	
Lys Phe Gly Asp Lys Leu Leu Glu Tyr Glu Leu Leu Gly Lys Ile Lys			
115	120	125	
Arg Ile Asn His Leu Val Val Leu Ala			
130	135		

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids

334

(B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400

Met	Val	Val	Glu	Leu	Lys	Asn	Ile	Glu	Lys	Ile	Tyr	Glu	Asn	Gly	Phe
1			5				10					15			
His	Ala	Leu	Lys	Gly	Val	Asn	Leu	Glu	Leu	Lys	Gly	Asp	Ile	Leu	
		20					25					30			
Gly	Val	Ile	Gly	Tyr	Ser	Gly	Ala	Gly	Lys	Ser	Thr	Leu	Ile	Arg	Leu
		35				40					45				
Ile	Asn	Cys	Leu	Glu	Arg	Pro	Ser	Ser	Gly	Glu	Val	Leu	Val	Asn	Gly
		50				55					60				
Val	Asn	Leu	Leu	Asn	Leu	Lys	Pro	Lys	Glu	Leu	Gln	Lys	Ala	Arg	Gln
		65			70			75			80				
Lys	Ile	Gly	Met	Ile	Phe	Gln	His	Phe	Asn	Leu	Leu	Ser	Ala	Lys	Asn
						85			90			95			
Val	Phe	Glu	Asn	Val	Ala	Phe	Ala	Leu	Glu	Ile	Ala	Arg	Trp	Glu	Lys
	100						105					110			
Thr	Lys	Ile	Lys	Ser	Arg	Val	His	Glu	Leu	Leu	Glu	Leu	Val	Gly	Leu
		115					120					125			
Glu	Asp	Lys	Val	His	Phe	Tyr	Pro	Lys	Gln	Leu	Ser	Gly	Gly	Gln	Lys
		130				135					140				
Gln	Arg	Val	Ala	Ile	Ala	Arg	Ser	Leu	Ala	Asn	Cys	Pro	Asn	Leu	Leu
		145			150			155			160				
Leu	Cys	Asp	Glu	Ala	Thr	Ser	Ala	Leu	Asp	Ser	Lys	Thr	Thr	His	Ser
			165				170					175			
Ile	Leu	Thr	Leu	Leu	Ser	Gly	Ile	Gln	Lys	Phe	Asp	Leu	Ser	Ile	
		180				185					190				
Val	Phe	Ile	Thr	His	Gln	Ile	Glu	Val	Val	Lys	Glu	Leu	Cys	Asn	Gln
		195					200					205			
Met	Cys	Val	Ile	Ser	Ser	Gly	Glu	Ile	Val	Glu	Arg	Gly	Ser	Val	Glu
		210				215					220				
Glu	Ile	Phe	Ala	Asn	Pro	Lys	His	Ala	Val	Thr	Lys	Glu	Leu	Leu	Gly
		225				230					235			240	
Ile	Lys	Asn	Glu	His	Ala	Asp	Gln	Lys	Ser	Gln	Asp	Ile	Tyr	Arg	Ile
			245				250					255			
Val	Phe	Leu	Gly	Glu	His	Leu	Asp	Glu	Pro	Ile	Ile	Ser	Unk	Phe	Unk
			260				265					270			

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 286 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401

Leu Unk Pro Met Lys Val Ile Gln Val Phe Leu Phe Ser Asn Pro Phe
 1 5 10 15
 Cys Ala Ile Val Pro Asn Thr Glu Pro Glu His Leu Glu His Tyr Asp
 20 25 30
 His Asp Leu Glu Arg Phe Phe Ala Tyr Lys Tyr Phe Leu Asp His
 35 40 45
 Ala Gln Lys Arg Val Ile Tyr Lys Glu Asp Pro Phe Leu Lys Asn Tyr
 50 55 60
 Ser Lys Asp Ala Ile Val Leu Glu Lys Asp Ile Tyr Asn Ile Gln
 65 70 75 80
 Tyr Ile Leu Lys Asp Gly Glu Pro Tyr Thr Ser Phe Glu Leu Lys Asn
 85 90 95
 Leu Gly Ala Phe Leu Val Trp Gly Leu Gly Glu His Asn Ala Thr Asn
 100 105 110
 Ala Ser Leu Ala Ile Leu Ser Ala Leu Asp Glu Leu Asn Leu Glu Glu
 115 120 125
 Ile Arg Asn Asn Unk Leu Asn Phe Lys Gly Ile Lys Lys Arg Phe Asp
 130 135 140
 Ile Leu Gln Lys Asn Asn Leu Ile Leu Ile Asp Asp Tyr Ala His His
 145 150 155 160
 Pro Thr Glu Ile Gly Unk Thr Leu Lys Ser Ala Arg Ile Tyr Ala Asn
 165 170 175
 Leu Leu Asn Thr Gln Glu Lys Ile Ile Val Ile Trp Gln Ala His Lys
 180 185 190
 Tyr Ser Arg Leu Met Asp Asn Leu Glu Glu Phe Lys Lys Cys Phe Leu
 195 200 205
 Glu His Cys Asp Arg Leu Ile Ile Leu Pro Val Tyr Ser Ala Ser Glu
 210 215 220
 Val Lys Arg Asp Ile Asp Leu Lys Ala His Phe Lys His Tyr Asn Pro
 225 230 235 240
 Thr Phe Ile Asp Arg Val Arg Lys Lys Gly Asp Phe Leu Glu Leu Leu
 245 250 255
 Val Asn Asp Asn Val Val Glu Thr Ile Glu Lys Gly Phe Val Ile Gly
 260 265 270
 Phe Gly Ala Gly Asp Ile Thr Tyr Gln Leu Arg Gly Glu Met
 275 280 285

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401

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Leu Unk Pro Met Lys Val Ile Gln Val Phe Leu Phe Ser Asn Pro Phe
 1 5 10 15
 Cys Ala Ile Val Pro Asn Thr Glu Pro Glu His Leu Glu His Tyr Asp
 20 25 30
 His Asp Leu Glu Arg Phe Phe Ala Tyr Lys Tyr Phe Leu Asp His
 35 40 45
 Ala Gln Lys Arg Val Ile Tyr Lys Glu Asp Pro Phe Leu Lys Asn Tyr
 50 55 60
 Ser Lys Asp Ala Ile Val Leu Glu Lys Lys Asp Ile Tyr Asn Ile Gln
 65 70 75 80
 Tyr Ile Leu Lys Asp Gly Glu Pro Tyr Thr Ser Phe Glu Leu Lys Asn
 85 90 95
 Leu Gly Ala Phe Leu Val Trp Gly Leu Gly Glu His Asn Ala Thr Asn
 100 105 110
 Ala Ser Leu Ala Ile Leu Ser Ala Leu Asp Glu Leu Asn Leu Glu Glu
 115 120 125
 Ile Arg Asn Asn Unk Leu Asn Phe Lys Gly Ile Lys Lys Arg Phe Asp
 130 135 140
 Ile Leu Gln Lys Asn Asn Leu Ile Leu Ile Asp Asp Tyr Ala His His
 145 150 155 160
 Pro Thr Glu Ile Gly Unk Thr Leu Lys Ser Ala Arg Ile Tyr Ala Asn
 165 170 175
 Leu Leu Asn Thr Gln Glu Lys Ile Ile Val Ile Trp Gln Ala His Lys
 180 185 190
 Tyr Ser Arg Leu Met Asp Asn Leu Glu Phe Lys Lys Cys Phe Leu
 195 200 205
 Glu His Cys Asp Arg Leu Ile Leu Pro Val Tyr Ser Ala Ser Glu
 210 215 220
 Val Lys Arg Asp Ile Asp Leu Lys Ala His Phe Lys His Tyr Asn Pro
 225 230 235 240
 Thr Phe Ile Asp Arg Val Arg Lys Lys Gly Asp Phe Leu Glu Leu Leu
 245 250 255
 Val Asn Asp Asn Val Val Glu Thr Ile Glu Lys Gly Phe Val Ile Gly
 260 265 270
 Phe Gly Ala Gly Asp Ile Thr Tyr Gln Leu Arg Gly Glu Met
 275 280 285

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402

Met Gly Ala Leu Ile Ala Met Phe Phe Leu Met Leu Ile Lys Lys Thr
 1 5 10 15
 Ile Ala Tyr Lys Glu Asp Lys Lys Ser Ala Ala Leu Lys Val Val Pro
 20 25 30
 Tyr Leu Val Ala Leu Met Ser Leu Ala Phe Ser Trp Tyr Leu Ile Val
 35 40 45
 Lys Val Leu Lys Arg Leu Tyr Ala Val Ser Phe Glu Ile Gln Leu Ala

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50	55	60	
Cys	Gly	Cys Val Leu Ala Leu Leu Ile Phe Ile Leu Phe Lys Arg Phe	
65	70	75	80
Val Leu Lys Lys Ala Pro Gln Leu Glu Asn Ser His Glu Ser Val Asn			
85	90	95	
Glu Leu Phe Asn Val Pro Leu Ile Phe Ala			
100	105		

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403

Met	Ile	Lys	Arg	Ile	Ala	Cys	Ile	Leu	Ser	Leu	Ser	Ala	Ser	Leu	Ala
1							5	10					15		
Leu	Ala	Gly	Glu	Val	Asn	Gly	Phe	Phe	Met	Gly	Ala	Gly	Tyr	Gln	Gln
							20	25	30						
Gly	Arg	Tyr	Gly	Pro	Tyr	Asn	Ser	Asn	Tyr	Ser	Asp	Trp	Arg	His	Gly
	35					40				45					
Asn	Asp	Leu	Tyr	Gly	Leu	Asn	Phe	Lys	Leu	Gly	Phe	Val	Gly	Phe	Ala
	50					55			60						
Asn	Lys	Trp	Phe	Gly	Ala	Arg	Val	Tyr	Gly	Phe	Leu	Asp	Trp	Phe	Asn
	65					70		75		80					
Thr	Ser	Gly	Thr	Glu	His	Thr	Lys	Thr	Asn	Leu	Leu	Thr	Tyr	Gly	Gly
						85		90		95					
Gly	Gly	Asp	Leu	Ile	Val	Asn	Leu	Ile	Pro	Leu	Asp	Lys	Phe	Ala	Leu
				100			105			110					
Gly	Leu	Ile	Gly	Gly	Val	Gln	Leu	Ala	Gly	Asn	Thr	Trp	Met	Phe	Pro
				115			120			125					
Tyr	Asp	Val	Asn	Gln	Thr	Arg	Gln	Phe	Leu	Trp	Asn	Leu	Gly	Gly	
	130					135			140						
Arg	Met	Arg	Val	Gly	Asp	Thr	Val	Arg	Leu	Lys	Arg	Ala			
	145					150			155						

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404

```

Met Tyr Arg His Val Leu Lys Asp Phe Ser Leu Asp Phe Ser Lys Glu
1          5           10          15
Ser Val Gln Glu Leu Phe Asn Gln Leu Ala Lys Asp Thr Phe Leu Leu
20         25           30
Leu Leu Pro Val Leu Ile Ile Leu Met Val Val Ala Phe Leu Ser Asn
35         40           45
Val Leu Gln Phe Gly Trp Leu Phe Ala Pro Lys Val Ile Glu Pro Lys
50         55           60
Phe Ser Lys Ile Asn Pro Ile Asn Gly Val Lys Asn Leu Phe Ser Leu
65         70           75           80
Lys Lys Ile Leu Asp Gly Ser Leu Ile Thr Leu Lys Val Phe Leu Ala
85         90           95
Phe Phe Leu Gly Phe Phe Ile Phe Ser Leu Phe Leu Gly Glu Leu Asn
100        105          110
His Ala Ala Leu Leu Asn Leu Gln Gly Gln Leu Leu Trp Phe Lys Ser
115        120          125
Lys Ala Leu Trp Leu Ile Ser Ser Leu Leu Phe Leu Phe Phe Val Leu
130        135          140
Ala Phe Val Asp Leu Ile Ile Lys Arg Arg Gln Tyr Thr Asn Ser Leu
145        150          155          160
Lys Met Thr Lys Gln Glu Val Lys Asp Glu Tyr Lys Gln Gln Glu Gly
165        170          175
Asn Pro Glu Ile Lys Ala Lys Ile Arg Gln Met Met Val Lys Asn Ala
180        185          190
Thr Asn Lys Met Met Gln Glu Ile Pro Lys Ser Asn Val Val Val Thr
195        200          205
Asn Pro Thr His Tyr Ala Val Ala Leu Lys Phe Asp Glu Glu His Pro
210        215          220
Val Pro Val Val Val Ala Lys Gly Thr Asp Tyr Leu Ala Ile Arg Ile
225        230          235          240
Lys Gly Ile Ala Arg Glu His Asp Ile Glu Ile Ile Glu Asn Lys Thr
245        250          255
Leu Ala Arg Glu Leu Tyr Arg Asp Val Lys Leu Asn Ala Thr Ile Pro
260        265          270
Glu Glu Leu Phe Glu Arg
275

```

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405

Met Asn Thr Unk Pro Leu Ile Ala Thr Leu Leu Gln Ala Pro Leu His

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1	5	10	15												
Val	Leu	Gly	Ile	Arg	Glu	Pro	Val	Ser	Phe	Gln	Pro	Phe	Tyr	Pro	Lys
20	25	30													
Thr	Glu	Lys	Pro	Asn	Arg	Pro	Gln	Lys	Phe	Ala	His	Val	Ser	Ser	Met
35	40	45													
Pro	Ser	Leu	Glu	Phe	Leu	Glu	Lys	Leu	Val	Ile	Arg	Tyr	Leu	Leu	Glu
50	55	60													
Asp	Arg	Ser	Leu	Leu	Asp	Leu	Ala	Val	Gly	Tyr	Ile	His	Ser	Gly	Val
65	70	75	80												
Phe	Leu	His	Lys	Lys	Gln	Glu	Phe	Asp	Ala	Leu	Cys	Gln	Glu	Lys	Leu
85	90	95													
Asp	Asp	Pro	Lys	Leu	Val	Ala	Leu	Leu	Asp	Ala	Asn	Leu	Pro	Leu	
100	105	110													
Lys	Lys	Gly	Gly	Phe	Glu	Lys	Glu								
115	120														

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406

Met	Gly	Gln	Ala	Phe	Phe	Lys	Ile	Val	Gly	Cys	Phe	Cys	Leu	Gly	
1	5	10	15												
Tyr	Leu	Phe	Leu	Ser	Ser	Ala	Ile	Glu	Ala	Val	Ala	Leu	Asp	Ile	Lys
20	25	30													
Asn	Phe	Asn	Arg	Gly	Arg	Val	Lys	Val	Val	Asn	Lys	Lys	Ile	Ala	Tyr
35	40	45													
Leu	Gly	Asp	Glu	Lys	Pro	Ile	Thr	Ile	Trp	Thr	Ser	Leu	Asp	Asn	Val
50	55	60													
Thr	Val	Ile	Gln	Leu	Glu	Lys	Asp	Glu	Thr	Ile	Ser	Tyr	Ile	Thr	Thr
65	70	75	80												
Gly	Phe	Asn	Lys	Gly	Trp	Ser	Ile	Val	Pro	Asn	Ser	Asn	His	Ile	Phe
85	90	95													
Ile	Gln	Pro	Lys	Ser	Val	Lys	Ser	Asn	Leu	Met	Phe	Glu	Lys	Glu	Ala
100	105	110													
Val	Asn	Phe	Ala	Leu	Met	Thr	Arg	Asp	Tyr	Gln	Glu	Phe	Leu	Lys	Thr
115	120	125													
Lys	Lys	Leu	Ile	Val	Asp	Ala	Pro	Asp	Pro	Lys	Glu	Leu	Glu	Gln	
130	135	140													
Lys	Lys	Ala	Leu	Glu	Lys	Glu	Lys	Glu	Ala	Lys	Gln	Ala	Gln	Lys	
145	150	155	160												
Ala	Gln	Lys	Asp	Lys	Arg	Glu	Lys	Arg	Lys	Glu	Glu	Arg	Ala	Lys	Asn
165	170	175													
Arg	Ala	Asn	Leu	Glu	Asn	Leu	Thr	Asn	Ala	Met	Ser	Asn	Pro	Gln	Asn
180	185	190													
Leu	Ser	Asn	Asn	Lys	Asn	Leu	Ser	Glu	Leu	Ile	Lys	Gln	Gln	Arg	Glu
195	200	205													
Asn	Glu	Leu	Asp	Gln	Met	Glu	Arg	Thr	Arg	Gly	His	Ala	Arg	Ala	Gly
210	215	220													

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Ser Ser
225

(2) INFORMATION FOR SEQ ID NO:407:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...61
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:407

Leu	Leu	Leu	Phe	Phe	Leu	Leu	Lys	Gly	Val	Val	Phe	Ser	Leu	Gly	Phe
1					5				10					15	
Phe	Ser	Phe	Phe	Glu	Glu	Val	Ser	Gly	Ser	Phe	Unk	Ala	Val	Ser	Leu
						20		25				30			
Unk	Val	Leu	Ala	Leu	Val	Met	Gly	Ser	Ser	Unk	Gly	Leu	Glu	Glu	Phe
						35		40			45				
Cys	Val	Leu	Glu	Glu	Leu	Ile	Asn	Ser	Gly	Leu	Ser	Val			
						50		55			60				

(2) INFORMATION FOR SEQ ID NO:407:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...61
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:407

Leu	Leu	Leu	Phe	Phe	Leu	Leu	Lys	Gly	Val	Val	Phe	Ser	Leu	Gly	Phe
1					5				10					15	
Phe	Ser	Phe	Phe	Glu	Glu	Val	Ser	Gly	Ser	Phe	Unk	Ala	Val	Ser	Leu
						20		25				30			
Unk	Val	Leu	Ala	Leu	Val	Met	Gly	Ser	Ser	Unk	Gly	Leu	Glu	Glu	Phe
						35		40			45				
Cys	Val	Leu	Glu	Glu	Leu	Ile	Asn	Ser	Gly	Leu	Ser	Val			
						50		55			60				

(2) INFORMATION FOR SEQ ID NO:408:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...50
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:408

Met Asn Thr Glu Ile Leu Thr Ile Met Leu Val Val Ser Val Leu Met
 1 5 10 15
 Gly Leu Val Gly Leu Ile Ala Phe Leu Trp Gly Val Lys Ser Gly Gln
 20 25 30
 Phe Asp Asp Glu Lys Arg Met Leu Glu Ser Val Leu Tyr Asp Ala Arg
 35 40 45
 Ala Thr
 50

(2) INFORMATION FOR SEQ ID NO:409:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...122
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:409

Met Gly Phe Leu Lys Val Leu Lys His Asp Ala Leu Gly Gln Val Gly
 1 5 10 15
 Asn Ile Val Ile Gly Asn Phe Leu Ile Thr Leu Thr Val Leu Ala Val
 20 25 30
 Cys Phe Ser Ser Gln Ser Ala Glu Glu Thr Thr Met Leu Thr Leu Ser
 35 40 45
 Tyr Thr Leu Phe Phe Ile Leu Gly Ala Phe Leu Leu Val Ala Ile Ser
 50 55 60
 Val Gly Ala Ile Lys Asn Leu Asn Ala Leu Phe Ser Lys Arg Gly Val
 65 70 75 80
 Leu Ser Phe Ser Leu Pro Ile Ser Leu Glu Ser Leu Leu Leu Pro Lys
 85 90 95
 Ile Leu Leu Pro Unk Val Phe Phe Tyr Leu Gln Phe Val Leu Val Cys
 100 105 110
 Gly Glu Arg Ala Phe Gly Leu Leu Pro Phe
 115 120

(2) INFORMATION FOR SEQ ID NO:409:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...122
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:409

```

Met Gly Phe Leu Lys Val Leu Lys His Asp Ala Leu Gly Gln Val Gly
1           5          10          15
Asn Ile Val Ile Gly Asn Phe Leu Ile Thr Leu Thr Val Leu Ala Val
20          25          30
Cys Phe Ser Ser Gln Ser Ala Glu Glu Thr Thr Met Leu Thr Leu Ser
35          40          45
Tyr Thr Leu Phe Phe Ile Leu Gly Ala Phe Leu Leu Val Ala Ile Ser
50          55          60
Val Gly Ala Ile Lys Asn Leu Asn Ala Leu Phe Ser Lys Arg Gly Val
65          70          75          80
Leu Ser Phe Ser Leu Pro Ile Ser Leu Glu Ser Leu Leu Leu Pro Lys
85          90          95
Ile Leu Leu Pro Unk Val Phe Phe Tyr Leu Gln Phe Val Leu Val Cys
100         105         110
Gly Glu Arg Ala Phe Gly Leu Leu Pro Phe
115         120

```

(2) INFORMATION FOR SEQ ID NO:410:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 187 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...187
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:410

```

Met Leu Lys Thr His Leu Ser Ser Ala Arg Gly Val Val Val Leu Ser
1           5          10          15
Lys Ile Leu Pro Val Asn Val Val Leu Met Val Ser Val Arg Leu Phe
20          25          30
Glu Lys Glu Leu Lys Arg Lys Pro Tyr Tyr Ile Ile Ala Ser Ala His

```

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35	40	45
Ser Asp Glu Gly Leu Glu Lys Leu Lys Lys Unk Gly Unk Asp Met Val		
50	55	60
Unk Unk Pro Thr Lys Leu Met Ala Gln Arg Val Ser Ala Asn Unk Trp		
65	70	75
Cys Unk Leu Asp Met Glu Asn Ile Leu Glu Arg Phe Ile Asn Lys Lys		
85	90	95
Asp Thr Leu Leu Asp Leu Glu Val Ile Val Pro Lys Thr Ser Trp		
100	105	110
Leu Val Leu Arg Lys Leu Lys Glu Ala His Phe Arg Glu Ile Ala Lys		
115	120	125
Ala Phe Val Ile Gly Ile Thr Gln Lys Asp Gly Lys Tyr Ile Pro Met		
130	135	140
Pro Asp Gly Glu Thr Ile Ile Ala Ser Glu Ser Lys Leu Leu Met Val		
145	150	155
Gly Thr Ser Glu Gly Val Ala Thr Cys Lys Gln Leu Ile Thr Ser His		
165	170	175
Gln Lys Pro Lys Glu Val Asp Tyr Ile Ser Leu		
180	185	

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410

Met Leu Lys Thr His Leu Ser Ser Ala Arg Gly Val Val Val Leu Ser		
1	5	10
Lys Ile Leu Pro Val Asn Val Val Leu Met Val Ser Val Arg Leu Phe		
20	25	30
Glu Lys Glu Leu Lys Arg Lys Pro Tyr Tyr Ile Ile Ala Ser Ala His		
35	40	45
Ser Asp Glu Gly Leu Glu Lys Leu Lys Lys Unk Gly Unk Asp Met Val		
50	55	60
Unk Unk Pro Thr Lys Leu Met Ala Gln Arg Val Ser Ala Asn Unk Trp		
65	70	75
Cys Unk Leu Asp Met Glu Asn Ile Leu Glu Arg Phe Ile Asn Lys Lys		
85	90	95
Asp Thr Leu Leu Asp Leu Glu Val Ile Val Pro Lys Thr Ser Trp		
100	105	110
Leu Val Leu Arg Lys Leu Lys Glu Ala His Phe Arg Glu Ile Ala Lys		
115	120	125
Ala Phe Val Ile Gly Ile Thr Gln Lys Asp Gly Lys Tyr Ile Pro Met		
130	135	140
Pro Asp Gly Glu Thr Ile Ile Ala Ser Glu Ser Lys Leu Leu Met Val		
145	150	155
Gly Thr Ser Glu Gly Val Ala Thr Cys Lys Gln Leu Ile Thr Ser His		
165	170	175
Gln Lys Pro Lys Glu Val Asp Tyr Ile Ser Leu		
180	185	

(2) INFORMATION FOR SEQ ID NO:411:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...130
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:411

```

Met Phe Val Ala Ala Gly Leu Gly Ala Tyr Ala Ile Ala Leu Phe His
1           5          10          15
Leu Phe Thr His Ala Phe Phe Lys Ser Leu Leu Phe Leu Gly Ser Gly
20          25          30
Asn Val Met His Ala Met Glu Asp Asn Leu Asp Ile Thr Lys Met Gly
35          40          45
Ala Leu Tyr Lys Pro Met Arg Ile Thr Ala Val Phe Met Ile Ile Gly
50          55          60
Ser Val Ala Leu Cys Gly Ile Tyr Pro Phe Ala Gly Tyr Phe Ser Lys
65          70          75          80
Asp Lys Ile Leu Glu Val Ala Phe Gly Met His His His Ile Leu Trp
85          90          95
Phe Val Leu Leu Ile Gly Ala Ile Phe Thr Ala Phe Tyr Ser Phe Arg
100         105         110
Leu Ile Met Leu Val Phe Phe Ala Pro Lys Gln His Glu Ile Asn His
115         120         125
Pro Pro
130

```

(2) INFORMATION FOR SEQ ID NO:412:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 183 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...183
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:412

```

Met Phe Ile Ser Ser Ser Tyr Thr Leu Ser Phe Val Trp Leu Phe Leu
1           5          10          15
Ile Phe Phe Phe Phe Lys Asn Lys Pro Leu Gly Leu Arg Phe Ser Leu

```

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	20	25	30												
Ser	Leu	Ile	Ser	Val	Ile	Leu	Ser	Asn	Ile	Ala	Leu	Lys	Asp	Ser	Leu
	35	40	45												
Ser	Leu	Asn	Glu	Phe	Leu	Ser	Ser	Phe	Thr	Ala	Pro	Leu	Ser	Pro	Phe
	50	55	60												
Ser	Cys	Leu	Leu	Ile	Leu	Ala	Tyr	Ala	Ser	Phe	Ser	Cys	His	Ile	Leu
	65	70	75												
Lys	Lys	Pro	Pro	Leu	Glu	Thr	Leu	Gln	Ser	Tyr	Ser	Val	Met	Leu	Phe
	85	90	95												
Phe	Asn	Leu	Leu	Leu	Leu	Thr	Asp	Ile	Leu	Gly	Phe	Leu	Pro	Phe	Ser
	100	105	110												
Ile	Tyr	His	His	Phe	Met	Ala	Ser	Leu	Ile	Phe	Ser	Ala	Leu	Phe	Cys
	115	120	125												
Ser	Ser	Leu	Phe	Leu	Ser	Ser	Pro	Leu	Leu	Gly	Val	Ile	Ala	Leu	Val
	130	135	140												
Ala	Leu	Ser	Ser	Ser	Leu	Leu	Met	Arg	Ser	Asn	Phe	Gln	Ile	Leu	Asp
	145	150	155												
Ser	Leu	Leu	Asp	Phe	Pro	Leu	Phe	Leu	Phe	Val	Phe	Phe	Lys	Thr	Leu
	165	170	175												
Tyr	Leu	Ala	Lys	Lys	Arg	Leu									
	180														

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413

Val	Gly	Ser	Phe	Leu	Phe	Val	Gly	Pro	Ser	Gly	Val	Gly	Lys	Thr	Glu
1				5					10				15		
Leu	Ala	Lys	Glu	Leu	Ala	Leu	Asn	Leu	Unk	Leu	His	Phe	Glu	Arg	Phe
				20					25				30		
Asp	Met	Ser	Glu	Tyr	Lys	Glu	Ala	His	Ser	Val	Ala	Lys	Leu	Ile	Gly
				35					40				45		
Ser	Pro	Ser	Gly	Tyr	Val	Gly	Phe	Glu	Gln	Gly	Gly	Leu	Leu	Val	Asn
				50					55				60		
Ala	Ile	Lys	Lys	His	Pro	His	Cys	Leu	Leu	Leu	Asp	Glu	Ile	Glu	
				65					70				75		80
Lys	Ala	His	Pro	Asn	Val	Tyr	Asp	Leu	Leu	Leu	Gln	Val	Met	Unk	Asn
				85					90				95		
Ala	Thr	Leu	Ser	Asp	Asn	Leu	Gly	Asn	Lys	Ala	Ser	Phe	Lys	His	Val
				100					105				110		
Ile	Leu	Ile	Met	Thr	Unk	Unk	Val	Gly	Ser	Lys	Asp	Lys	Asp	Thr	Leu
				115					120				125		
Gly	Phe	Phe	Ser	Thr	Lys	Asn	Ala	Lys	Tyr	Asp	Arg	Ala	Val	Lys	Glu
				130					135				140		
Leu	Leu	Thr	Pro	Glu	Leu	Arg	Ser	Arg	Ile	Asp	Ala	Ile	Val	Pro	Phe
				145					150				155		160
Asn	Ala	Leu	Ser	Leu	Glu	Asp	Phe	Glu	Thr	His	Cys	Phe	Cys	Gly	Ile
				165					170				175		

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Gly Arg Val Lys Ser Pro Ser Thr Arg Ala Arg Arg Asp Leu Lys Ile
 180 185 190
 Pro

(2) INFORMATION FOR SEQ ID NO:413:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...193
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:413

Val Gly Ser Phe Leu Phe Val Gly Pro Ser Gly Val Gly Lys Thr Glu
 1 5 10 15
 Leu Ala Lys Glu Leu Ala Leu Asn Leu Unk Leu His Phe Glu Arg Phe
 20 25 30
 Asp Met Ser Glu Tyr Lys Glu Ala His Ser Val Ala Lys Leu Ile Gly
 35 40 45
 Ser Pro Ser Gly Tyr Val Gly Phe Glu Gln Gly Gly Leu Leu Val Asn
 50 55 60
 Ala Ile Lys Lys His Pro His Cys Leu Leu Leu Asp Glu Ile Glu
 65 70 75 80
 Lys Ala His Pro Asn Val Tyr Asp Leu Leu Leu Gln Val Met Unk Asn
 85 90 95
 Ala Thr Leu Ser Asp Asn Leu Gly Asn Lys Ala Ser Phe Lys His Val
 100 105 110
 Ile Leu Ile Met Thr Unk Unk Val Gly Ser Lys Asp Lys Asp Thr Leu
 115 120 125
 Gly Phe Phe Ser Thr Lys Asn Ala Lys Tyr Asp Arg Ala Val Lys Glu
 130 135 140
 Leu Leu Thr Pro Glu Leu Arg Ser Arg Ile Asp Ala Ile Val Pro Phe
 145 150 155 160
 Asn Ala Leu Ser Leu Glu Asp Phe Glu Thr His Cys Phe Cys Gly Ile
 165 170 175
 Gly Arg Val Lys Ser Pro Ser Thr Arg Ala Arg Arg Asp Leu Lys Ile
 180 185 190
 Pro

(2) INFORMATION FOR SEQ ID NO:414:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 235 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414

```

Met Arg Leu Asp Tyr Ala Leu Phe Asn Gln His Leu Ala Asn Ser Arg
 1           5          10          15
Glu Lys Ala Lys Ala Leu Val Leu Lys Lys Gln Val Leu Val Asn Lys
 20          25          30
Met Val Val Ser Lys Pro Ser Phe Ile Val Lys Glu Gly Asp Gln Ile
 35          40          45
Glu Leu Ile Ala Pro Asn Leu Phe Val Ser Arg Ala Gly Glu Lys Leu
 50          55          60
Gly Ala Phe Leu Glu Asp His Phe Ile Asp Phe Lys Glu Lys Val Val
 65          70          75          80
Leu Asp Val Gly Ala Ser Lys Gly Gly Phe Ser Gln Val Ala Leu Leu
 85          90          95
Lys Gly Ala Lys Lys Val Leu Cys Val Asp Val Gly Lys Met Gln Leu
100         105         110
Asp Glu Ser Leu Lys Asn Asp Gln Arg Ile Glu Cys Tyr Glu Glu Cys
115         120         125
Asp Ile Arg Gly Phe Lys Thr Pro Glu Lys Ile Asp Leu Ala Leu Cys
130         135         140
Asp Val Ser Phe Ile Ser Leu Tyr Cys Ile Leu Glu Ala Ile Leu Pro
145         150         155         160
Leu Ser Gly Glu Phe Leu Thr Leu Phe Lys Pro Gln Phe Glu Val Gly
165         170         175
Arg Thr Ile Lys Arg Asn Lys Lys Gly Val Val Met Asp Lys Glu Ala
180         185         190
Ile Leu Asn Ala Leu Glu Asn Phe Lys Asn His Leu Lys Thr Lys Asp
195         200         205
Phe Gln Ile Leu Thr Ile Gln Glu Ser Leu Val Lys Gly Lys Asn Gly
210         215         220
Asn Val Glu Phe Phe Ile His Phe Lys Arg Ala
225         230         235

```

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415

```

Met Ser Leu Pro Pro Val Cys Ile Leu Lys Asp Val Asn His Leu Leu
 1           5          10          15
Gln Val Leu His Ser Leu Val Ala Leu Gly Asn Ser Met Leu Val Ile
 20          25          30

```

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Glu	His	Asn	Leu	Asp	Ile	Ile	Lys	Asn	Ala	Asp	Tyr	Ile	Ile	Asp	Met
35							40							45	
Gly	Pro	Asp	Gly	Gly	Asp	Lys	Gly	Gly	Lys	Val	Ile	Ala	Ser	Gly	Thr
50							55							60	
Pro	Leu	Glu	Val	Ala	Gln	Asn	Cys	Glu	Lys	Thr	Gln	Ser	Tyr	Thr	Gly
65							70							75	
Lys	Phe	Leu	Ala	Leu	Glu	Leu	Lys								80
															85

(2) INFORMATION FOR SEQ ID NO:416:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...109
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:416

Met	Gln	Asn	Arg	Ser	His	Glu	Ile	Gln	Gly	Val	Ser	His	Ile	Lys	Asn
1							5					10			15
Asn	Tyr	Lys	Phe	Phe	Thr	Lys	Glu	Leu	Asp	Asn	Tyr	Ile	Ser	Lys	Gly
							20					25			30
Tyr	Arg	Ile	Glu	Glu	Ile	Tyr	Gly	Ala	Phe	Leu	Trp	Leu	Lys	Ile	Val
							35					40			45
Ala	Ile	Gly	Leu	Glu	Leu	Gly	Glu	Asp	Asp	Pro	Gln	Val	Val	Phe	Glu
							50				55			60	
Ser	Ile	Asn	Ala	Thr	Gly	Val	Gln	Leu	Lys	Gly	Leu	Asp	Ile	Arg	
							65				70			75	
Asn	Tyr	Leu	Met	Met	Gly	Glu	Asn	Unk	Asp	Asn	Gln	Asn	Arg	Leu	Tyr
							85				90			95	
Asn	Thr	Tyr	Trp	Val	Pro	Leu	Glu	Asn	Trp	Leu	Gly	Glu			
							100				105				

(2) INFORMATION FOR SEQ ID NO:417:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...107
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:417

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Met Asp Thr Ile Lys Ser Ile Pro Ile Arg Thr Phe Ile Leu Leu Tyr
 1 5 10 15
 Lys Ser Ser Pro Lys Cys Val Val Leu Ala Ser Ile Thr Val Leu Phe
 20 25 30
 Val Gly Ile Leu Unk Ser Leu Asn Ile Leu Val Met Ile Lys Leu Ile
 35 40 45
 Asp Ile Val Val Asn Leu Leu Gln Lys His Thr His Phe Glu Tyr Ser
 50 55 60
 Leu Leu Leu Pro Thr Leu Leu Leu Trp Gly Ala Leu Leu Phe Leu Thr
 65 70 75 80
 His Val Phe Ser Gly Asn Phe Ile Lys Leu Ala Asn His Tyr Cys Arg
 85 90 95
 Thr Ile Phe Tyr Lys Tyr His His Ser Ala Cys
 100 105

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418

Met Ile Phe Tyr Thr Thr Ile Lys Glu Pro Leu Lys Asn Leu Gln Tyr
 1 5 10 15
 Arg Tyr Ala Gln Phe Phe Gly Lys Ile Lys Pro Cys Ser Phe Leu Glu
 20 25 30
 Ser Leu Lys Ser Cys Phe Phe Gln Thr Tyr Ser Phe Ser Leu Thr Arg
 35 40 45
 Lys Gln Asp Phe Lys Ser His Leu Arg His Phe Ile Asp Ser Ala His
 50 55 60
 Ser Asn Ala Leu Val Gly Asn Leu Tyr Arg Ala Leu Phe Ile Gly Asp
 65 70 75 80
 Ser Leu Asn Lys Asp Leu Arg Asp Arg Ala Asn Ala Leu Gly Ile Asn
 85 90 95
 His Leu Leu Ala Ile Ser Gly Phe His Leu Gly Ile Leu Ser Ala Ser
 100 105 110
 Val Tyr Phe Leu Phe Ser Leu Phe Tyr Thr Pro Leu Gln Lys Arg Tyr
 115 120 125
 Phe Pro Tyr Arg Asn Ala Phe Unk
 130 135

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419

Met	Asn	Lys	Pro	Phe	Leu	Ile	Leu	Ile	Ala	Leu	Ile	Ala	Phe	Ser	
1				5				10					15		
Gly	Cys	Asn	Met	Arg	Lys	Tyr	Phe	Lys	Pro	Ala	Lys	His	Gln	Ile	Lys
				20				25				30			
Ala	Lys	Arg	Ile	Ser	Leu	Thr	Ile	Cys	Lys	Lys	Ala	Ser	Phe	Arg	Leu
				35				40				45			
Ile	Val	Met	Glu	Pro	Phe										
				50											

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420

Met	Ala	Ala	Trp	Asn	Thr	Leu	Val	Glu	Lys	Ile	Ile	Ala	Pro	Lys	His
1						5			10				15		
Lys	Val	Lys	Ile	Gly	Phe	Val	Gly	Lys	Tyr	Leu	Ser	Leu	Lys	Glu	Ser
						20			25			30			
Tyr	Lys	Ser	Leu	Ile	Glu	Ala	Leu	Ile	His	Ala	Gly	Ala	His	Leu	Asp
						35			40			45			
Thr	Gln	Val	Asn	Ile	Glu	Trp	Leu	Asp	Ser	Glu	Asn	Phe	Asn	Glu	Lys
						50			55			60			
Thr	Asp	Leu	Glu	Gly	Val	Asp	Ala	Ile	Leu	Val	Pro	Gly	Gly	Phe	Gly
						65			70			75			80
Glu	Arg	Gly	Ile	Glu	Gly	Lys	Ile	Cys	Ala	Ile	Gln	Arg	Ala	Arg	Leu
						85			90			95			
Glu	Lys	Leu	Pro	Phe	Leu	Gly	Ile	Cys	Leu	Gly	Met	Gln	Leu	Ala	Ile
						100			105			110			
Val	Glu	Phe	Cys	Arg	Lys	Cys	Phe	Arg	Leu	Glu	Arg	Gly			
						115			120			125			

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids
(B) TYPE: amino acid**SUBSTITUTE SHEET (RULE 26)**

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421

Met	Thr	Lys	Ala	Phe	Val	Pro	Leu	Ser	Leu	Leu	Val	Ser	Ala	Ile	Leu
1				5					10				15		
Leu	Ala	Phe	Ser	Leu	Ile	Leu	Ile	Pro	Thr	Ser	Lys	Ser	Ala	Tyr	Tyr
				20				25				30			
Gly	Phe	Leu	Arg	Gln	Lys	Lys	Asp	Lys	Ile	Asp	Ile	Asn	Ile	Arg	Ala
				35			40				45				
Gly	Glu	Phe	Gly	Gln	Lys	Leu	Gly	Asp	Trp	Leu	Val	Tyr	Val	Asp	Lys
	50				55				60						
Thr	Glu	Asn	Asn	Ser	Tyr	Asp	Asn	Leu	Val	Leu	Phe	Ser	Asn	Lys	Ser
65					70				75				80		
Leu	Ser	Gln	Glu	Ser	Phe	Ile	Leu	Ala	Gln	Lys	Gly	Asn	Ile	Asn	Asn
					85				90				95		
Gln	Asn	Gly	Val	Phe	Glu	Leu	Asn	Leu	Tyr	Asn	Gly	His	Ala	Tyr	Phe
				100			105				110				
Thr	Gln	Gly	Asp	Lys	Met	Arg	Lys	Val	Asp	Phe	Glu	Glu	Leu	His	Leu
					115			120				125			
Arg	Asn	Lys	Leu	Lys	Ser	Phe	Asn	Ser	Asn	Asp	Ala	Ala	Tyr	Leu	Gln
					130			135			140				
Gly	Thr	Asp	Tyr	Leu	Gly	Tyr	Trp	Lys	Lys	Ala	Phe	Gly	Lys	Asn	Ala
145					150			155			160				
Asn	Lys	Asn	Gln	Lys	Arg	Arg	Phe	Ser	Gln	Ala	Ile	Leu	Val	Ser	Leu
					165			170			175				
Phe	Pro	Leu	Ala	Ser	Val	Phe	Leu	Ile	Pro	Leu	Phe	Gly	Ile	Ala	Asn
					180			185			190				
Pro	Arg	Phe	Lys	Thr	Asn	Trp	Ser	Tyr	Phe	Unk	Val	Leu	Gly	Ala	Val
					195		200		205						
Gly	Val	Tyr	Phe	Leu	Met	Val	His	Val	Ile	Ser	Thr	Asp	Leu	Phe	Leu
					210		215		220						
Met	Thr	Phe	Phe	Pro	Phe	Ile	Trp	Ala	Phe	Ile	Ser	Tyr	Leu	Leu	
					225		230		235			240			
Phe	Arg	Lys	Phe	Ile	Leu	Lys	Arg	Tyr							
					245										

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

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(B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422

Met Ser Lys Ser Ala Ile Phe Val Leu Ser Gly Phe Leu Ala Phe Leu
 1 5 10 15
 Leu Tyr Ala Leu Leu Leu Tyr Gly Leu Leu Leu Glu Arg His Asn Lys
 20 25 30
 Glu Ala Glu Lys Ile Leu Leu Asp Leu Asn Lys Lys Asp Glu Gln Ala
 35 40 45
 Ile Asp Leu Asn Leu Glu Asp Leu Pro Ser Glu Lys Lys Asn Glu Lys
 50 55 60
 Ile Lys Lys Val Thr Glu Lys Gln Asp Asp Phe Leu Glu Pro Lys Arg
 65 70 75 80
 Arg Thr Gln Arg Gly Ala
 85

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423

Val Met Ala Gln Ser Leu Leu Val His Ala Phe Phe Ala Ala Leu Leu
 1 5 10 15
 Ala Leu Ala Phe Met Ile Asn Leu Tyr Thr Leu Phe Lys Glu Lys Asn
 20 25 30
 Phe Ile Gln Leu Asn Arg Lys Ile Tyr Leu Val Met Pro Ala Ile Tyr
 35 40 45
 Ile Leu Leu Ser Ile Ala Leu Leu Ser Gly Val Phe Ile Trp Ala Met
 50 55 60
 Gln Gln Phe Glu Phe Ser Phe Ser Ala Val Val Met Leu Leu Gly Leu
 65 70 75 80
 Leu Leu Met Leu Ile Ala Glu Ile Lys Arg His Lys Ser Val Lys Phe
 85 90 95
 Ala Ile Thr Lys Lys Glu Arg Met Lys Ala Tyr Ile Lys Lys Ala Lys
 100 105 110
 Ile Leu Tyr Phe Leu Glu Thr Ile Leu Ile Ile Val Leu Met Gly Ile
 115 120 125

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424

Val	Arg	Asn	Val	Val	Leu	Phe	Ile	Leu	Thr	Ala	Ile	Phe	Leu	Ala	Phe
1					5				10						15
Met	Leu	Leu	Val	Ser	Tyr	Cys	Met	Pro	His	Tyr	Ser	Val	Ala	Val	Ile
					20				25						30
Ser	Gly	Val	Glu	Val	Lys	Arg	Met	Asn	Glu	Asn	Glu	Asn	Thr	Pro	Asn
					35			40						45	
Asn	Lys	Glu	Val	Lys	Thr	Leu	Ala	Arg	Asp	Val	Tyr	Phe	Val	Gln	Thr
					50			55			60				
Tyr	Asp	Pro	Lys	Asp	Gln	Lys	Ser	Val	Thr	Val	Tyr	Arg	Asn	Glu	Asp
					65			70			75			80	
Thr	Arg	Phe	Gly	Phe	Pro	Phe	Tyr	Phe	Lys	Phe	Asn	Ser			
					85				90						

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425

Met	Phe	Lys	Lys	Ile	Ile	Phe	Leu	Cys	Val	Phe	Leu	Ile	Gly	Gly	Phe
1						5			10						15
Val	Ile	Pro	Pro	Leu	Glu	Ala	Met	Pro	Ile	Leu	Arg	Asn	Lys	Thr	Pro
						20			25					30	
Lys	Lys	Asn	Tyr	Gln	Glu	Ala	His	Glu	Lys	Leu	Tyr	Arg	Ser	Ile	Ile
						35			40					45	
Asn	Arg	Gln	Unk	Unk	Thr	Arg	Lys	Lys	Ser	Gly	Trp	Tyr	Phe	Leu	Gly
					50			55			60				
Gly	Val	Gly	Ala	Val	Glu	Ala	Ile	Lys	Asp	Tyr	Gln	Gly	Lys	Glu	Met
					65			70			75			80	
Lys	Asp	Trp	Met	Pro	Arg	Ser	Ile								
					85										

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

354

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426

Val	His	Phe	Thr	Cys	Ile	Phe	Leu	Thr	Leu	Leu	Lys	Trp	Ile	Leu	Pro
1						5					10				15
Ala	Lys	Asn	Lys	Gln	Ala	Cys	Lys	Lys	Ala	Thr	Asn	Gln	Ile	His	Ser
							20			25				30	
Arg	Unk	Ala	Lys	His	Pro	Ala	Lys	Tyr	Pro	Pro	Ser	Ser	Ile	Asn	Pro
							35			40				45	
Ser	Ile	Gln	Ala	Gly	Ile	Gln	Gly	Val	Met	Gln	Gly	Phe	Gly	Ala	Leu
						50			55			60			
Ser	Ser	Unk	Leu	Glu	Unk	Pro	Unk	Phe	Val	Unk	Unk	Ala	Lys	Cys	Gly
						65			70			75			80
Trp	Ile	Gly	Gly	Phe	Glu	His	Tyr	Leu	Ser	Pro	Leu	Tyr	Gly	Trp	Gly
							85			90				95	
Lys	Ile	His	Asp	Gly	Ala	His	Cys	Asp	Leu	Met	Gln	Lys	Asp	Ala	Asn
						100			105			110			
Gly	Arg	Gly	Ile	Gly	Leu	Glu	Lys	Gly	Leu	Pro	Pro	Phe	Lys	Gly	Leu
						115			120			125			

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427

Met	Gln	Lys	Phe	Phe	Ser	Arg	Phe	Arg	Arg	Trp	Ala	Leu	Pro	Phe	Tyr
1							5			10				15	
Phe	Val	Ser	Ala	Leu	Ala	Ala	Ile	Asp	Ile	Asp	Glu	Val	Thr	Glu	Ala
							20			25				30	
Gln	Ala	Asn	Ser	Ile	Lys	Leu	Ser	Asp	Gln	Leu	Val	Ser	Leu	Ser	Asp
							35			40				45	
Lys	Leu	Leu	Glu	Lys	Ala	Val	Asp	Arg	Gly	Arg	Asn	Thr	Asp	His	Leu
							50			55				60	
Lys	Asp	Leu	Asn	Asp	Leu	His	Glu	Lys	Ile	Lys	His	Leu	Arg	Leu	Ile
							65			70				80	
Leu	Glu	Pro	Lys	Pro	Lys	Gly	Lys	Glu	Asp	Ser	Pro	Asn	Leu	Gly	Gly
							85			90				95	
Asn	Lys	Asp	Met	Lys	Thr	Val	Glu	Ile	Gly	Ser	Gly				

SUBSTITUTE SHEET (RULE 26)

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(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428

Val	Ile	Leu	Ala	Phe	Ala	Phe	Gly	Met	Ser	Leu	Leu	Gly	Leu	Ala	Gly
1								5		10			15		
Met	Phe	Ile	Asp	Ile	Pro	Phe	Leu	Ser	Thr	Gly	Val	Mis	Ile	Pro	Arg
								20		25			30		
Lys	Glu	Asp	Ile	Leu	Trp	Ile	Ser	Leu	Ile	Gly	Ile	Ser	Gly	Thr	Leu
								35		40			45		
Gly	Gln	Tyr	Phe	Leu	Thr	Tyr	Ala	Tyr	Met	Asn	Ala	Pro	Ala	Gly	Ile
								50		55			60		
Ile	Ala	Pro	Ile	Glu	Tyr	Thr	Arg	Ile	Val	Trp	Gly	Leu	Leu	Phe	Gly
								65		70			75		80
Leu	Tyr	Leu	Gly	Asp	Thr	Phe	Leu	Asp	Leu	Lys	Ser	Ser	Leu	Gly	Val
								85		90			95		
Ala	Leu	Ile	Leu	Cys	Ser	Gly	Leu	Leu	Ile	Ala	Leu	Pro	Ala	Leu	Leu
								100		105			110		
Lys	Glu	Leu	Lys	Lys	Ile										
								115							

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429

Met	Ile	Tyr	Leu	Gly	Lys	Lys	Asn	Phe	Asn	Ala	Leu	Leu	Lys	Gly	Ala
1								5		10			15		
Tyr	Leu	Met	Asp	Glu	His	Phe	Arg	Asn	Ala	Pro	Phe	Glu	Ser	Asn	Leu
								20		25			30		

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Pro Val Leu Met Gly Leu Ile Trp Arg Val Val Tyr Leu Thr Phe Phe
 35 40 45
 Pro Ile Gln Lys Ala Thr
 50

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430

Met Ala Ala Lys Ser Lys Ala Unk Thr Leu Lys Val Phe Ser Lys Phe
 1 5 10 15
 Phe Ser Asn Phe Lys Ile Thr Lys Leu Lys Asp Asn His Glu Glu Ala
 20 25 30
 His Lys Leu Phe Gly Glu Asn Ser Arg Lys Ala His Asp Thr Glu Ile
 35 40 45
 Ile Tyr Ser Thr Leu Gln Val Val Pro Arg Tyr Ser Ile Glu Thr Val
 50 55 60
 Gly Phe Ser Leu Leu Ile Leu Ala Val Ala Tyr Ile Leu Phe Lys Tyr
 65 70 75 80
 Gly Glu Ala Arg Met Val Leu Pro Thr Ile Ser Met Tyr Ala Leu Ala
 85 90 95
 Leu Tyr Arg Ile Leu Pro Ser Val Thr Gly Val Ile Ser Tyr Tyr Asn
 100 105 110
 Glu Ile Ala Tyr Asn Gln Leu Ala Thr Asn Val Val Phe Lys Ser Leu
 115 120 125
 Ser Lys Thr Ile Val Glu Glu Asp Leu Val Pro Leu Asp Phe Asn Glu
 130 135 140
 Lys Ile Thr Leu Gln Asn Ile Ser Phe Ala Tyr Lys Ser Lys His Pro
 145 150 155 160
 Val Leu Lys Asn Phe Asn Leu Thr Ile Gln Lys Gly Gln Lys Ile Ala
 165 170 175
 Leu Ile Gly His Ser Gly Cys Gly Lys Ser Thr Leu Ala Asp Ile Ile
 180 185 190
 Met Gly Leu Thr Tyr Pro Lys Ser Gly Glu Ile Phe Ile Asp Asn Thr
 195 200 205
 Leu Leu Thr Ser Glu Asn Arg Arg Ser Trp Arg Lys Lys Ile Gly Tyr
 210 215 220
 Ile Pro Gln Asn Ile Tyr Leu Phe Asp Gly Thr Val Gly Asp Asn Ile
 225 230 235 240
 Ala Phe Gly Ser Ala Ile Asp Glu Lys Arg Leu Ile Lys Val Cys Lys
 245 250 255
 Met Ala His Ile Tyr Asp Phe Leu Cys Glu His Glu Gly Leu Lys Thr
 260 265 270
 Gln Val Gly Glu Gly Ala Leu Ser Leu Ala Ala Val Lys Asn Ser Ala
 275 280 285

(2) INFORMATION FOR SEQ ID NO:431:

SUBSTITUTION SHEET (RULE 26)

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 303 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431

```

Met Ala Phe Gln Val Asn Thr Asn Ile Asn Ala Met Asn Ala His Val
 1           5          10          15
Gln Ser Ala Leu Thr Gln Asn Ala Leu Lys Thr Ser Leu Glu Arg Leu
 20          25          30
Ser Ser Gly Leu Arg Ile Asn Lys Ala Ala Asp Asp Ala Ser Gly Met
 35          40          45
Thr Val Ala Asp Ser Leu Arg Ser Gln Ala Ser Ser Leu Gly Gln Ala
 50          55          60
Ile Ala Asn Thr Asn Asp Gly Met Gly Ile Ile Gln Val Ala Asp Lys
 65          70          75          80
Ala Met Asp Glu Gln Leu Lys Ile Leu Asp Thr Val Lys Val Lys Ala
 85          90          95
Thr Gln Ala Ala Gln Asp Gly Gln Thr Thr Glu Ser Arg Lys Ala Ile
100         105         110
Gln Ser Asp Ile Val Arg Leu Ile Gln Gly Leu Asp Asn Ile Gly Asn
115         120         125
Thr Thr Thr Tyr Asn Gly Gln Ala Leu Leu Ser Gly Gln Phe Thr Asn
130         135         140
Lys Glu Phe Gln Val Gly Ala Tyr Ser Asn Gln Ser Ile Lys Ala Ser
145         150         155         160
Ile Gly Ser Thr Thr Ser Asp Lys Ile Gly Gln Val Arg Ile Ala Thr
165         170         175
Gly Ala Leu Ile Thr Ala Ser Gly Asp Ile Ser Leu Thr Phe Lys Gln
180         185         190
Val Asp Gly Val Asn Asp Val Thr Leu Glu Ser Val Lys Val Ser Ser
195         200         205
Ser Ala Gly Thr Gly Ile Gly Val Leu Ala Glu Val Ile Asn Lys Asn
210         215         220
Ser Asn Arg Thr Gly Val Lys Ala Tyr Ala Ser Val Ile Thr Thr Ser
225         230         235         240
Asp Val Ala Val Gln Ser Gly Ser Leu Ser Asn Leu Thr Leu Asn Gly
245         250         255
Ile His Leu Gly Asn Ile Ala Asp Ile Lys Unk Asn Asp Ser Asp Gly
260         265         270
Arg Leu Val Thr Ala Ile Asn Ala Val Thr Ser Glu Thr Gly Val Unk
275         280         285
Ala Tyr Thr Asp Gln Lys Gly Arg Leu Asn Leu Arg Ser Ile Gly
290         295         300

```

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 303 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431

Met	Ala	Phe	Gln	Val	Asn	Thr	Asn	Ile	Asn	Ala	Met	Asn	Ala	His	Val
1				5					10					15	
Gln	Ser	Ala	Leu	Thr	Gln	Asn	Ala	Leu	Lys	Thr	Ser	Leu	Glu	Arg	Leu
					20				25					30	
Ser	Ser	Gly	Leu	Arg	Ile	Asn	Lys	Ala	Ala	Asp	Asp	Ala	Ser	Gly	Met
					35				40					45	
Thr	Val	Ala	Asp	Ser	Leu	Arg	Ser	Gln	Ala	Ser	Ser	Leu	Gly	Gln	Ala
					50				55					60	
Ile	Ala	Asn	Thr	Asn	Asp	Gly	Met	Gly	Ile	Ile	Gln	Val	Ala	Asp	Lys
					65				70			75		80	
Ala	Met	Asp	Glu	Gln	Leu	Lys	Ile	Leu	Asp	Thr	Val	Lys	Val	Lys	Ala
					85				90					95	
Thr	Gln	Ala	Ala	Gln	Asp	Gly	Gln	Thr	Thr	Glu	Ser	Arg	Lys	Ala	Ile
					100				105					110	
Gln	Ser	Asp	Ile	Val	Arg	Leu	Ile	Gln	Gly	Leu	Asp	Asn	Ile	Gly	Asn
					115				120					125	
Thr	Thr	Thr	Tyr	Asn	Gly	Gln	Ala	Leu	Leu	Ser	Gly	Gln	Phe	Thr	Asn
					130				135					140	
Lys	Glu	Phe	Gln	Val	Gly	Ala	Tyr	Ser	Asn	Gln	Ser	Ile	Lys	Ala	Ser
					145				150			155		160	
Ile	Gly	Ser	Thr	Thr	Ser	Asp	Lys	Ile	Gly	Gln	Val	Arg	Ile	Ala	Thr
					165				170					175	
Gly	Ala	Leu	Ile	Thr	Ala	Ser	Gly	Asp	Ile	Ser	Leu	Thr	Phe	Lys	Gln
					180				185					190	
Val	Asp	Gly	Val	Asn	Asp	Val	Thr	Leu	Glu	Ser	Val	Lys	Val	Ser	Ser
					195				200					205	
Ser	Ala	Gly	Thr	Gly	Ile	Gly	Val	Leu	Ala	Glu	Val	Ile	Asn	Lys	Asn
					210				215					220	
Ser	Asn	Arg	Thr	Gly	Val	Lys	Ala	Tyr	Ala	Ser	Val	Ile	Thr	Thr	Ser
					225				230			235		240	
Asp	Val	Ala	Val	Gln	Ser	Gly	Ser	Leu	Ser	Asn	Leu	Thr	Leu	Asn	Gly
					245				250					255	
Ile	His	Leu	Gly	Asn	Ile	Ala	Asp	Ile	Lys	Unk	Asn	Asp	Ser	Asp	Gly
					260				265					270	
Arg	Leu	Val	Thr	Ala	Ile	Asn	Ala	Val	Thr	Ser	Glu	Thr	Gly	Val	Unk
					275				280					285	
Ala	Tyr	Thr	Asp	Gln	Lys	Gly	Arg	Leu	Asn	Leu	Arg	Ser	Ile	Gly	
					290				295					300	

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432

```

Met Leu Asp Ile Trp Ile Asp Met Ile Ile Cys Ile Phe Tyr Leu Leu
1      5          10          15
Phe Phe Thr Thr Pro Tyr Ile Val Gly Asp Ile Leu Gln Leu Lys Phe
20     25          30
Ile Arg Gln Lys Leu Cys Glu Lys Pro Val Leu Leu Pro Gln Lys Asp
35     40          45
Tyr Glu Glu Ala Gly Asn Tyr Ala Ile Arg Lys Met Gln Leu Ser Ile
50     55          60
Ile Ser Gln Ile Leu Asp Gly Val Ile Phe Ala Gly Trp Val Phe Phe
65     70          75          80
Gly Leu Thr His Leu Glu Asp Leu Thr His Tyr Leu Asn Leu Pro Glu
85     90          95
Thr Leu Gly Tyr Leu Val Phe Ala Leu Phe Leu Ala Ile Gln Ser
100    105         110
Val Leu Ala Leu Pro Ile Ser Tyr Tyr Thr Thr Met His Leu Asp Lys
115    120         125
Glu Phe Gly Phe Ser Lys Val Ser Leu Ser Leu Phe Phe Lys Asp Phe
130    135         140
Phe Lys Gly Leu Leu Leu Thr Leu Gly Val Gly Leu Leu Leu Ile Tyr
145    150         155         160
Thr Leu Ile Met Ile Ile Glu His Val Glu His Trp Glu Ile Ser Ser
165    170         175
Phe Phe Val Val Phe Val Phe Met Ile Leu Ala Asn Leu Phe Leu Pro
180    185         190

```

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 168 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433

```

Met Leu Lys Lys Ile Phe Leu Thr Asn Ser Leu Gly Ile Leu Cys Ser
1      5          10          15
Arg Ile Phe Gly Phe Leu Arg Asp Leu Met Met Ala Asn Ile Leu Gly
20     25          30
Ala Gly Val Tyr Ser Asp Ile Phe Phe Val Ala Phe Lys Leu Pro Asn
35     40          45
Leu Phe Arg Arg Ile Phe Ala Glu Gly Ser Phe Ser Gln Ser Phe Leu
50     55          60
Pro Ser Phe Ile Arg Ser Ser Ile Lys Gly Gly Phe Ala Ser Leu Val
65     70          75          80

```

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Gly Leu Ile Phe Cys Gly Val Leu Phe Met Trp Cys Leu Leu Val Ala
 85 90 95
 Leu Asn Pro Leu Trp Leu Thr Lys Leu Leu Ala Tyr Gly Phe Asp Glu
 100 105 110
 Glu Thr Leu Lys Leu Cys Thr Pro Ile Val Ala Ile Asn Phe Trp Tyr
 115 120 125
 Leu Leu Leu Val Phe Ile Thr Thr Phe Leu Gly Ala Leu Leu Gln Tyr
 130 135 140
 Lys His Ser Phe Phe Ala Ala Leu Met Arg Lys Leu Thr Gln Phe Met
 145 150 155 160
 His Asp Phe Ser Pro Phe Asp Phe
 165

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434

Met Asn Leu Glu Val Ala Leu Lys Ala Phe Glu Thr Leu Leu Pro Cys
 1 5 10 15
 Asn Lys Gln Glu Val Leu Lys Asn Leu Lys Pro Leu Asp Leu Ile Gly
 20 25 30
 Arg Cys Glu Leu Leu Ser Pro Asn Ile Leu Ile Asp Val Gly His Asn
 35 40 45
 Pro His Ser Ala Lys Ala Leu Lys Glu Glu Ile Lys Arg Ile Phe Asn
 50 55 60
 Ala Pro Ile Val Leu Ile Tyr Asn Cys Tyr Gln Asp Lys Asp Ala Phe
 65 70 75 80
 Leu Val Leu Glu Ile Leu Lys Ser Val Val Lys Lys Val Leu Ile Leu
 85 90 95
 Glu Leu His Asn Glu Arg Ile Ile Gln Leu Glu Lys Leu Lys Gly Ile
 100 105 110
 Leu Glu Thr Leu Gly Leu Glu His Ala Leu Phe Glu Glu Leu Lys Glu
 115 120 125
 Asn Glu Asn Tyr Leu Val Tyr Gly Ser Phe Leu Val Ala Asn Ala Phe
 130 135 140
 Tyr Glu Arg Tyr Pro Lys Lys Arg Asp
 145 150

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

361

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435

Met	Phe	Phe	Lys	Thr	Tyr	Gln	Lys	Leu	Leu	Gly	Ala	Ser	Cys	Leu	Ala
1								5		10				15	
Leu	Tyr	Leu	Val	Gly	Cys	Gly	Asn	Gly	Gly	Gly	Gly	Glu	Ser	Pro	Val
								20		25				30	
Glu	Met	Ile	Unk	Asn	Ser	Glu	Gly	Thr	Phe	Gln	Ile	Asp	Ser	Lys	Ala
								35		40			45		
Asp	Ser	Ile	Thr	Ile	Gln	Gly	Val	Lys	Leu	Asn	Arg	Gly	Asn	Cys	Ala
								50		55			60		
Val	Asn	Phe	Val	Pro	Val	Ser	Glu	Thr	Phe	Gln	Met	Gly	Val	Leu	Ser
								65		70			75		80
Gln	Val	Thr	Pro	Ile	Ser	Ile	Gln	Asp	Phe	Lys	Asp	Met	Ala	Ser	Thr
								85		90			95		
Tyr	Lys	Ile	Phe	Asp	Gln	Lys	Gly	Leu	Ala	Asn	Ile	Ala	Asn	Lys	
								100		105			110		
Ile	Ser	Gln	Leu	Glu	Gln	Lys	Gly	Val	Met	Met	Lys	Pro	Unk	Thr	Leu
								115		120			125		
Asn	Phe	Gly	Glu	Ser	Leu	Lys	Gly	Ile	Ser	Gln	Gly	Cys	Asn	Ile	Ile
								130		135			140		
Glu	Ala	Glu	Ile	Gln	Thr	Asp	Lys	Gly	Ala	Trp	Thr	Phe	Asn	Phe	Asp
								145		150			155		160
															Lys

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435

Met	Phe	Phe	Lys	Thr	Tyr	Gln	Lys	Leu	Leu	Gly	Ala	Ser	Cys	Leu	Ala
1								5		10				15	
Leu	Tyr	Leu	Val	Gly	Cys	Gly	Asn	Gly	Gly	Gly	Gly	Glu	Ser	Pro	Val
								20		25			30		
Glu	Met	Ile	Unk	Asn	Ser	Glu	Gly	Thr	Phe	Gln	Ile	Asp	Ser	Lys	Ala
								35		40			45		
Asp	Ser	Ile	Thr	Ile	Gln	Gly	Val	Lys	Leu	Asn	Arg	Gly	Asn	Cys	Ala
								50		55			60		
Val	Asn	Phe	Val	Pro	Val	Ser	Glu	Thr	Phe	Gln	Met	Gly	Val	Leu	Ser
								65		70			75		80

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Gln Val Thr Pro Ile Ser Ile Gln Asp Phe Lys Asp Met Ala Ser Thr
 85 90 95
 Tyr Lys Ile Phe Asp Gln Lys Lys Gly Leu Ala Asn Ile Ala Asn Lys
 100 105 110
 Ile Ser Gln Leu Glu Gln Lys Gly Val Met Met Lys Pro Unk Thr Leu
 115 120 125
 Asn Phe Gly Glu Ser Leu Lys Gly Ile Ser Gln Gly Cys Asn Ile Ile
 130 135 140
 Glu Ala Glu Ile Gln Thr Asp Lys Gly Ala Trp Thr Phe Asn Phe Asp
 145 150 155 160
 Lys

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...59

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436

Met Ala Ile Gly Phe Pro Leu Val Phe Gly Ile Leu Leu Thr Leu Phe
 1 5 10 15
 Ser Arg Ser Tyr Trp Arg Glu Phe Gly Gly Val Ser Gly Val Leu Trp
 20 25 30
 Arg Ala Ser Gly Phe Ser Gly Ala Lys Val Glu Arg Asn Leu Glu Arg
 35 40 45
 Asp Pro His Ala Phe Phe Thr His Cys Asp Phe
 50 55

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 222 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437

Met Lys Lys Lys Ala Lys Val Phe Trp Cys Cys Phe Lys Met Ile Arg

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1	5	10	15												
Trp	Leu	Tyr	Leu	Ala	Val	Phe	Phe	Leu	Leu	Ser	Val	Ser	Asp	Ala	Lys
20	25	30													
Glu	Ile	Ala	Met	Gln	Arg	Phe	Asp	Lys	Gln	Asn	His	Lys	Ile	Phe	Glu
35	40	45													
Ile	Leu	Ala	Asp	Lys	Val	Ser	Ala	Lys	Asp	Asn	Val	Ile	Thr	Ala	Ser
50	55	60													
Gly	Asn	Ala	Ile	Leu	Leu	Asn	Tyr	Asp	Val	Tyr	Ile	Leu	Ala	Asp	Lys
65	70	75	80												
Val	Arg	Tyr	Asp	Thr	Lys	Thr	Lys	Glu	Ala	Leu	Leu	Glu	Gly	Asn	Ile
85	90	95													
Lys	Val	Tyr	Arg	Gly	Glu	Gly	Leu	Leu	Val	Lys	Thr	Asp	Tyr	Val	Lys
100	105	110													
Leu	Ser	Leu	Asn	Glu	Lys	Tyr	Glu	Ile	Ile	Phe	Pro	Phe	Tyr	Val	Gln
115	120	125													
Asp	Ser	Val	Ser	Gly	Ile	Trp	Val	Ser	Ala	Asp	Ile	Ala	Ser	Gly	Lys
130	135	140													
Asp	Gln	Lys	Tyr	Lys	Ile	Lys	Asn	Met	Ser	Ala	Ser	Gly	Cys	Ser	Ile
145	150	155	160												
Asp	Asn	Pro	Ile	Trp	His	Val	Asn	Ala	Thr	Ser	Gly	Ser	Phe	Asn	Met
165	170	175													
Gln	Lys	Ser	His	Leu	Ser	Met	Trp	Asn	Pro	Lys	Ile	Tyr	Val	Gly	Asp
180	185	190													
Ile	Pro	Val	Leu	Tyr	Leu	Pro	Tyr	Ile	Phe	Met	Ser	Thr	Ser	Asn	Lys
195	200	205													
Arg	Thr	Thr	Gly	Phe	Leu	Tyr	Pro	Glu	Phe	Gly	Thr	Ser	Thr		
210	215	220													

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...53

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438

Met	Leu	Asp	Phe	Asp	Leu	Val	Leu	Phe	Gly	Ala	Thr	Gly	Asp	Leu	Ala
1	5	10	15												
Met	Arg	Lys	Leu	Phe	Val	Ser	Leu	Tyr	Glu	Ile	Tyr	Ile	Ser	Phe	Met
20	25	30													
Val	Leu	Lys	Thr	Ile	Leu	Gly	Leu	Ser	His	Arg	Gly	Val	Arg	Ser	Tyr
35	40	45													
Pro	Met	Lys	Ser	Phe											
50															

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439

Met	Gln	Asp	Leu	Pro	Pro	Cys	Pro	Lys	Arg	Asn	Asp	Ala	Tyr	Thr	Tyr
1				5		.		10						15	
His	Asp	Gly	Thr	Gln	Phe	Val	Cys	Ser	Ser	Cys	Leu	Tyr	Glu	Trp	Asn
				20				25					30		
Gly	Asn	Glu	Ile	Ser	Asn	Glu	Glu	Leu	Ile	Val	Lys	Asp	Cys	His	Asn
		35					40					45			
Asn	Leu	Leu	Gln	Asn	Gly	Asp	Ser	Val	Ile	Leu	Ile	Lys	Asp	Leu	Lys
		50					55				60				
Val	Lys	Gly	Ser	Ser	Leu	Val	Leu	Lys	Lys	Gly	Thr	Lys	Ile	Lys	Asn
		65					70			75				80	
Ile	Lys	Leu	Val	Asn	Ser	Asp	His	Asn	Val	Asp	Cys	Lys	Val	Glu	Gly
							85			90				95	
Gln	Ser	Leu	Ser	Leu	Lys	Ser	Glu	Phe	Leu	Lys	Lys	Ala			
				100					105						

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

4.1.1. Molecular sieve protein

(iii) UNDERSIGNED - YES

(iii) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

FEATURE:

(A) NAME
(B) LOC

(B) LOCATION 1.....3

SEQUENCE DESCRIPTION

• 100-11-53 The Club has Two Alas

1	5	10	15
Thr Gly Ala Leu Phe Ser Glu Asp Lys Asp.	Ser Pro Tyr Ala Asn Leu		
20	25	30	
Val Ala Ser Arg Glu Asp Asn Ala Gln Asp Glu Ala Ile Lys Ala Leu			
35	40	45	
Ile Glu Ala Leu Gln Ser Glu Lys Thr Arg Lys Phe Ile Leu Asp Thr			
50	55	60	
Tyr Lys Gly Ala Ile Ile Pro Ala Phe			
65	70		

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441

Val	Phe	Thr	Met	Leu	Val	Leu	Val	Leu	Ser	Asp	Asn	Phe	Leu	Gly	Leu
1				5				10						15	
Phe	Ile	Gly	Trp	Glu	Gly	Val	Gly	Leu	Cys	Ser	Tyr	Leu	Leu	Ile	Gly
				20				25						30	
Phe	Trp	Tyr	His	Lys	Lys	Ser	Ala	Asn	Asn	Ala	Ser	Ile	Glu	Ala	Phe
				35				40						45	
Val	Met	Asn	Arg	Ile	Thr	Asp	Leu	Gly	Met	Leu	Met	Gly	Ile	Ile	Leu
							50	55				60			
Ile	Phe	Trp	Asn	Phe	Gly	Thr	Leu	Gln	Tyr	Lys	Glu	Val	Phe	Ser	Met
					65		70		75						80
Leu	Asn	Asn	Ala	Asp	Tyr	Ser	Met	Leu	Phe	Tyr	Ile	Ser	Val	Phe	Leu
							85		90						95
Phe	Ile	Gly	Ala	Met	Gly	Lys	Ser	Ala	Gln	Phe	Pro	Met	His	Thr	Trp
					100			105							110
Leu	Ala	Asn	Ala	Met	Glu	Gly	Pro	Thr	Pro	Val	Ser	Ala	Leu	Ile	His
					115			120							125
Ala	Thr	Thr	Met	Val	Thr	Ala	Gly	Val	Tyr	Leu	Ile	Ile	Arg	Ala	Asn
					130		135								140
Pro	Leu	Tyr	Ser	Ala	Val	Phe	Glu	Val	Gly	Tyr	Phe	Ile	Ala	Cys	Leu
						145		150			155				160
Gly	Ala	Phe	Val	Ala	Leu	Phe	Gly	Ala	Ser	Met	Ala	Leu	Val	Asn	Lys
							165			170					175
Asp	Leu	Lys	Arg	Ile	Val	Glu	Tyr	Ser	Thr	Leu	Ser	Gln	Leu	Gly	Leu
						180			185						190
Tyr	Val	Cys	Ser	Gly	Arg	Ala	Trp	Gly	Leu	Cys	Asp	Arg	Ala	Phe	Pro
						195			200						205
Pro	Leu	Tyr	Ala	Cys	Val	Leu	Gln	Ile	Pro	Pro	Phe	Leu	Arg	Leu	Arg
						210		215			220				
Gln	Cys	His	Ala	Cys	Asp	Gly	Arg	Gln	Ser	Gly	Tyr	Tyr			
						225		230			235				

(2) INFORMATION FOR SEO ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:-

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...91

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442

Val	Cys	Leu	Gly	Leu	Ala	Asp	Val	Met	Val	Val	Leu	Ser	Leu	His	Leu
1								5			10			15	
Asn	Leu	Asn	Pro	Thr	Asn	Pro	Lys	Trp	Leu	Asn	Arg	Asp	Arg	Leu	Val
								20			25			30	
Phe	Ser	Gly	Gly	His	Ala	Ser	Ala	Leu	Val	Tyr	Ser	Leu	Leu	His	Leu
								35			40			45	
Trp	Gly	Phe	Asp	Leu	Ser	Leu	Asp	Asp	Leu	Lys	Arg	Phe	Arg	Gln	Leu
								50			55			60	
His	Ser	Lys	Thr	Pro	Gly	His	Pro	Glu	Leu	His	His	Thr	Glu	Gly	Ile
								65			70			75	
Glu	Ile	Thr	Thr	Unk	Phe	Arg	Ala	Arg	Phe	Cys					80
								85			90				

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...91

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442

Val	Cys	Leu	Gly	Leu	Ala	Asp	Val	Met	Val	Val	Leu	Ser	Leu	His	Leu
1								5			10			15	
Asn	Leu	Asn	Pro	Thr	Asn	Pro	Lys	Trp	Leu	Asn	Arg	Asp	Arg	Leu	Val
								20			25			30	
Phe	Ser	Gly	Gly	His	Ala	Ser	Ala	Leu	Val	Tyr	Ser	Leu	Leu	His	Leu
								35			40			45	
Trp	Gly	Phe	Asp	Leu	Ser	Leu	Asp	Asp	Leu	Lys	Arg	Phe	Arg	Gln	Leu
								50			55			60	
His	Ser	Lys	Thr	Pro	Gly	His	Pro	Glu	Leu	His	His	Thr	Glu	Gly	Ile
								65			70			75	
Glu	Ile	Thr	Thr	Unk	Phe	Arg	Ala	Arg	Phe	Cys					80
								85			90				

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443

Met Met Ile Thr Lys Gln Ser Tyr Gln Arg Phe Ala Leu Met Arg Val
 1 5 10 15
 Phe Val Phe Ser Leu Ser Ala Phe Ile Phe Asn Thr Thr Glu Phe Val
 20 25 30
 Pro Val Ala Leu Leu Ser Asp Ile Ala Lys Ser Phe Glu Met Glu Ser
 35 40 45
 Ala Thr Val Gly Leu Met Ile Thr Ala Tyr Ala Trp Val Val Ser Leu
 50 55 60
 Gly Ser Leu Pro Leu Met Leu Leu Ser Ala Lys Ile Glu Arg Lys Arg
 65 70 75 80
 Leu Leu Leu Phe Leu Phe Ala Leu Phe Ile Phe Ser His Ile Leu Ser
 85 90 95
 Arg

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444

Met Lys Leu Arg Ala Ser Val Leu Ile Gly Val Ala Ile Leu Cys Leu
 1 5 10 15
 Ile Leu Ser Ala Cys Ser Asn Tyr Ala Lys Lys Val Val Lys Gln Lys
 20 25 30
 Asn His Val Tyr Thr Pro Val Tyr Asn Glu Leu Ile Glu Lys Tyr Ser
 35 40 45
 Glu Ile Pro Leu Asn Asp Lys Leu Lys Asp Thr Pro Phe Met Val Gln
 50 55 60
 Val Lys Leu Pro Asn Tyr Lys Asp Tyr Leu Leu Asp Asn Lys Gln Val
 65 70 75 80
 Val Leu Thr Phe Lys Leu Val His His Ser Lys Lys Ile Thr Leu Ile
 85 90 95
 Gly Asp Ala Asn Lys Ile Leu Gln Tyr Lys Asn Tyr Phe Gln Ala Asn
 100 105 110
 Gly Ala Arg Ser Asp Ile Asp Phe Tyr Leu Gln Pro Thr Leu Asn Gln
 115 120 125
 Lys Gly Val Val Met Ile Ala Ser Asn Tyr Asn Asp Asn Pro Asn Asn
 130 135 140
 Lys Glu Iys Pro Gln Thr Phe Asp Val Leu Gln Gly Ser Gln Pro Met
 145 150 155 160
 Leu Gly Ala Asn Thr Lys Asn Leu His Gly Tyr Asp Val Ser Gly Ala
 165 170 175

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Asn	Asn	Lys	Gln	Val	Ile	Asn	Glu	Val	Ala	Arg	Glu	Lys	Ala	Gln	Leu
180						185					190				
Glu	Lys	Ile	Asn	Gln	Tyr	Tyr	Lys	Thr	Leu	Leu	Gln	Asp	Lys	Glu	Gln
195						200					205				
Glu	Tyr	Thr	Thr	Arg	Lys	Asn	Asn	Gln	Arg	Glu	Ile	Leu	Glu	Thr	Leu
210						215				220					
Ser	Asn	Arg	Ala	Gly	Tyr	Gln	Met	Arg	Gln	Asn	Val	Ile	Ser	Ser	Glu
225						230				235				240	
Ile	Phe	Lys	Asn	Gly	Asn	Leu	Asn	Met	Gln	Ala	Lys	Glu	Glu	Glu	Val
											245		250		255
Arg	Glu	Lys	Leu	Gln	Glu	Glu	Arg	Glu	Asn	Glu	Tyr	Leu	Arg	Asn	Gln
											260		265		270
Ile	Arg	Ser	Leu	Leu	Ser	Gly	Lys								
						275									
															280

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445

Met	Thr	Thr	Pro	Met	Ile	Ile	Ile	Ser	Leu	Glu	Met	Gly	Leu	Ser	Leu
1					5				10				15		
Val	Pro	Met	Arg	Gln	Cys	Leu	Val	Cys	Gln	Ala	Leu	Ala	Arg	Ser	Ile
							20		25				30		
Ser	Trp	Asn	Gly	Leu	Gly	Gly	Asn	Val	Arg	Asn	Thr	Lys	Val	Tyr	Gly
							35		40			45			
Lys	Phe	Ala	Ala	Tyr	His	His	Leu	Gln	Lys	Tyr	Leu	Leu	Ile	Asp	Leu
							50		55			60			
Ile	Ala	Arg	Phe	Lys	Thr	Gln	Gly	Gly	Tyr	Ile	Phe	Arg	Tyr	Asn	Thr
							65		70		75		80		
Asp	Asp	Tyr	Leu	Pro	Leu	Asn	Ser	Thr	Phe	Tyr	Met	Gly	Gly	Val	Thr
							85		90			95			
Thr	Val	Arg	Gly	Phe	Arg	Asn	Gly	Ser	Ile	Thr	Pro	Lys	Asp	Glu	Phe
							100		105			110			
Gly	Leu	Trp	Leu	Gly	Gly	Asp	Gly	Ile	Phe	Thr	Unk	Ser	Thr	Glu	Leu
							115		120			125			
Ser	Tyr	Gly	Val	Leu	Lys	Ala	Ala	Lys	Met	Arg	Leu	Ala	Trp	Phe	Phe
							130		135			140			
Asp	Phe	Gly	Phe	Leu	Thr	Phe	Unk	Thr	Pro	Thr	Arg	Gly	Ser	Phe	Phe
							145		150		155			160	
Tyr	Asn	Ala	Unk	Thr	Thr	Thr	Ala	Asn	Phe	Lys	Asp	Tyr	Unk	Val	Val
							165		170			175			
Gly	Unk	Unk	Phe	Glu	Unk	Ala	Thr	Trp	Arg	Ala					
							180		185						

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 187 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445

Met	Thr	Thr	Pro	Met	Ile	Ile	Ser	Leu	Glu	Met	Gly	Leu	Ser	Leu	
1					5			10				15			
Val	Pro	Met	Arg	Gln	Cys	Leu	Val	Cys	Gln	Ala	Leu	Ala	Arg	Ser	Ile
					20			25				30			
Ser	Trp	Asn	Gly	Leu	Gly	Gly	Asn	Val	Arg	Asn	Thr	Lys	Val	Tyr	Gly
					35			40				45			
Lys	Phe	Ala	Ala	Tyr	His	His	Gln	Lys	Tyr	Leu	Leu	Ile	Asp	Leu	
					50			55				60			
Ile	Ala	Arg	Phe	Lys	Thr	Gln	Gly	Gly	Tyr	Ile	Phe	Arg	Tyr	Asn	Thr
					65			70				75			80
Asp	Asp	Tyr	Leu	Pro	Leu	Asn	Ser	Thr	Phe	Tyr	Met	Gly	Gly	Val	Thr
					85			90				95			
Thr	Val	Arg	Gly	Phe	Arg	Asn	Gly	Ser	Ile	Thr	Pro	Lys	Asp	Glu	Phe
					100			105				110			
Gly	Leu	Trp	Leu	Gly	Gly	Asp	Gly	Ile	Phe	Thr	Unk	Ser	Thr	Glu	Leu
					115			120				125			
Ser	Tyr	Gly	Val	Leu	Lys	Ala	Ala	Lys	Met	Arg	Leu	Ala	Trp	Phe	Phe
					130			135				140			
Asp	Phe	Gly	Phe	Leu	Thr	Phe	Unk	Thr	Pro	Thr	Arg	Gly	Ser	Phe	Phe
					145			150				155			160
Tyr	Asn	Ala	Unk	Thr	Thr	Thr	Ala	Asn	Phe	Lys	Asp	Tyr	Unk	Val	Val
					165			170				175			
Gly	Unk	Unk	Phe	Glu	Unk	Ala	Thr	Trp	Arg	Ala					
					180			185							

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446

Met	Trp	Leu	Asp	His	Ile	Ala	Lys	Glu	Ile	Arg	Ser	Leu	Val	Glu	Asn
1					5			10				15			

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Asp	Ile	Glu	Val	Gly	Ile	Val	Ile	Gly	Gly	Gly	Asn	Ile	Ile	Arg	Gly
					20			25				30			
Val	Ser	Ala	Ala	Leu	Gly	Gly	Ile	Ile	Arg	Arg	Thr	Ser	Gly	Asp	Tyr
					35			40			45				
Met	Gly	Met	Leu	Ala	Thr	Val	Ile	Lys	Arg						
					50			55							

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...85

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447

Val	His	Asn	Phe	His	Trp	Asn	Val	Lys	Gly	Thr	Asp	Phe	Phe	Asn	Val
1							5		10					15	
His	Lys	Ala	Thr	Glu	Glu	Ile	Tyr	Glu	Gly	Phe	Ala	Asp	Met	Phe	Asp
							20		25			30			
Asp	Leu	Ala	Glu	Arg	Ile	Val	Gln	Leu	Gly	His	His	Pro	Leu	Val	Thr
							35		40			45			
Leu	Ser	Glu	Ala	Ile	Lys	Leu	Thr	Arg	Val	Lys	Glu	Glu	Thr	Lys	Thr
					50		55			60					
Ser	Phe	His	Ser	Lys	Asp	Ile	Phe	Lys	Glu	Ile	Leu	Glu	Asp	Tyr	Lys
	65					70			75			80			
His	Leu	Glu	Lys	Glu											
					85										

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448

Met	Asn	Lys	Thr	Ile	Lys	Ala	Ala	Leu	Ala	Tyr	Asn	Met	Gly	Gln
1						5		10		15				
Asp	His	Ala	Pro	Lys	Val	Ile	Ala	Ser	Gly	Val	Glu	Val	Ala	Lys

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20	25	30
Arg Ile Ile Gln Lys Ala Lys Glu Tyr Asp Ile Ala Leu Phe Ser Asn		
35	40	45
Pro Met Leu Val Asp Ser Leu Leu Lys Val Glu Leu Asp Cys Ala Ile		
50	55	60
Pro Glu Glu Leu Tyr Glu Ser Val Val Gln Val Phe Leu Trp Leu Asn		
65	70	75
Ser Val Glu Asn Asn Ala Gln Met Ser Lys		
85	90	

(2) INFORMATION FOR SEQ ID NO:449:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - iii) HYPOTHETICAL: YES
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...104
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:441

```

Met Gln Ala Leu Lys Ser Leu Leu Glu Val Ile Thr Lys Leu Gln Asn
1      5           10          15
Leu Gly Gly Tyr Leu Met His Ile Ala Ile Phe Ile Ile Phe Ile Trp
20        25          30
Ile Gly Gly Leu Lys Phe Val Pro Tyr Glu Ala Glu Gly Ile Ala Pro
35        40          45
Phe Val Unk Asn Ser Pro Phe Phe Ser Phe Met Tyr Lys Phe Glu Lys
50        55          60
Pro Ala Tyr Lys Gln His Lys Met Ser Glu Ser Gln Ser Met Gln Glu
65        70          75          80
Glu Met Gln Asp Asn Pro Lys Ile Val Glu Asn Lys Unk Trp His Lys
85        90          95
Glu Asn Arg Thr Ser Phe Ser Gly
100

```

(2) INFORMATION FOR SEQ ID NO:449:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - iii) HYPOTHETICAL: YES
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449

Met Gln Ala Leu Lys Ser Leu Leu Glu Val Ile Thr Lys Leu Gln Asn
 1 5 10 15
 Leu Gly Gly Tyr Leu Met His Ile Ala Ile Phe Ile Ile Phe Ile Trp
 20 25 30
 Ile Gly Gly Leu Lys Phe Val Pro Tyr Glu Ala Glu Gly Ile Ala Pro
 35 40 45
 Phe Val Unk Asn Ser Pro Phe Phe Ser Phe Met Tyr Lys Phe Glu Lys
 50 55 60
 Pro Ala Tyr Lys Gln His Lys Met Ser Glu Ser Gln Ser Met Gln Glu
 65 70 75 80
 Glu Met Gln Asp Asn Pro Lys Ile Val Glu Asn Lys Unk Trp His Lys
 85 90 95
 Glu Asn Arg Thr Ser Phe Ser Gly
 100

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450

Met Gly Lys Ile Ser Ala His Leu Ala His Glu Ile Arg Asn Pro Val
 1 5 10 15
 Gly Ser Ile Ser Leu Leu Ala Ser Val Leu Leu Lys His Ala Asn Glu
 20 25 30
 Lys Thr Lys Pro Ile Val Val Glu Leu Gln Lys Ala Leu Trp Arg Val
 35 40 45
 Glu Arg Ile Ile Lys Ala Thr Leu Leu Phe Ser Lys Gly Ile Gln Ala
 50 55 60
 Asn Arg Thr Lys Gln Ser Leu Lys Thr Leu Glu Ser Asp Leu Lys Glu
 65 70 75 80
 Ala Leu Asn Cys Tyr Thr Ser Lys Asp Ile Asp Phe Leu Phe Asn
 85 90 95
 Phe Ser Asp Glu Glu Gly Phe Phe Asp Phe Asp Leu Met Gly Ile Val
 100 105 110
 Leu Gln Asn Phe Leu Tyr Asn Ala Ile Asp Ala Ile Glu Ala Leu Glu
 115 120 125
 Glu Ser Glu Gln Gly Gln Val Lys Ile Glu Ala Phe Ile Gln Asn Glu
 130 135 140
 Phe Ile Val Phe Thr Ile Ile Asp Asn Gly Lys Glu Val Glu Asn Lys
 145 150 155 160
 Ser Ala Leu Phe Glu Pro Phe Glu Thr Thr Lys Leu
 165 170

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 212 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451

Val	Ser	Glu	Phe	His	Gln	Val	Tyr	Asp	Pro	Leu	Gly	Asn	Ile	Trp	Leu
1						5				10				15	
Ser	Ala	Leu	Val	Ala	Leu	Leu	Pro	Ile	Leu	Leu	Phe	Phe	Leu	Ser	Leu
						20				25				30	
Met	Val	Phe	Lys	Leu	Lys	Gly	Tyr	Thr	Ala	Ala	Phe	Leu	Ser	Val	Ala
						35				40				45	
Leu	Ser	Ala	Ile	Ile	Ala	Val	Leu	Val	Tyr	Lys	Met	Pro	Val	Ser	Met
						50				55				60	
Val	Gly	Ser	Ser	Phe	Leu	Tyr	Gly	Phe	Leu	Tyr	Gly	Leu	Trp	Leu	Phe
						65				70				75	
Ala	Trp	Ile	Ile	Ile	Ala	Ile	Phe	Leu	Tyr	Lys	Leu	Ser	Val	Lys	
						85				90				95	
Ser	Gly	Tyr	Phe	Glu	Ile	Leu	Lys	Glu	Ser	Val	Gln	Ser	Ile	Thr	Leu
						100				105				110	
Asp	His	Arg	Ile	Leu	Val	Ile	Leu	Ile	Gly	Phe	Cys	Phe	Gly	Ser	Phe
						115				120				125	
Leu	Glu	Gly	Ala	Ile	Gly	Phe	Gly	Gly	Pro	Ile	Ala	Ile	Thr	Ala	Ala
						130				135				140	
Ile	Ile	Leu	Val	Gly	Leu	Ser	Pro	Leu	Tyr	Ser	Ala	Gly	Leu	Cys	
						145				150				155	
Leu	Ile	Ala	Asn	Thr	Ala	Pro	Val	Ala	Phe	Gly	Ala	Val	Gly	Ile	Pro
						165				170				175	
Ile	Ser	Ala	Met	Ala	Ser	Ala	Val	Gly	Val	Pro	Ala	Ile	Leu	Ile	Ser
						180				185				190	
Ala	Met	Thr	Gly	Lys	Ile	Leu	Phe	Phe	Val	Ser	Leu	Leu	Val	Pro	Phe
						195				200				205	
Phe	Ile	Val	Phe												
						210									

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...182

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452

Met Glu Ile Lys Met Ala Lys Asp Tyr Gly Phe Cys Phe Gly Val Lys
 1 5 10 15
 Arg Ala Ile Gln Ile Ala Glu Lys Asn Gln Asn Ser Leu Ile Phe Gly
 20 25 30
 Ser Leu Ile His Asn Ala Lys Glu Ile Asn Arg Leu Glu Lys Asn Phe
 35 40 45
 Asn Val Lys Ile Glu Glu Asp Pro Lys Lys Ile Pro Lys Asn Lys Ser
 50 55 60
 Val Ile Ile Arg Thr His Gly Ile Pro Lys Gln Asp Leu Glu Tyr Leu
 65 70 75 80
 Lys Asn Lys Gly Val Lys Ile Thr Asp Ala Thr Cys Pro Tyr Val Ile
 85 90 95
 Lys Pro Gln Gln Ile Val Glu Ser Met Ser Lys Glu Gly Tyr Gln Ile
 100 105 110
 Val Leu Phe Gly Asp Ile Asn His Pro Glu Val Lys Gly Val Ile Ser
 115 120 125
 Tyr Ala Thr Asn Gln Ala Leu Val Gly Asn Ser Leu Glu Glu Leu Gln
 130 135 140
 Glu Lys Lys Leu Gln Arg Lys Val Ala Leu Val Ser Gln Thr Thr Gln
 145 150 155 160
 Ala Asn Pro Lys Thr Leu Ala Asn Arg Phe Leu Phe Gly Gly Unk Cys
 165 170 175
 Thr Glu Val Arg Ile Phe
 180

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear.

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453

Met Asp His Glu Phe Leu Ile Thr Met Arg Leu Ser Phe Ser Leu Ala
 1 5 10 15
 Leu Ile Thr Thr Leu Ile Leu Pro Ile Gly Ile Phe Leu Gly Tyr
 20 25 30
 Phe Leu Ser Leu Lys Arg Asn Leu Leu Thr Ser Leu Thr Glu Thr Leu
 35 40 45
 Val Tyr Met Pro Leu Val Leu Pro Pro Ser Val Leu Gly Phe Tyr Leu
 50 55 60
 Leu Leu Ile Phe Ser Pro Ser Ser Phe Leu Gly Ala Phe Leu Gln Asp
 65 70 75 80
 Val Leu Asn Val Lys Leu Val Phe Ser Phe Gln Gly Leu Ile Leu Gly
 85 90 95
 Ser Val Ile Phe Ser Leu Pro Phe Met Val Ser Pro Ile Lys Ser Ala
 100 105 110
 Leu Ile Ser Leu Pro Thr Ser Leu Lys Glu Ala Ser Tyr Ser Leu Gly
 115 120 125
 Lys Gly Glu Tyr Tyr Thr Leu Phe Phe Val Leu Leu Pro Asn Ile Lys

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130	135	140
Pro Ser Val Leu Met Ala Ile Ile Thr Thr Phe Met His Thr Ile Gly		
145	150	155
Glu Phe Gly Val Val Met Met Leu Gly Gly Asp Ile Leu Gly Glu Thr		160
165	170	175
Arg Val Ala Ser Ile Thr Ile Phe Asn Glu Ala Glu Ala Leu Asn Tyr		
180	185	190
Ser Lys Ala His Gln Tyr Ala Leu Thr Leu Thr Leu Ile Ser Phe Ser		
195	200	205
Leu Leu Phe Val Thr Leu Phe Leu Asn Lys Lys Gln Ser Ser Phe Leu		
210	215	220

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454

Met His Pro Ile Met Phe Ala Tyr Ile Ala Asn Ala Leu Ala Gln Ala		
1	5	10
Arg Lys Ile Asn Gly Thr Leu Cys Met Ala Phe Gln Lys Ile Ser Gln		15
20	25	30
Val Lys Glu Leu Gly Ile Asp Lys Ala Lys Ser Leu Ile Gly Asn Leu		
35	40	45
Ser Gln Val Ile Ile Tyr Pro Thr Lys Asp Thr Asp Glu Leu Ile Glu		
50	55	60
Cys Gly Val Pro Leu Ser Asp Ser Glu Ile Asn Phe Leu His Asn Thr		
65	70	75
Asp Met Arg Ala Arg Gln Val Leu Val Lys Asn Ile Val Thr Asn Ala		80
85	90	95
Ser Ala Phe Ile Glu Ile Asp Leu Lys Lys Ile Cys Lys Asn Tyr Phe		
100	105	110
Ile Phe Leu Ile Ala Met Leu Val Ile Glu Lys Ser Ser Met Ile Leu		
115	120	125
Lys Lys Gln		
130		

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...73

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455

Met	Cys	Leu	Thr	Gly	Gly	Leu	Met	Arg	Trp	Leu	Lys	Ser	Val	Lys	Pro
1				5				10						15	
Glu	Arg	Ile	Leu	His	Ser	Val	Val	Glu	Phe	Val	Asp	Ile	Ala	Gly	Leu
							20		25				30		
Ile	Lys	Gly	Ala	Ser	Lys	Gly	Glu	Gly	Leu	Gly	Asn	Gln	Phe	Leu	Ala
	35					40					45				
Asn	Ile	Lys	Glu	Cys	Glu	Val	Ile	Leu	Gln	Val	Val	Arg	Cys	Phe	Glu
	50					55				60					
Asp	Asp	Asn	Asn	His	Ala	Cys	Glu	Arg							
	65					70									

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...92

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456

Met	His	Val	Ala	Cys	Leu	Leu	Ala	Leu	Gly	Asp	Asn	Leu	Ile	Thr	Leu
1					5				10				15		
Ser	Leu	Leu	Lys	Glu	Ile	Ala	Ser	Lys	Gln	Gln	Gln	Ser	Leu	Lys	Ile
								20	25				30		
Leu	Gly	Thr	His	Leu	Thr	Leu	Lys	Ile	Ala	Lys	Leu	Leu	Glu	Cys	Glu
	35					40				45					
Lys	His	Phe	Glu	Ile	Ile	Pro	Val	Phe	Glu	Asn	Ile	Pro	Ala	Phe	Tyr
	50					55				60					
Asp	Leu	Lys	Gln	Gly	Val	Phe	Trp	Ala	Met	Lys	Asp	Phe	Leu	Trp	
	65				70				75			80			
Leu	Leu	Lys	Gln	Leu	Lys	Asn	Ile	Lys	Ser	Asn	Val				
					85				90						

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457

```

Met Lys Lys Lys Pro Leu Met Trp Arg Ile Cys Ala Leu Arg Arg Leu
1      5          10          15
Leu Leu Gly Phe Lys Arg Glu Arg Glu Leu Leu Ser Phe Ala Lys His
20     25          30
Trp Asn Ile Pro Thr Ile Val Val Phe Thr His Thr Gln Ala Glu Ala
35     40          45
Gly Asp Ala Phe Val Gln Glu Thr Lys Gly Ile Ile Asp Glu Glu Trp
50     55          60
Gly Phe Lys Gly Phe Val Arg Ala Tyr Val Arg Val Asn Ser Val Ala
65     70          75          80
Phe Ser Phe Arg Gly Leu Lys Val Pro Val Glu Gly Leu Glu Glu Leu
85     90          95
Val Asp Glu Thr Lys Lys Cys Leu Ser Asp Ala Glu Lys Asn Lys Lys
100    105         110
Arg His Phe Leu Ser Ile Gln Arg Val Lys Ile Gln Glu Arg Lys Gln
115    120         125
Ala Met Ile Glu Glu Cys Lys Thr Ile Ile His Val Ala Ser Gly Ala
130    135         140
Ala Gly Val Ala Gly Leu Ile Pro Ile Pro Phe Ser Asp Ala Leu Ala
145    150         155         160
Ile Ala Pro Ile Gln Ala Gly Met Ile Tyr Lys Met Asn Asp Ala Phe
165    170         175
Gly Met Asp Leu Asp Lys Ser Val Gly Ala Ser Leu Val Ala Gly Leu
180    185         190
Leu Gly Val Asn Cys Arg Ala Ser Gly Glu Asp Ser Arg
195    200         205

```

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...41

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458

```

Val Leu Gly Val Unk Asn Leu Arg Gly Asn Val Phe Pro Leu Ile Ser
1      5          10          15
Leu Arg Leu Lys Phe Gly Leu Lys Ala Glu Lys Gln Asn Lys Asp Thr
20     25          30
Arg Tyr Ile Val Val Arg His Asn Asp
35     40

```

(2) INFORMATION FOR SEQ ID NO:459:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - iii) HYPOTHETICAL: YES
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...219
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45

(2) INFORMATION FOR SEQ ID NO:460:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 188 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - ii) MOLECULE TYPE: protein
 - iii) HYPOTHETICAL: YES
 - vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
 - ix) FEATURE:

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(A) NAME/KEY: misc_feature
 (B) LOCATION 1...188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460

```

Met Lys Ser Ile Gly Glu Val Met Ala Ile Gly Gly Asn Phe Leu Glu
1      5          10          15
Ala Leu Gln Lys Ala Leu Cys Ser Leu Glu Asn Asn Trp Leu Gly Phe
20     25          30
Glu Ser Leu Ser Lys Asp Leu Glu Ala Ile Lys Lys Glu Ile Arg Arg
35     40          45
Pro Asn Pro Lys Arg Leu Leu Tyr Ile Ala Asp Ala Phe Arg Leu Gly
50     55          60
Val Ser Val Asp Glu Val Phe Glu Leu Cys Gln Ile Asp Arg Trp Phe
65     70          75          80
Leu Ser Gln Ile Gln Lys Leu Val Lys Ala Glu Glu Gly Ile Asn Ser
85     90          95
Ser Val Leu Thr Asp Ala Lys Lys Leu Arg Gly Leu Lys Asn Leu Gly
100    105         110
Phe Ser Asp Ala Arg Ile Ala Thr Lys Ile Lys Glu Asn Glu Asn Leu
115    120         125
Glu Val Ser Pro Phe Glu Val Glu Leu Ala Arg Ser Asn Leu Gln Ile
130    135         140
Ala Pro His Phe Glu Glu Val Asp Thr Cys Ala Ala Glu Phe Leu Ser
145    150         155         160
Leu Thr Leu Ile Cys Ile Pro Pro Met Pro Leu Thr Leu Cys Pro Leu
165    170         175
Leu Glu Thr Asn Lys Lys Asn Lys Lys Arg Lys Ser
180    185

```

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 231 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461

```

Met Phe Gly Asn Lys Gln Leu Gln Ile Ser Gln Lys Asp Ser
1      5          10          15
Glu Ile Ala Glu Leu Lys Lys Glu Val Asn Leu Tyr Gln Ser Leu Leu
20     25          30
Asn Leu Cys Leu His Glu Gly Phe Val Gly Ile Lys Asn Asn Lys Val
35     40          45
Val Phe Lys Ser Gly Asn Leu Ala Ser Leu Asn Asn Leu Glu Glu Gln
50     55          60
Ser Val His Phe Lys Glu Asn Ala Glu Ser Val Asn Leu Gln Gly Val
65     70          75          80
Ser Tyr Ser Leu Lys Ser Gln Asn Ile Asp Gly Val Gln Tyr Phe Ser
85     90          95
Leu Ala Lys Lys Thr Gly Gly Val Gly Glu Tyr His Lys Asn Asp Leu
100    105         110

```

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Phe Lys Thr Phe Cys Thr Ser Leu Lys Glu Gly Leu Asn Ala Gln
 115 120 125
 Glu Ser Met Gln Tyr Phe His Gln Glu Thr Gly Leu Leu Leu Asn Ala
 130 135 140
 Ala Lys Asn Gly Glu Glu His Ser Asn Glu Gly Leu Ile Thr Val Asn
 145 150 155 160
 Lys Thr Gly Gln Asp Ile Glu Ser Leu Tyr Glu Lys Met Gln Asn Ala
 165 170 175
 Thr Ser Leu Ala Asp Ser Leu Asn Gln Arg Ser Asn Glu Ile Thr Gln
 180 185 190
 Val Ile Ser Leu Ile Asp Asp Ile Ala Glu Gln Thr Asn Leu Leu Ala
 195 200 205
 Leu Asn Ala Ala Ile Glu Ala Ala Arg Ala Val Asn Met Ala Glu Gly
 210 215 220
 Leu Arg Trp Trp Leu Met Arg
 225 230

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462

Met Trp Ile Met Ser Ser Leu Ser Ser Phe Phe His Ser Leu Phe
 1 5 10 15
 Phe Ile Lys Ser Asn Pro Gly Gln Leu Lys Gly Trp Gly Ser Lys
 20 25 30
 Ile Phe Phe Ile Asn Arg Lys Phe Val Leu Ala Gln Tyr Asn Pro Ser
 35 40 45
 Val Ser Ile Phe Ile Leu Leu Asn Arg Val Phe Gly Val Gly Val
 50 55 60

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463

Met Gln Phe Glu Glu Met Lys Glu Leu Ala His Gln Ile Gly Val Phe
 1 5 10 15
 Tyr His Val Gly Val Asp Gly Ile Ala Leu Phe Leu Leu Leu Asn
 20 25 30
 Ala Ile Val Val Leu Leu Ser Val Val Tyr Val Lys Glu Arg Arg Lys
 35 40 45
 Asp Phe Val Ile Cys Leu Leu Leu Unk Gly Ile Leu Met Gly Val
 50 55 60
 Phe Ser Ser Leu Asn Val Ile Phe Phe Tyr Ala Phe Trp Glu Ile Ser
 65 70 75 80
 Leu Leu Pro Val Leu Tyr Leu Ile Gly Arg Phe Gly Arg Asn Asn Lys
 85 90 95
 Ile Tyr Ser Gly Met Lys Phe Phe Leu Tyr Thr Phe Leu Ala Ser Leu
 100 105 110
 Cys Met Leu Leu Gly Ile Leu Tyr Ile Gly Tyr Asp Tyr Ala Asn Asn
 115 120 125
 Tyr Gly Met Met Ser Phe Asp Ile Leu Asp Trp Tyr Gln Leu Asn Phe
 130 135 140
 Ser Ser Gly Ile Lys Thr Trp Leu Phe Val Ala Phe Leu Ile Gly Ile
 145 150 155 160
 Ala Val Lys Ile Pro Leu Phe Pro Phe Thr His Gly Cys Leu Met Arg
 165 170 175
 Ile Leu Thr Pro Pro Leu
 180

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463

Met Gln Phe Glu Glu Met Lys Glu Leu Ala His Gln Ile Gly Val Phe
 1 5 10 15
 Tyr His Val Gly Val Asp Gly Ile Ala Leu Phe Leu Leu Leu Asn
 20 25 30
 Ala Ile Val Val Leu Leu Ser Val Val Tyr Val Lys Glu Arg Arg Lys
 35 40 45
 Asp Phe Val Ile Cys Leu Leu Leu Unk Gly Ile Leu Met Gly Val
 50 55 60
 Phe Ser Ser Leu Asn Val Ile Phe Phe Tyr Ala Phe Trp Glu Ile Ser
 65 70 75 80
 Leu Leu Pro Val Leu Tyr Leu Ile Gly Arg Phe Gly Arg Asn Asn Lys
 85 90 95
 Ile Tyr Ser Gly Met Lys Phe Phe Leu Tyr Thr Phe Leu Ala Ser Leu
 100 105 110
 Cys Met Leu Leu Gly Ile Leu Tyr Ile Gly Tyr Asp Tyr Ala Asn Asn
 115 120 125

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Tyr	Gly	Met	Met	Ser	Phe	Asp	Ile	Leu	Asp	Trp	Tyr	Gln	Leu	Asn	Phe
130					135					140					
Ser	Ser	Gly	Ile	Lys	Thr	Trp	Leu	Phe	Val	Ala	Phe	Leu	Ile	Gly	Ile
145					150				155					160	
Ala	Val	Lys	Ile	Pro	Leu	Phe	Pro	Phe	Thr	His	Gly	Cys	Leu	Met	Arg
					165				170					175	
Ile	Leu	Thr	Pro	Pro	Leu										
					180										

(2) INFORMATION FOR SEQ ID NO:464:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 116 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...116
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:464

Val	Lys	Lys	Tyr	Ala	Glu	Asp	Phe	Ile	Thr	Lys	Asp	Glu	Val	Lys	Ser
1					5				10				15		
Leu	Leu	Glu	Arg	Leu	Ala	Lys	Asp	Tyr	Pro	Thr	Ile	Val	Glu	Glu	Ser
					20				25				30		
Lys	Lys	Ile	Pro	Thr	Gly	Ala	Ile	Arg	Ser	Val	Leu	Gln	Ala	Leu	Leu
					35				40			45			
His	Glu	Ile	Pro	Ile	Lys	Asp	Met	Leu	Thr	Ile	Leu	Glu	Thr	Ile	
	50					55				60					
Thr	Asp	Ile	Ala	Pro	Leu	Val	Gln	Asn	Asp	Val	Asn	Ile	Leu	Thr	Glu
65						70			75			80			
Gln	Val	Arg	Ala	Arg	Leu	Ser	Arg	Val	Ile	Thr	Asn	Ala	Phe	Lys	Ser
	85						90				95				
Glu	Asp	Gly	Arg	Leu	Lys	Phe	Leu	Thr	Phe	Ser	Thr	Asp	Unk	Glu	Gln
	100					105				110					
Phe	Unk	Ala	Gln												
					115										

(2) INFORMATION FOR SEQ ID NO:464:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 116 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464

(2) INFORMATION FOR SEQ ID NO:465:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 153 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - iii) HYPOTHETICAL: YES
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...153
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:461

```

Val Gly Ala Asn Pro Val Pro His Ala Gln Ile Leu Gln Ser Val Val
1 5 10 15
Asp Asp Leu Lys Glu Lys Gly Ile Lys Leu Val Ile Val Ser Phe Thr
20 25 30
Asp Tyr Val Leu Pro Asn Leu Ala Leu Asn Asp Gly Ser Leu Asp Ala
35 40 45
Asn Tyr Phe Gln His Arg Pro Tyr Leu Asp Arg Phe Asn Leu Asp Arg
50 55 60
Lys Met His Leu Val Gly Leu Ala Asn Ile His Val Glu Pro Leu Arg
65 70 75 80
Phe Tyr Ser Gln Ile Thr Asp Ile Lys Asn Leu Lys Lys Gly Ser
85 90 95
Val Ile Ala Val Pro Asn Asp Pro Ala Asn Gln Gly Arg Ala Leu Ile
100 105 110
Leu Leu His Lys Gln Gly Leu Ile Ala Leu Lys Asp Pro Ser Asn Leu
115 120 125
Tyr Ala Thr Glu Phe Asp Ile Val Lys Asn Pro Tyr Asn Ile Lys Ile
130 135 140
Lys Pro Leu Glu Ala Ala Val Ile Ala
145 150

```

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...43

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466

```
Met Gly Leu Val Ala Ser Gly Ile Asn Asp Glu Glu Leu Leu Lys Trp
1           5          10          15
Leu Gln Ala Phe Gly Leu Lys Met Gly Leu Cys Phe Gln Val Leu Asp
20          25          30
Asp Ile Ile Asp Val Thr Gln Asp Glu Lys Glu
35          40
```

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 240 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467

```
Met Met Lys Asn Lys Arg Ser Gln Asn Ser Pro Tyr Val Thr Pro Asp
1           5          10          15
Asn Pro Tyr Leu Thr Leu Glu Lys Ala Leu Gly Tyr Ser Phe Lys Asp
20          25          30
Lys Arg Leu Leu Glu Gln Ala Leu Thr His Lys Ser Cys Lys Leu Ala
35          40          45
Leu Asn Asn Glu Arg Leu Glu Phe Leu Gly Asp Ala Val Leu Gly Leu
50          55          60
Val Ile Gly Glu Leu Leu Tyr His Lys Phe Unk Unk Unk Asp Gly Gly
65          70          75          80
Lys Leu Ser Lys Leu Arg Ala Ser Ile Val Ser Ala His Gly Phe Thr
85          90          95
Lys Leu Ala Lys Ala Ile Ala Leu Gln Asp Tyr Leu Arg Val Ser Ser
100         105         110
Ser Glu Glu Ile Ser Lys Gly Arg Glu Lys Pro Ser Ile Leu Ser Ser
115         120         125
Ala Phe Glu Ala Leu Met Ala Gly Val Tyr Leu Glu Ala Gly Leu Ala
130         135         140
Lys Val Arg Lys Ile Ile Gln Asn Leu Leu Asn Arg Ala Tyr Lys Arg
```

145	150	155	160
Leu Asp Leu Glu His	Leu Phe Met Asp Tyr	Lys Thr Ala Leu Gln Glu	
165	170	175	
Leu Thr Gln Unk Gln Phe Cys Val Ile Pro Thr Tyr Gln Leu Leu Gln			
180	185	190	
Glu Lys Gly Pro Asp His His Lys Glu Phe Glu Met Ala Leu Tyr Ile			
195	200	205	
Gln Asp Lys Met Tyr Ala Thr Ala Lys Gly Lys Ser Lys Lys Glu Ala			
210	215	220	
Glu Gln Gln Cys Ala Tyr Gln Ala Leu Gln Asn Leu Arg Lys Pro Asn			
225	230	235	240

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467

Met Met Lys Asn Lys Arg Ser Gln Asn Ser Pro Tyr Val Thr Pro Asp			
1	5	10	15
Asn Pro Tyr Leu Thr Leu Glu Lys Ala Leu Gly Tyr Ser Phe Lys Asp			
20	25	30	
Lys Arg Leu Leu Glu Gln Ala Leu Thr His Lys Ser Cys Lys Leu Ala			
35	40	45	
Leu Asn Asn Glu Arg Leu Glu Phe Leu Gly Asp Ala Val Leu Gly Leu			
50	55	60	
Val Ile Gly Glu Leu Leu Tyr His Lys Phe Unk Unk Unk Asp Gly Gly			
65	70	75	80
Lys Leu Ser Lys Leu Arg Ala Ser Ile Val Ser Ala His Gly Phe Thr			
85	90	95	
Lys Leu Ala Lys Ala Ile Ala Leu Gln Asp Tyr Leu Arg Val Ser Ser			
100	105	110	
Ser Glu Glu Ile Ser Lys Gly Arg Glu Lys Pro Ser Ile Leu Ser Ser			
115	120	125	
Ala Phe Glu Ala Leu Met Ala Gly Val Tyr Leu Glu Ala Gly Leu Ala			
130	135	140	
Lys Val Arg Lys Ile Ile Gln Asn Leu Leu Asn Arg Ala Tyr Lys Arg			
145	150	155	160
Leu Asp Leu Glu His Leu Phe Met Asp Tyr Lys Thr Ala Leu Gln Glu			
165	170	175	
Leu Thr Gln Unk Gln Phe Cys Val Ile Pro Thr Tyr Gln Leu Leu Gln			
180	185	190	
Glu Lys Gly Pro Asp His His Lys Glu Phe Glu Met Ala Leu Tyr Ile			
195	200	205	
Gln Asp Lys Met Tyr Ala Thr Ala Lys Gly Lys Ser Lys Lys Glu Ala			
210	215	220	
Glu Gln Gln Cys Ala Tyr Gln Ala Leu Gln Asn Leu Arg Lys Pro Asn			
225	230	235	240

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(2) INFORMATION FOR SEQ ID NO:468:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 209 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...209
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:468

Met Gly Asn Arg Leu Val Asp Arg Asp Ile Asp Lys Asn Pro
 1 5 10 15
 Arg Thr Lys Asn Arg Pro Ser Val Asp Gly Arg Ile Ser Val Lys Gly
 20 25 30
 Met Val Ile Phe Ser Val Ser Asn Ala Leu Leu Phe Val Gly Val Ser
 35 40 45
 Tyr Phe Ile Asn Pro Leu Ala Phe Lys Leu Ser Leu Pro Phe Leu Ile
 50 55 60
 Ile Leu Gly Gly Tyr Ser Tyr Phe Lys Arg Phe Ser Ser Leu Ala His
 65 70 75 80
 Phe Val Val Gly Leu Ala Leu Gly Leu Ala Pro Ile Ala Gly Ser Val
 85 90 95
 Ala Val Leu Gly Asp Ile Pro Leu Trp Asn Val Phe Leu Ala Leu Gly
 100 105 110
 Val Met Leu Trp Val Ala Gly Phe Asp Leu Leu Tyr Ser Leu Gln Asp
 115 120 125
 Met Glu Phe Asp Lys Glu Arg Gly Leu Phe Ser Ile Pro Ser Gln Leu
 130 135 140
 Gly Glu Lys Trp Cys Leu Asn Leu Ser Arg Leu Ser His Leu Val Ala
 145 150 155 160
 Leu Ile Cys Trp Leu Cys Phe Val Lys Cys Tyr His Gly Gly Leu Phe
 165 170 175
 Ala Tyr Leu Gly Leu Gly Val Ser Ala Leu Ile Leu Leu Tyr Glu Gln
 180 185 190
 Ile Leu Val Ala Arg Asp Tyr Lys Asn Ile Pro Lys Ser Leu Phe Cys
 195 200 205
 Glu

(2) INFORMATION FOR SEQ ID NO:469:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:

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(A) NAME/KEY: misc_feature
 (B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469

Val	Glu	Gln	Asn	Lys	Ile	Ile	Lys	Leu	Phe	Thr	Val	Ala	Thr	Met	Ala
1					5				10					15	
Met	Met	Pro	Pro	Thr	Leu	Ile	Gly	Thr	Ile	Asn	Gly	Met	Asn	Phe	Lys
					20				25					30	
Phe	Met	Pro	Glu	Leu	Glu	Trp	Gln	Tyr	Gly	Tyr	Leu	Phe	Ala	Leu	Ile
					35				40					45	
Val	Met	Ala	Ile	Ser	Thr	Ile	Leu	Pro	Val	Ile	Tyr	Phe	Lys	Lys	Lys
					50				55					60	
Gly	Leu	Val	Val	Ala	Phe	His	Gly	Ile	Phe	Ile	Leu	Thr	Leu	Arg	Arg
					65				70					75	80
Ser	Phe	Tyr	Thr	Ala	Trp	His	Ser	Leu	Leu	Gly	Tyr	Ala	Thr	Leu	
					85				90					95	

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470

Leu	Leu	Val	Leu	Leu	Asn	Leu	Lys	Unk	Thr	Pro	Asn	Leu	Met	Trp	Pro
1					5				10					15	
Leu	Asp	Ile	Ile	Val	Val	Val	Ala	Trp	Val	Leu	Trp	Gly	Val	Asn	Met
					20				25					30	
Phe	Gly	Ser	Met	Ser	Val	Arg	Arg	Glu	Asn	Thr	Ile	Tyr	Val	Ser	Leu
					35				40					45	
Trp	Tyr	Tyr	Ile	Ala	Thr	Tyr	Val	Gly	Ile	Ala	Val	Met	Tyr	Ile	Phe
					50				55					60	
Asn	Asn	Leu	Ser	Ile	Pro	Thr	Tyr	Phe	Val	Ala	Asp	Met	Gly	Ser	Val
					65				70					75	80
Trp	His	Unk	Ile	Ser	Met	Tyr	Ser	Gly	Ser	Asn	Asp	Ala	Leu	Ile	Gln
					85				90					95	
Trp	Trp	Trp	Gly	Asn	Ala	Val	Ala	Phe	Val	Phe	Thr	Ser	Gly	Val	
					100				105					110	
Ile	Gly	Thr	Ile	Tyr	Tyr	Phe	Leu	Pro	Lys	Glu	Ser	Gly	Gln	Pro	Ile
					115				120					125	
Phe	Ser	Tyr	Lys	Leu	Thr	Leu	Phe	Ser	Phe	Trp	Ser	Leu	Met	Phe	Val
					130				135					140	
Tyr	Ile	Trp	Ala	Gly	Gly	His	His	Leu	Ile	Tyr	Ser	Thr	Val	Unk	Asp
					145				150					155	160
Unk	Val	Gln	Thr	Leu	Ser	Ser	Unk	Phe	Ser	Val	Val	Leu	Ile	Leu	Pro
					165				170					175	
Ser	Unk	Gly	Thr	Ala	Ile	Asn	Met	Leu	Leu	Unk	Met	Arg	Gly	Gln	Trp
					180				185					190	
His	Gln	Unk	Lys	Glu	Ser	Pro	Leu	Ile	Lys	Phe	Leu	Val	Leu	Ala	Ser
					195				200					205	

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Thr Phe Tyr Met Leu Ser Thr Leu Glu Gly Ser Ile Gln Ala Ile Lys
 210 215 220
 Ser Val Asn Ala
 225

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470

Leu Leu Val Leu Leu Asn Leu Lys Unk Thr Pro Asn Leu Met Trp Pro
 1 5 10 15
 Leu Asp Ile Ile Val Val Ala Trp Val Leu Trp Gly Val Asn Met
 20 25 30
 Phe Gly Ser Met Ser Val Arg Arg Glu Asn Thr Ile Tyr Val Ser Leu
 35 40 45
 Trp Tyr Tyr Ile Ala Thr Tyr Val Gly Ile Ala Val Met Tyr Ile Phe
 50 55 60
 Asn Asn Leu Ser Ile Pro Thr Tyr Phe Val Ala Asp Met Gly Ser Val
 65 70 75 80
 Trp His Unk Ile Ser Met Tyr Ser Gly Ser Asn Asp Ala Leu Ile Gln
 85 90 95
 Trp Trp Trp Gly His Asn Ala Val Ala Phe Val Phe Thr Ser Gly Val
 100 105 110
 Ile Gly Thr Ile Tyr Tyr Phe Leu Pro Lys Glu Ser Gly Gln Pro Ile
 115 120 125
 Phe Ser Tyr Lys Leu Thr Leu Phe Ser Phe Trp Ser Leu Met Phe Val
 130 135 140
 Tyr Ile Trp Ala Gly Gly His His Leu Ile Tyr Ser Thr Val Unk Asp
 145 150 155 160
 Unk Val Gln Thr Leu Ser Ser Unk Phe Ser Val Val Leu Ile Leu Pro
 165 170 175
 Ser Unk Gly Thr Ala Ile Asn Met Leu Leu Unk Met Arg Gly Gln Trp
 180 185 190
 His Gln Unk Lys Glu Ser Pro Leu Ile Lys Phe Leu Val Leu Ala Ser
 195 200 205
 Thr Phe Tyr Met Leu Ser Thr Leu Glu Gly Ser Ile Gln Ala Ile Lys
 210 215 220
 Ser Val Asn Ala
 225

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(iii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...92

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471

Met	Phe	Asp	Ser	Ile	Val	Tyr	Phe	Phe	Asn	Lys	Ser	Gly	Phe	Val	Thr
1				5					10						15
Thr	Leu	Val	Leu	Val	Trp	Ile	Ser	Leu	Tyr	Leu	Val	Met	Thr	Leu	Trp
					20				25						30
Val	Phe	Leu	Tyr	Lys	Ser	Ile	Val	Leu	Lys	Ile	Glu	Leu	Arg	Arg	Glu
						35			40				45		
Met	Gln	Ser	Leu	Ser	Asn	Ile	Leu	Asn	Gly	Ala	Gln	Asp	Ala	Pro	Glu
	50					55				60					
His	Phe	Met	Phe	Asn	Lys	Lys	Arg	Asn	Asp	Glu	Thr	Lys	Arg	Tyr	Ser
	65					70			75			80			
Asn	Glu	Leu	Leu	Gln	Asp	Leu	Glu	Thr	Pro	Gly	Ser				
	85					90									

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...96

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472

Met	Ala	Met	Leu	Tyr	Cys	Met	Arg	Leu	Leu	Met	Pro	Ile	Leu	Gly	Ala
1					5				10					15	
Ile	Lys	Gly	Gly	Asp	Ile	Gly	Glu	Trp	Phe	Pro	Asp	Asn	Asp	Pro	Lys
					20			25						30	
Tyr	Lys	Asn	Ala	Ser	Ser	Lys	Glu	Leu	Leu	Lys	Ile	Val	Leu	Asp	Phe
						35		40				45			
Ser	Gln	Ser	Ile	Gly	Phe	Glu	Leu	Leu	Glu	Met	Gly	Ala	Thr	Ile	Phe
	50					55			60						
Ser	Glu	Ile	Pro	Lys	Ile	Thr	Pro	Tyr	Lys	Pro	Ala	Ile	Leu	Glu	Asn
	65					70			75			80			
Leu	Ser	Gln	Leu	Leu	Gly	Leu	Glu	Lys	Ser	Gln	Ile	Ser	Leu	Lys	Ala
						85			90						95

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1178 amino acids

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(B) TYPE: amino acid
 (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473

```

Met Ile Pro Asn Leu Asp Ile Glu Gly Glu Thr Met Thr Asn Glu Ala
1           5          10          15
Ile Asn Gln Gln Pro Gln Thr Glu Ala Ala Phe Asn Pro Gln Gln Phe
20          25          30
Ile Asn Asn Leu Gln Val Ala Phe Ile Lys Val Asp Asn Val Val Ala
35          40          45
Ser Phe Asp Pro Asn Gln Lys Pro Ile Val Asp Lys Asn Asp Arg Asp
50          55          60
Asn Arg Gln Ala Phe Glu Lys Ile Ser Gln Leu Arg Glu Glu Phe Ala
65          70          75          80
Asn Lys Ala Ile Lys Asn Pro Thr Lys Lys Asn Gln Tyr Phe Ser Ser
85          90          95
Phe Ile Ser Lys Ser Asn Asp Leu Ile Asp Lys Asp Asn Leu Ile Asp
100         105         110
Thr Gly Ser Ser Ile Lys Ser Phe Gln Lys Phe Gly Thr Gln Arg Tyr
115         120         125
Gln Ile Phe Met Asn Trp Val Ser His Gln Asn Asp Pro Ser Lys Ile
130         135         140
Asn Thr Gln Lys Ile Arg Gly Phe Met Glu Asn Ile Ile Gln Pro Pro
145         150         155         160
Ile Ser Asp Asp Lys Glu Lys Ala Glu Phe Leu Arg Ser Ala Lys Gln
165         170         175
Ala Phe Ala Gly Ile Ile Gly Asn Ile Arg Ser Asp Gln Lys
180         185         190
Phe Met Gly Val Phe Asp Glu Ser Leu Lys Glu Arg Gln Glu Ala Glu
195         200         205
Lys Asn Gly Glu Pro Asn Gly Asp Pro Thr Gly Gly Asp Trp Leu Asp
210         215         220
Ile Phe Leu Ser Phe Val Phe Asn Lys Lys Gln Ser Ser Asp Leu Lys
225         230         235         240
Glu Thr Leu Asn Gln Glu Pro Val Pro His Val Gln Pro Asp Val Ala
245         250         255
Thr Thr Thr Thr Asp Ile Gln Ser Leu Pro Pro Glu Ala Arg Asp Leu
260         265         270
Leu Asp Glu Arg Gly Asn Phe Ser Lys Phe Thr Leu Gly Asp Met Asn
275         280         285
Met Leu Asp Val Glu Gly Val Ala Asp Ile Asp Pro Asn Tyr Lys Phe
290         295         300
Asn Gln Leu Leu Ile His Asn Asn Ala Leu Ser Ser Val Leu Met Gly
305         310         315         320
Ser His Asn Gly Ile Glu Pro Glu Lys Val Ser Leu Leu Tyr Gly Asn
325         330         335
Asn Gly Gly Pro Glu Ala Arg His Asp Trp Asn Ala Thr Val Gly Tyr
340         345         350
Lys Asn Gln Arg Gly Asp Asn Val Ala Thr Leu Ile Asn Val His Met
355         360         365
Lys Asn Gly Ser Gly Leu Val Ile Ala Gly Gly Glu Lys Gly Ile Asn
370         375         380
Asn Pro Ser Phe Tyr Leu Tyr Lys Glu Asp Gln Leu Thr Gly Ser Gln

```

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385	390	395	400
Arg Ala Leu Ser Gln Glu Glu Ile Gln Asn Lys Val Asp Phe Met Glu			
405	410	415	
Phe Leu Ala Gln Asn Asn Ala Lys Leu Asp Asn Leu Ser Lys Lys Glu			
420	425	430	
Lys Glu Lys Phe Gln Asn Glu Ile Glu Asp Phe Gln Lys Asp Ser Lys			
435	440	445	
Ala Tyr Leu Asp Ala Leu Gly Asn Asp His Ile Ala Phe Val Ser Lys			
450	455	460	
Lys Asp Lys Lys His Leu Ala Leu Val Ala Glu Phe Gly Asn Gly Glu			
465	470	475	480
Leu Ser Tyr Thr Leu Lys Asp Tyr Gly Lys Lys Ala Asp Lys Ala Leu			
485	490	495	
Asp Arg Glu Ala Lys Thr Thr Leu Gln Gly Ser Leu Lys His Asp Gly			
500	505	510	
Val Met Phe Val Asp Tyr Ser Asn Phe Lys Tyr Thr Asn Ala Ser Lys			
515	520	525	
Ser Pro Asp Lys Gly Val Gly Ala Thr Asn Gly Val Ser His Leu Glu			
530	535	540	
Ala Gly Phe Ser Lys Val Ala Val Phe Asn Leu Pro Asn Leu Asn Asn			
545	550	555	560
Leu Ala Ile Thr Ser Val Val Arg Gln Asp Leu Glu Asp Lys Leu Ile			
565	570	575	
Ala Lys Gly Leu Ser Pro Gln Glu Ala Asn Lys Leu Val Lys Asp Phe			
580	585	590	
Leu Ser Ser Asn Lys Glu Leu Val Gly Lys Ala Leu Asn Phe Asn Lys			
595	600	605	
Ala Val Ala Glu Ala Lys Asn Thr Gly Asn Tyr Asp Glu Val Lys Gln			
610	615	620	
Ala Gln Lys Asp Leu Glu Lys Ser Leu Lys Lys Arg Glu Arg Leu Glu			
625	630	635	640
Lys Asp Val Ala Lys Asn Leu Glu Ser Lys Ser Gly Asn Lys Asn Lys			
645	650	655	
Met Glu Ala Lys Ser Gln Ala Asn Ser Gln Lys Asp Glu Ile Phe Ala			
660	665	670	
Leu Ile Asn Lys Glu Ala Asn Arg Asp Ala Arg Ala Ile Ala Tyr Ala			
675	680	685	
Gln Asn Leu Lys Gly Ile Lys Arg Glu Leu Ser Asp Lys Leu Glu Asn			
690	695	700	
Ile Asn Lys Asp Leu Lys Asp Phe Ser Lys Ser Phe Asp Glu Phe Lys			
705	710	715	720
Asn Gly Lys Asn Lys Asp Phe Ser Lys Ala Glu Glu Thr Leu Lys Ala			
725	730	735	
Leu Lys Gly Ser Val Lys Asp Leu Gly Ile Asn Pro Glu Trp Ile Ser			
740	745	750	
Lys Val Glu Asn Leu Asn Ala Ala Leu Asn Glu Phe Lys Asn Gly Lys			
755	760	765	
Asn Lys Asp Phe Ser Lys Val Thr Gln Ala Lys Ser Asp Leu Glu Asn			
770	775	780	
Ser Ile Lys Asp Val Ile Ile Asn Gln Lys Ile Thr Asp Lys Val Asp			
785	790	795	800
Asn Leu Asn Gln Ala Val Ser Val Ala Lys Ala Thr Gly Asp Phe Ser			
805	810	815	
Gly Val Glu Gln Ala Leu Ala Asp Leu Lys Asn Phe Ser Lys Glu Gln			
820	825	830	
Leu Ala Gln Gln Ala Gln Lys Asn Glu Asp Phe Asn Thr Gly Lys Asn			
835	840	845	
Ser Ala Leu Tyr Gln Ser Val Lys Asn Gly Val Asn Gly Thr Leu Val			
850	855	860	
Gly Asn Gly Leu Ser Lys Ala Glu Ala Thr Thr Leu Ser Lys Asn Phe			
865	870	875	880
Ser Asp Ile Lys Lys Glu Leu Asn Ala Lys Leu Gly Asn Phe Asn Asn			
885	890	895	
Asn Asn Asn Gly Leu Glu Asn Ser Thr Glu Pro Ile Tyr Thr Gln			
900	905	910	

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Val Ala Lys Lys Val Lys Ala Lys Ile Asp Arg Leu Asp Gln Ile Ala
 915 920 925
 Ser Gly Leu Gly Asp Val Gly Gln Ala Ala Ser Phe Leu Leu Lys Arg
 930 935 940
 His Asp Lys Val Asp Asp Leu Ser Lys Val Gly Leu Ser Ala Asn His
 945 950 955 960
 Glu Pro Ile Tyr Ala Thr Ile Asp Asp Leu Gly Gly Pro Phe Pro Leu
 965 970 975
 Lys Arg His Asp Lys Val Asp Asp Leu Ser Lys Val Gly Leu Ser Arg
 980 985 990
 Glu Gln Lys Leu Thr Gln Lys Ile Asp Asn Leu Asn Gln Ala Val Ser
 995 1000 1005
 Glu Ala Lys Ala Ser His Phe Asp Asn Leu Asp Gln Met Ile Asp Lys
 1010 1015 1020
 Leu Lys Asp Ser Thr Lys Lys Asn Val Val Asn Leu Tyr Val Glu Ser
 1025 1030 1035 1040
 Ala Lys Lys Val Pro Thr Ser Leu Ser Ala Lys Leu Asp Asn Tyr Ala
 1045 1050 1055
 Thr Asn Ser His Thr Arg Ile Asn Ser Asn Val Lys Asn Gly Thr Ile
 1060 1065 1070
 Asn Glu Lys Ala Thr Gly Met Leu Thr Gln Lys Asn Ser Glu Trp Leu
 1075 1080 1085
 Lys Leu Val Asn Asp Lys Ile Val Ala His Asn Val Gly Ser Ala Pro
 1090 1095 1100
 Leu Ser Ala Tyr Asp Lys Ile Gly Phe Asn Gln Lys Asn Met Lys Asp
 1105 1110 1115 1120
 Tyr Ser Asp Ser Phe Lys Phe Ser Thr Arg Leu Ser Asn Ala Val Lys
 1125 1130 1135
 Asp Ile Lys Ser Gly Phe Val Gln Phe Leu Thr Asn Ile Phe Ser Met
 1140 1145 1150
 Gly Ser Tyr Ser Leu Met Lys Ala Ser Val Glu His Gly Val Lys Asn
 1155 1160 1165
 Thr Asn Thr Lys Gly Gly Phe Gln Lys Ser
 1170 1175

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 162 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474

Met Lys Ala Pro Ser Gln Unk Asp Leu Lys Lys Ile Leu Gly Ile Glu
 1 5 10 15
 Glu Val Ile Unk Unk Ser Thr Ser Pro Met Glu Leu Arg Leu Ala Asn
 20 25 30
 Gln Lys Leu Gly Asn Arg Phe Ile Lys Thr Leu Gln Ala Met Asn Glu
 35 40 45
 Leu Asp Met Gly Ala Phe Phe Asn Ala Tyr Ala Gln Thr Thr Lys Asp
 50 55 60
 Pro Thr His Ala Thr Ser Tyr Gly Val Phe Ala Ala Ser Leu Asn Met

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65	70	75	80		
Glu	Leu	Lys Lys Ala Leu Arg His Tyr	Leu Tyr Ala Gln Thr Ser Asn		
		85	90	95	
Met	Val	Ile Asn Cys Val Lys Ser Val Pro	Leu Ser Gln Asn Asp Gly		
		100	105	110	
Gln	Lys	Ile Leu Leu Ser Leu Gln Ser Pro	Phe Asn Gln Leu Ile Glu		
		115	120	125	
Lys	Thr	Leu Glu Leu Asp Glu Ser His Leu	Cys Ala Ala Ser Val Gln		
		130	135	140	
Asn	Asp	Ile Lys Ala Met Gln His Glu Ser	Leu Tyr Ser Arg Leu Tyr		
		145	150	155	160
Met	Ser				

(2) INFORMATION FOR SEQ ID NO:474:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 162 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...162
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:474

Met	Lys	Ala	Pro	Ser	Gln	Unk	Asp	Leu	Lys	Ile	Leu	Gly	Ile	Glu	
1						5			10				15		
Glu	Val	Ile	Unk	Unk	Ser	Thr	Ser	Pro	Met	Glu	Leu	Arg	Leu	Ala	Asn
						20			25				30		
Gln	Lys	Leu	Gly	Asn	Arg	Phe	Ile	Lys	Thr	Leu	Gln	Ala	Met	Asn	Glu
						35			40				45		
Leu	Asp	Met	Gly	Ala	Phe	Phe	Asn	Ala	Tyr	Ala	Gln	Thr	Thr	Lys	Asp
						50			55				60		
Pro	Thr	His	Ala	Thr	Ser	Tyr	Gly	Val	Phe	Ala	Ala	Ser	Leu	Asn	Met
						65			70				75		80
Glu	Leu	Lys	Lys	Ala	Leu	Arg	His	Tyr	Leu	Tyr	Ala	Gln	Thr	Ser	Asn
						85			90				95		
Met	Val	Ile	Asn	Cys	Val	Lys	Ser	Val	Pro	Leu	Ser	Gln	Asn	Asp	Gly
						100			105				110		
Gln	Lys	Ile	Leu	Leu	Ser	Leu	Gln	Ser	Pro	Phe	Asn	Gln	Leu	Ile	Glu
						115			120				125		
Lys	Thr	Leu	Glu	Leu	Asp	Glu	Ser	His	Leu	Cys	Ala	Ala	Ser	Val	Gln
						130			135				140		
Asn	Asp	Ile	Lys	Ala	Met	Gln	His	Glu	Ser	Leu	Tyr	Ser	Arg	Leu	Tyr
						145			150				155		160
Met	Ser														

(2) INFORMATION FOR SEQ ID NO:475:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 466 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475

Met Lys Ala Leu Lys Thr Phe Leu Lys Ser Leu Ile Leu Leu Leu
 1 5 10 15
 Ala Ile Ala Leu Asn His Leu Asn Ala Val Ala Met Ile Val Asp Asn
 20 25 30
 Pro Thr Gln Asn Ala Trp Asn Gly Ala Lys Arg Ala Trp Asp Glu Ser
 35 40 45
 Lys Trp Ala Lys His Leu Ala Thr Ile Thr Glu Arg Ile Lys Leu Ala
 50 55 60
 Gln Asp Thr Leu Asp Arg Ala Asn Gln Thr Leu Asn Ser Ile Asn Lys
 65 70 75 80
 Val Asn Asp Val Leu Asn Lys Thr Asn Gln Phe Leu Thr Gly Ser Ile
 85 90 95
 Leu Ser Ile Pro Asn Pro Met Gln Tyr Val Glu Lys Ile Gln Ser Phe
 100 105 110
 Ala Lys Gln Val Gln Ala Asn Thr Glu Arg Ile Lys Glu Asn Ala Gln
 115 120 125
 Asn Tyr Asp Ile Arg Asn Gln Ile Ala Ala Lys Arg Ile Ser Glu Lys
 130 135 140
 Cys Pro Glu Leu Asn Trp Asp Val Ser Gln Asp Ala Ser Pro Thr Glu
 145 150 155 160
 Lys Asn Leu His Gln Phe Phe Thr Ser Lys Gly Lys Glu Ser Ala Asn
 165 170 175
 Thr Lys Ala Leu Lys Asp Phe Ala Asn Ala Ile Gly Asn Thr Gln Ile
 180 185 190
 Ser Thr Ala Asn Asp Leu Gly Ala Gly Leu Arg Gly Arg Ala Leu Leu
 195 200 205
 Glu Tyr Ile Cys Ile Gln Lys Gly Asn Leu Glu Ala Ala Lys Lys Ile
 210 215 220
 Gln Leu Leu Asp Ser Gln Met Thr Leu Ala Leu Leu Asn Asn Asp Tyr
 225 230 235 240
 Thr Ala Tyr Glu Lys Leu Arg Ala Glu Lys Glu Glu Leu Lys Arg Gln
 245 250 255
 Ile Ala Ser Asn Val Tyr Ala Lys Val Lys Gln Leu Val Val Ala Ser
 260 265 270
 Gln Asp Arg Ala Phe Ser Gln Met Asp Asn Glu Leu Gly Val Lys Thr
 275 280 285
 Phe Gly Phe Asn Asp Glu Asn Val Lys Lys Gly Tyr Cys Lys Lys Glu
 290 295 300
 Asn Arg Asn Gly Lys Ser Glu Cys Ile Pro Asn Met Leu Asn Val Asn
 305 310 315 320
 Arg Leu Lys Ala Gln Phe Asp Glu Leu Asn Leu Asp Tyr Ser Arg Asp
 325 330 335
 Ile Ala Gly Lys Gly Glu Ala Ala Lys Val Phe Asn Asp Tyr
 340 345 350
 Lys His Arg Phe Gln Gln Leu Ser Val Glu Thr Ala Leu Glu Ile Ala
 355 360 365
 Gln Asn Leu Ser Phe Met Asn Lys Thr Leu Gly Leu Met Val Gln Met
 370 375 380
 Gln Ser Tyr Ala Phe Lys Gln Gln Met Gly Tyr Phe Glu Asp Ile Ile
 385 390 395 400
 Pro Ala Asp Ala Leu Lys Asp Asp Lys Glu His Gln Glu Asn Leu Glu

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405	410	415
Gln Lys Gln Gln	Glu Ile Glu Lys Val Tyr Arg Ala Lys Leu Asp Ala	
420	425	430
Tyr Gly Phe Pro Asn Gly Ser Val Val Gly Lys Ala Ser Gly Val Asn Ser		
435	440	445
Asn Ser Asn Asn Glu Ala Pro Ser Ser Asp Asn Ile Gln Ser Phe Asn		
450	455	460
Pro Tyr		
465		

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...59

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476

Met Ala Phe Ile Leu Thr Thr Asn Leu Phe Ile Lys Ser Phe Thr Asn			
1	5	10	15
Ser Ile Arg Ile Thr Gly Cys Ile Ile Ser Pro Asn Val Phe Phe Ala			
20	25	30	
Tyr Glu Phe Cys Ala Leu Gly Phe Arg Lys Gly Gly Leu Ile Leu Asp			
35	40	45	
Asn Phe Ser Lys Phe Val Ser His Arg Leu Gln			
50	55		

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...59

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476

Met Ala Phe Ile Leu Thr Thr Asn Leu Phe Ile Lys Ser Phe Thr Asn			
1	5	10	15
Ser Ile Arg Ile Thr Gly Cys Ile Ile Ser Pro Asn Val Phe Phe Ala			
20	25	30	

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Tyr	Glu	Phe	Cys	Ala	Leu	Gly	Phe	Arg	Lys	Gly	Gly	Leu	Ile	Leu	Asp
	35					40				45					
Asn	Phe	Ser	Lys	Phe	Val	Ser	His	Arg	Leu	Gln					
	50					55									

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477

Val	Arg	Phe	Phe	Ile	Phe	Leu	Ile	Leu	Ile	Cys	Pro				
1				5				10			15				
Leu	Met	Ser	Ala	Asp	Ser	Ala	Leu	Pro	Ser	Val	Asn	Leu	Ser	Leu	Asn
							20		25			30			
Ala	Pro	Ser	Asp	Pro	Lys	Gln	Leu	Val	Thr	Thr	Leu	Asn	Val	Ile	Ala
					35		40			45					
Leu	Leu	Thr	Leu	Leu	Val	Leu	Ala	Pro	Ser	Leu	Ile	Leu	Val	Met	Thr
	50				55				60						
Ser	Phe	Thr	Arg	Leu	Ile	Val	Val	Phe	Ser	Phe	Leu	Arg	Thr	Ala	Leu
	65				70				75			80			
Gly	Thr	Gln	Gln	Thr	Pro	Pro	Thr	Gln	Ile	Leu	Val	Ser	Leu		
	85				90				95						
Ile	Leu	Thr	Phe	Phe	Ile	Met	Glu	Pro	Ser	Leu	Lys	Lys	Ala	Tyr	Asp
	100				105				110						
Thr	Gly	Ile	Lys	Pro	Tyr	Met	Asp	Lys	Lys	Ile	Ser	Tyr	Thr	Glu	Ala
	115				120				125						
Phe	Glu	Lys	Ser	Thr	Leu	Pro	Phe	Lys	Glu	Phe	Met	Leu	Lys	Asn	Thr
	130				135				140						
Arg	Glu	Lys	Asp	Leu	Ala	Leu	Phe	Phe	Arg	Ile	Arg	Asn	Leu	Pro	Asn
	145				150				155			160			
Pro	Lys	Thr	Pro	Asp	Asp	Val	Ser	Leu	Ser	Val	Leu	Ile	Pro	Ala	Phe
	165				170				175						
Met	Ile	Ser	Glu	Leu	Lys	Thr	Ala	Phe	Gln	Ile	Gly	Phe	Leu	Leu	Tyr
	180				185				190						
Leu	Pro	Phe	Leu	Val	Ile	Asp	Met	Val	Ile	Ser	Ser	Ile	Leu	Met	Ala
	195				200				205						
Met	Gly	Met	Met	Met	Leu	Pro	Pro	Val	Met	Ile	Ser	Leu	Pro	Phe	Lys
	210				215				220						
Ile	Leu	Val	Phe	Ile	Leu	Val	Asp	Gly	Phe	Asn	Leu	Leu	Thr	Glu	Asn
	225				230				235			240			
Leu	Val	Ala	Ser	Phe	Lys	Met	Val								
	245														

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477

Val	Arg	Phe	Phe	Ile	Phe	Leu	Ile	Leu	Ile	Cys	Pro	Leu	Ile	Cys	Pro
1				5					10					15	
Leu	Met	Ser	Ala	Asp	Ser	Ala	Leu	Pro	Ser	Val	Asn	Leu	Ser	Leu	Asn
				20					25					30	
Ala	Pro	Ser	Asp	Pro	Lys	Gln	Leu	Val	Thr	Thr	Leu	Asn	Val	Ile	Ala
				35					40					45	
Leu	Leu	Thr	Leu	Leu	Val	Leu	Ala	Pro	Ser	Leu	Ile	Leu	Val	Met	Thr
				50					55					60	
Ser	Phe	Thr	Arg	Leu	Ile	Val	Val	Phe	Ser	Phe	Leu	Arg	Thr	Ala	Leu
	65				70				75					80	
Gly	Thr	Gln	Gln	Thr	Pro	Pro	Thr	Gln	Ile	Leu	Val	Ser	Leu	Ser	Leu
				85				90						95	
Ile	Leu	Thr	Phe	Phe	Ile	Met	Glu	Pro	Ser	Leu	Lys	Lys	Ala	Tyr	Asp
			100				105						110		
Thr	Gly	Ile	Lys	Pro	Tyr	Met	Asp	Lys	Lys	Ile	Ser	Tyr	Thr	Glu	Ala
			115				120						125		
Phe	Glu	Lys	Ser	Thr	Leu	Pro	Phe	Lys	Glu	Phe	Met	Leu	Lys	Asn	Thr
	130				135			140							
Arg	Glu	Lys	Asp	Leu	Ala	Leu	Phe	Phe	Arg	Ile	Arg	Asn	Leu	Pro	Asn
	145				150				155						160
Pro	Lys	Thr	Pro	Asp	Asp	Val	Ser	Leu	Ser	Val	Leu	Ile	Pro	Ala	Phe
			165				170							175	
Met	Ile	Ser	Glu	Leu	Lys	Thr	Ala	Phe	Gln	Ile	Gly	Phe	Leu	Leu	Tyr
			180				185						190		
Leu	Pro	Phe	Leu	Val	Ile	Asp	Met	Val	Ile	Ser	Ser	Ile	Leu	Met	Ala
		195			200			205							
Met	Gly	Met	Met	Met	Leu	Pro	Pro	Val	Met	Ile	Ser	Leu	Pro	Phe	Lys
		210			215			220							
Ile	Leu	Val	Phe	Ile	Leu	Val	Asp	Gly	Phe	Asn	Leu	Leu	Thr	Glu	Asn
	225				230			235						240	
Leu	Val	Ala	Ser	Phe	Lys	Met	Val								
		245													

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

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(B) LOCATION 1...44

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478

Val	Met	Asp	Ala	Glu	Asn	Gly	Glu	Leu	Leu	Val	Ala	Gly	Ser	Tyr	Pro
1				5				10						15	
Glu	Tyr	Asn	Leu	Asn	Asp	Phe	Val	Gly	Gly	Ile	Ser	Gln	Asp	Lys	Trp
					20			25					30		
Gln	Lys	Leu	Gln	Asp	Asp	Ile	Tyr	Asn	Pro	Leu	Leu				
					35			40							

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479

Met	Asn	Phe	Phe	Asp	Thr	Leu	Met	Gly	Met	Phe	Val	Glu	Pro	Ser	Gln
1						5			10					15	
Lys	Val	Ala	Lys	Ser	Leu	Ala	Glu	His	Val	Gly	Ser	Phe	Phe	His	Ala
						20			25				30		
Gln	Leu	Ile	Leu	Asn	Thr	Ile	Ile	Thr	Ile	Leu	Phe	Met	Ile	Trp	Ala
						35			40			45			
Tyr	Lys	Arg	Val	Lys	Glu	Gly	Asp	Met	Phe	Glu	Phe	Lys	Thr	Ala	Met
						50			55			60			
Gly	Val	Val	Val	Phe	Ile	Ala	Phe	Val	Gly	Phe	Ile	Asn	Trp	Gly	Ile
						65			70			75		80	
Lys	Asn	Pro	Asn	Asp	Phe	Asn	Thr	Tyr	Phe	Ile	Asn	Thr	Ile	Phe	Tyr
						85			90			95			
Pro	Ser	Glu	Lys	Leu	Ala	Ile	Leu	Ile	Ala	Gln	Ser	Leu	Asn	Asp	Gly
						100			105			110			
Leu	Glu	Ile	Pro	Thr	Asn	Thr	Asn	Leu	Ser	Pro	Ser	Glu	Ile	Phe	Ser
						115			120			125			
Ile	Gly	Asn	Leu	Ala	Ser	Ser	Ala	Tyr	Ala	Met	Ile	Val	Asn	Leu	Trp
						130			135			140			
Asp	Asn	Ala	Phe	Asp	Gly	Ile	Asn	Met	Phe	Asn	Trp	Leu	Thr	Met	Ile
						145			150			155		160	
Pro	Lys	Ile	Ile	Met	Phe	Phe	Leu	Val	Ile	Leu	Gly	Glu	Leu	Phe	
						165			170			175			
Leu	Gly	Leu	Leu	Ile	Ile	Ile	Val	Leu	Leu	Val	Thr	Ala	Glu	Ile	Phe
						180			185			190			
Met	Trp	Ser	Ala	Leu	Gly	Leu	Ile	Val	Leu	Pro	Leu	Gly	Leu	Ile	Pro
						195			200			205			
Gln	Thr	Lys	Gly	Met	Leu	Phe	Ser	Tyr	Leu	Lys	Lys	Leu	Ile	Ser	Leu
						210			215			220			
Thr	Leu	Tyr	Lys	Pro	Cys	Met	Met	Leu	Val	Ala	Phe	Phe	Asn	Tyr	Gly
						225			230			235		240	
Ile	Ile	Tyr	Lys	Val	Asn	Thr	Leu	Ile	Pro	Thr	Lys	His	Glu	Val	Thr
						245			250			255			
Gln	Gly	Phe	Tyr	Gly	Asn	Ala	Asp	Lys	Met	Ala	Asn	Glu	Gly	Lys	Ile

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Ile	Asp	Val	Phe	Gly	Asn	Val	Leu	Glu	Gly	Asp	Trp	Asn	Ser	Tyr	Ile
260						265						270			
275						280						285			
Ala	His	Ser	Ser	Ile	Val	Gly	Leu	Thr	Ile	Ile	Val	Leu	Gly	Ser	
290						295						300			
Val	Ile	Cys	Phe	Phe	Leu	Val	Lys	Arg	Val	Pro	Asp	Phe	Ile	Asn	Asn
305						310					315			320	
Ile	Phe	Gly	Thr	Ser	Gly	Gly	Val	Gly	Ala	Val	Thr	Glu	Met	Met	Gln
325						330						335			
Lys	Ile	Gly	Met	Thr	Ile	Gly	Gly	Ala	Val	Phe	Gly	Gly	Ser	Ala	Val
340						345						350			
Met	Val	Ala	Asn	Gln	Val	Lys	Gln	Ala	Tyr	Gln	Ser	Ala	Gly	Gly	Gly
355						360						365			
Leu	Ala	Gly	Leu	Gln	Ala	Gly	Ala	Lys	Ala	Phe	Gly	Leu	Gly	Ala	Ile
370						375						380			
Ser	Gly	Gly	Ala	Ser	Ala	Met	Ala	Asn	His	Arg	Ser	Val	Lys	Ala	Gly
385						390					395			400	
Val	Lys	His	Phe	Val	Ala	Ser	Val	Lys	Ser	Gly	Phe	Gly	Phe	Asp	Asn
405						410						415			
Asp	Lys	Asn	Asn	Lys											
					420										

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480

Leu	Leu	Val	Thr	Phe	Leu	Asn	Gly	Phe	Asp	Pro	Lys	Ile	Ala	Asn	Leu
1				5				10				15			
Arg	Lys	Ala	Cys	Asn	Val	Tyr	Ser	Val	Gly	Val	Ile	Tyr	Ile	Val	Thr
						20		25				30			
Thr	Asn	Thr	Leu	Asn	Ile	Leu	Ser	Cys	Glu	Ser	Phe	Glu	Ile	Leu	Glu
						35		40				45			
Lys	Arg	Glu	Leu	Asp	Thr	Ser	Gly	Val	Thr	Lys	Thr	Ser	Thr	Pro	Phe
						50		55			60				
Phe	Ser	Arg	Val	Glu	Ile	Asp	Ala	Gly	Thr	Leu	Gly	Lys	Leu	Phe	
						65		70			75			80	
Ser	Gly	Ser	Gln	Ser	Lys	Asn	Tyr	Phe	Ala	Tyr	Tyr	Asp	Ala	Leu	Val
						85		90			95				
Lys	Lys	Glu	Lys	Arg	Lys	Glu	Val	Arg	Ile	Glu	Lys	Glu	Glu	Arg	
						100		105			110				
Ile	Asp	Ala	Arg	Glu	Asn	Lys	Arg	Glu	Ile	Lys	Gln	Glu	Ala	Ile	Lys
						115		120			125				
Glu	Pro	Lys	Lys	Ala	Asn	Gln	Gly	Thr	Glu	Asn	Ala	Pro	Thr	Leu	Glu
						130		135			140				
Glu	Lys	Unk	Tyr	Gln	Lys	Ala	Glu	Arg	Lys	Phe	Asp	Ala	Lys	Unk	Unk
						145		150			155			160	
Arg	Arg	Ser	Phe	Lys	Unk										
					165										

(2) INFORMATION FOR SEQ ID NO:480:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...166
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:480

Leu	Leu	Val	Thr	Phe	Leu	Asn	Gly	Phe	Asp	Pro	Lys	Ile	Ala	Asn	Leu
1				5				10				15			
Arg	Lys	Ala	Cys	Asn	Val	Tyr	Ser	Val	Gly	Val	Ile	Tyr	Ile	Val	Thr
					20			25			30				
Thr	Asn	Thr	Leu	Asn	Ile	Leu	Ser	Cys	Glu	Ser	Phe	Glu	Ile	Leu	Glu
					35			40			45				
Lys	Arg	Glu	Leu	Asp	Thr	Ser	Gly	Val	Thr	Lys	Thr	Ser	Thr	Pro	Phe
					50			55		60					
Phe	Ser	Arg	Val	Glu	Gly	Ile	Asp	Ala	Gly	Thr	Leu	Gly	Lys	Leu	Phe
					65			70		75		80			
Ser	Gly	Ser	Gln	Ser	Lys	Asn	Tyr	Phe	Ala	Tyr	Tyr	Asp	Ala	Leu	Val
					85			90		95					
Lys	Lys	Glu	Lys	Arg	Glu	Val	Arg	Ile	Glu	Lys	Glu	Glu	Arg		
					100			105		110					
Ile	Asp	Ala	Arg	Glu	Asn	Lys	Arg	Glu	Ile	Lys	Gln	Glu	Ala	Ile	Lys
					115			120		125					
Glu	Pro	Lys	Lys	Ala	Asn	Gln	Gly	Thr	Glu	Asn	Ala	Pro	Thr	Leu	Glu
					130			135		140					
Glu	Lys	Unk	Tyr	Gln	Lys	Ala	Glu	Arg	Lys	Phe	Asp	Ala	Lys	Unk	Unk
					145			150		155		160			
Arg	Arg	Ser	Phe	Lys	Unk										
					165										

(2) INFORMATION FOR SEQ ID NO:481:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...89
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:481

Met Asp Glu Pro Glu Thr Ser Leu Glu Gln Asn Ala Leu Ile Arg Leu
 1 5 10 15
 Ser Asn Leu Ile Ser Leu Arg Asn Thr Gln Gln Leu Thr Ser Ile Ile
 20 25 30
 Ala Thr His Asp Pro Ile Val Leu Asp Ser Cys Glu Trp Val Leu Leu
 35 40 45
 Leu Lys Asn Gly Asn Ile Ala Gln Tyr Lys Pro Leu Asn Ser Ile Leu
 50 55 60
 Lys Ser Val Ala Lys Thr Phe Asn Phe Lys Glu Lys Pro Thr Thr Lys
 65 70 75 80
 Asp Leu Leu Ala Leu Lys Asp Ile
 85

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 237 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482

Val Lys Thr Leu Gly Leu Ser Ser Leu Gly Gly Thr Leu Glu Phe Tyr
 1 5 10 15
 Asp Phe Ile Ile Phe Val Phe Phe Thr Ser Ile Ile Ala Lys His Phe
 20 25 30
 Phe Pro Asn Thr Leu Ser Pro Ile Trp Ser Glu Ile Asn Thr Tyr Gly
 35 40 45
 Ile Phe Ala Ala Gly Tyr Leu Ala Arg Pro Leu Gly Gly Ile Val Met
 50 55 60
 Ala His Phe Gly Asp Lys Phe Gly Arg Lys Asn Met Phe Met Leu Ser
 65 70 75 80
 Ile Leu Leu Met Val Ile Pro Thr Phe Ala Leu Ala Leu Met Pro Thr
 85 90 95
 Phe Asn Asp Leu Val Gly Phe Gly Val Asp Ser Met Gly Leu Thr Pro
 100 105 110
 Lys Asn Ala His Tyr Leu Gly Tyr Ile Ala Pro Val Phe Leu Val Leu
 115 120 125
 Val Arg Ile Cys Gln Gly Val Ala Val Gly Gly Glu Leu Pro Gly Ala
 130 135 140
 Trp Val Phe Val His Glu His Ala Pro Gln Gly Gln Lys Asn Thr Tyr
 145 150 155 160
 Ile Gly Phe Leu Thr Ala Ser Val Val Ser Gly Ile Leu Leu Gly Ser
 165 170 175
 Leu Val Tyr Ile Gly Ile Tyr Met Val Phe Asp Lys Pro Val Val Glu
 180 185 190
 Asp Trp Ala Trp Arg Val Ala Phe Gly Leu Gly Gly Ile Phe Gly Ile
 195 200 205
 Ile Ser Val Tyr Leu Arg Arg Phe Leu Glu Glu Thr Pro Val Phe Gln
 210 215 220
 Gln Met Lys Gln Gly Arg Cys Leu Ser Gln Ile Pro Ala
 225 230 235

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483

Met Arg Lys Phe Leu Asp Gly Ala Lys Ser Glu Val Leu Lys Tyr Asp
 1 5 10 15
 Val Ile Ser Phe Asp Ile Phe Asp Thr Leu Leu Leu Arg Pro Phe Ile
 20 25 30
 Lys Pro Thr Asp Leu Phe Leu Tyr Ile Glu Thr Lys Tyr Asn Ile Lys
 35 40 45
 Gly Phe His Gln Ala Arg Ile Leu Ala Glu Met Gln Ser Arg Lys Leu
 50 55 60
 Ser Lys Arg Gln Asp Ile Thr Leu Asp Glu Ile Tyr His Gln Ile Pro
 65 70 75 80
 Lys Glu Phe His Ser Tyr Lys Gly Val Glu Ile Ala Thr Glu Lys Glu
 85 90 95
 Val Leu Val Pro Asn Leu Glu Met Leu Glu Leu Tyr Arg Phe Ala Lys
 100 105 110
 Glu Asn Asn Lys Arg Val Ile Ile Val Ser Asp Met Tyr Leu Pro Leu
 115 120 125
 Glu Val Leu Glu Asp Ile Leu Ile Ser Lys Gly Phe Asp Gly Tyr Thr
 130 135 140
 Asn Phe Tyr Leu Ser Asn His Ile Met Leu Thr Lys His Ser Lys Asp
 145 150 155 160
 Leu Phe Lys His Val Leu Lys Gln Glu Asn Ile Thr Asn Thr Gln Ile
 165 170 175
 Leu His Ile Gly Asp Asn Ser Trp Ala Asp Asp Ala Met Pro Lys Ser
 180 185 190
 Leu Gly Ile Ala Thr Leu Phe Arg Lys Ser Val Leu Lys Gln Leu Glu
 195 200 205
 Glu Val Phe Pro Lys Tyr Lys Thr Phe Asn Pro Thr Ser Val Ala Gln
 210 215 220
 Ser Phe Ile Leu Gly Ser Leu Cys Val Phe Tyr Lys Asn Tyr Ile Gln
 225 230 235 240
 Lys His Glu Lys Phe Asp Tyr Trp Phe Leu Leu Gly Ala Met Gln Ala
 245 250 255
 Gly Ile Ala Ala Val Ala Tyr Cys Gln Phe Ile Tyr Lys Glu Ile His
 260 265 270
 Lys Arg Asn Ile Asp Thr Leu Val Phe Val Ala Arg Asp Gly Tyr Leu
 275 280 285
 Leu Gln Lys Ile Phe Asn Ile Leu Tyr Pro Asn Ser Tyr Lys Thr Thr
 290 295 300
 Tyr Val Tyr Ala Pro Arg Ile Leu Lys Lys Ala Val Phe Leu Glu Val
 305 310 315 320
 Val Glu Gly Glu Ser Leu Glu Ile Leu Arg Ile Leu Glu Gly Glu Glu
 325 330 335
 Glu Val Lys Lys Lys Gln Ile Thr Thr Asn Gln Gln Ala Tyr Val Tyr

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340	345	350
Leu Tyr Ser Asn Phe Glu His Cys Arg His Leu Ala Leu Lys Cys Leu		
355	360	365
Asp Asn Tyr Arg Lys Tyr Leu Phe Ser Ser Asn Leu Glu Gly Asn Ile		
370	375	380
Ala Ile Val Asp Thr Ile Thr Leu Gly Tyr Ser Ser Gln Gly Leu Ile		
385	390	395
Gln Lys Ala Leu Asn Lys Glu Val Phe Gly Cys Tyr Val Asp Leu Leu		
405	410	415
Arg Ile Leu Asn Tyr Asp Cys Val Ser Phe Leu Pro Phe Ser His Pro		
420	425	430
Lys Pro Val Tyr Phe His Asn Trp Asp Phe Met Glu Phe Leu Leu Thr		
435	440	445
Ser Pro Glu Tyr Pro Ile Leu Asn Val Glu Asn Gly Val Pro Ile Leu		
450	455	460
Ser Lys Arg Arg Phe Ile Leu		
465	470	

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484

Val Leu Lys Phe Phe Glu Asp Ser Lys Gln Leu Ser Thr Pro Met Gly		
1	5	10
		15
Lys Ser Ala Val Gly Ile Leu Ile Phe Gln Asp Ile Ala Ala Ile Pro		
20	25	30
Met Leu Leu Ile Leu Thr Ile Leu Gly Ser Lys Asp Ser His Val Asn		
35	40	45
Leu Leu Ile Leu Lys Thr Leu Ile Ser Ala Gly Ile Ile Leu Ile Leu		
50	55	60
Leu Leu Leu Pro Gly Lys Lys Gly Ala Asn Leu Ile Leu Glu Gln Ala		
65	70	75
		80
Lys Asp Thr Arg Leu Pro Glu Ile Phe Ile Gly Thr Asp Phe Ser Asp		
85	90	95
Cys Leu Gln Arg Gly Gly Val Glu Pro Phe Phe Trp Val Phe Tyr Val		
100	105	110
Phe Gly Gly Val His Cys Gly His Gly Asp Phe		
115	120	

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485

Met	Glu	Asn	Ser	Thr	Leu	Tyr	Ile	Val	Ile	Ala	Gly	Leu	Trp	Leu	Ala
1	5							10					15		
Val	Gly	Phe	Gly	Ile	Phe	Leu	Lys	Lys	Leu	Asp	Met	Pro	Val	Ile	Ile
	20						25						30		
Gly	Tyr	Ile	Cys	Thr	Gly	Thr	Val	Leu	Ala	Ala	Phe	Phe	Lys	Ile	Asn
	35						40						45		
Asp	Phe	Asn	Leu	Leu	Ser	Asp	Ile	Gly	Glu	Phe	Gly	Ile	Val	Phe	Leu
	50						55						60		
Met	Phe	Met	Ile	Gly	Ile	Glu	Phe	Asn	Phe	Asp	Lys	Leu	Lys	Ser	Ile
	65						70					75			80
Lys	Gln	Glu	Val	Leu	Val	Phe	Gly	Leu	Leu	Gln	Val	Val	Leu	Cys	Ala
	85						90						95		
Leu	Ile	Ala	Phe	Leu	Leu	Gly	Tyr	Phe	Val	Leu	Gly	Leu	Ser	Pro	Ile
	100						105						110		
Phe	Ser	Leu	Val	Leu	Gly	Met	Gly	Leu	Ser	Leu	Ser	Ser	Thr	Ala	
	115						120						125		

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485

Met	Glu	Asn	Ser	Thr	Leu	Tyr	Ile	Val	Ile	Ala	Gly	Leu	Trp	Leu	Ala
1	5							10					15		
Val	Gly	Phe	Gly	Ile	Phe	Leu	Lys	Lys	Leu	Asp	Met	Pro	Val	Ile	Ile
	20						25						30		
Gly	Tyr	Ile	Cys	Thr	Gly	Thr	Val	Leu	Ala	Ala	Phe	Phe	Lys	Ile	Asn
	35						40						45		
Asp	Phe	Asn	Leu	Leu	Ser	Asp	Ile	Gly	Glu	Phe	Gly	Ile	Val	Phe	Leu
	50						55						60		
Met	Phe	Met	Ile	Gly	Ile	Glu	Phe	Asn	Phe	Asp	Lys	Leu	Lys	Ser	Ile
	65						70					75			80
Lys	Gln	Glu	Val	Leu	Val	Phe	Gly	Leu	Leu	Gln	Val	Val	Leu	Cys	Ala
	85						90						95		
Leu	Ile	Ala	Phe	Leu	Leu	Gly	Tyr	Phe	Val	Leu	Gly	Leu	Ser	Pro	Ile
	100						105						110		
Phe	Ser	Leu	Val	Leu	Gly	Met	Gly	Leu	Ser	Leu	Ser	Ser	Thr	Ala	

405

115

120

125

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486

Met	Ile	Leu	Ala	Leu	Leu	Ile	Ser	Lys	Glu	Lys	Thr	His	Leu	Glu	Ala
1						5			10						15
Leu	Tyr	Tyr	Leu	Ser	Tyr	Gly	Val	Leu	Leu	Gly	Gly	Val	Ala	Gln	Ile
						20			25						30
Leu	Leu	His	Phe	Tyr	Pro	Leu	Val	Lys	Leu	Gly	Leu	Trp	Asp	Leu	Leu
						35			40						45
Phe	Lys	Gly	Leu	Leu	Gly	Phe	Lys	Thr	Lys	Asn	Thr	Asn	Lys	Lys	Glu
	50					55			60						
Tyr	Arg	Leu	Asn	Arg	Ala	Lys	Lys	Asp	Leu	Lys	Ala	Phe	Phe	Lys	Gln
	65					70			75						80
Phe	Phe	Pro	Ser	Val	Leu	Gly	Asn	Ser	Ser	Ala	Gln	Ile	Ala	Ser	Phe
						85			90						95
Leu	Asp	Thr	Thr	Ile	Ala	Ser	Phe	Leu	Ala	Ser	Gly	Ser	Val	Ser	Tyr
				100			105								110
Leu	Tyr	Tyr	Ala	Asn	Arg	Val	Phe	Gln	Leu	Pro	Leu	Ala	Leu	Phe	Ala
				115			120								125
Ile	Ala	Ile	Ser	Thr	Ala	Leu	Phe	Pro	Ser	Ile	Ala	Ile	Ala	Leu	Lys
	130					135									140
Asn	Asn	Gln	Gln	Asp	Leu	Ile	Leu	Gln	Arg	Leu	Gln	Lys	Ala	Trp	Phe
	145					150				155					160
Phe	Leu	Val	Gly	Val	Leu	Leu	Leu	Cys	Ser	Ile	Gly	Gly	Ile	Met	Leu
						165			170						175
Ser	Lys	Glu	Ile	Thr	Glu	Leu	Leu	Phe	Glu	Arg	Gly	Gln	Phe	Ser	Pro
				180			185								190
Lys	Asp	Thr	Leu	Ile	Thr	Ser	Gln	Val	Phe	Ser	Leu	Tyr	Leu	Leu	Gly
				195			200								205
Leu	Leu	Pro	Phe	Gly	Leu	Thr	Lys	Leu	Phe	Ser	Leu	Trp	Leu	Tyr	Ala
				210			215								220
Lys	Leu	Glu	Gln	Lys	Lys	Ala	Ala	Lys	Ile	Ser	Ile	Ile	Ser	Leu	Phe
	225					230				235					240
Leu	Gly	Leu	Ala	Ala	Ser	Leu	Ser	Leu	Met	Pro	Leu	Leu	Gly	Val	Leu
						245				250					255
Gly	Leu	Arg													

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...16
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:487

Leu Leu Leu Met Leu Asn Lys Pro Lys Pro Leu Phe Leu Unk Leu Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:487:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...16
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:487

Leu Leu Leu Met Leu Asn Lys Pro Lys Pro Leu Phe Leu Unk Leu Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:488:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...77
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:488

Val Leu Lys Tyr Pro Thr Met Phe Met Cys Ala Asp Ala Val Ile Ile
1 5 10 15
Ser Lys Ala Asp Met Ile Glu Val Phe Asn Phe Arg Val Ser Gln Val

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20	25	30
Lys Glu Asp Met Gln Lys Leu Lys Pro Glu Ala Pro Ile Phe Leu Met		
35	40	45
Ser Ser Lys Asp Pro Lys Ser Leu Glu Asp Phe Lys Asn Phe Leu Leu		
50	55	60
Glu Lys Lys Arg Glu Asn Tyr Gln Ser Thr His Ser Phe		
65	70	75

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 180 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489

Met Leu Leu Cys Ala Gly Arg Asn Glu Thr Leu Lys Lys Ala Val Pro		
1	5	10
Ile Gly Val Gly Leu Ile Glu Ser Ala Ile Asn Leu Thr Arg Met Cys		
20	25	30
Leu Lys Asn Pro Asp Thr Glu Ser Leu Ile Phe Ile Gly Ser Ala Gly		
35	40	45
Ser Tyr Ser Pro Glu Thr Glu Ile Leu Ser Val Phe Glu Ser Ile Glu		
50	55	60
Gly Tyr Gln Ile Glu Glu Ser Phe Ser His Leu Asn Ser Tyr Thr Pro		
65	70	75
Leu Asp Asn Phe Ile His Ile Glu Thr Lys Glu Gln Ala Leu Phe Glu		
85	90	95
Arg Val Arg Val Asn Ser Ser Asn Tyr Ile His Thr Ser Glu Met Phe		
100	105	110
Ala Lys Lys Met Val Gln Lys Gly Val Leu Leu Glu Asn Met Glu Phe		
115	120	125
Phe Ser Val Leu Ser Val Ala Lys Ile Phe Ser Leu Lys Ala Lys Gly		
130	135	140
Ile Phe Cys Val Ser Asn His Val Gly Leu Asn Ala His Lys Glu Phe		
145	150	155
Lys Glu Asn His Ala Lys Val Lys Gln Ile Leu Glu Asn Ile Ile Asp		
165	170	175
Ser Leu Ile Val		
180		

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490

Val Tyr Glu Glu Arg Ile Thr Leu Ala Ser Gln Gly Ile Pro Lys Thr
 1 5 10 15
 Ser Lys Val Gly Phe Glu Ile Phe Asp Thr Lys Asp Phe Gly Ala Thr
 20 25 30
 Asp Phe Asp Gln Asn Ile Lys Leu Ile Arg Ala Ile Glu Gly Glu Leu
 35 40 45
 Ser Arg Thr Ile Glu Ser Leu Asn Pro Ile Leu Lys Ala Asn Val His
 50 55 60
 Ile Ala Ile Pro Lys Asp Ser Val Phe Val Ala Lys Glu Val Pro Pro
 65 70 75 80
 Ser Ala Ser Val Met Leu Lys Leu Lys Pro Asp Met Lys Leu Ser Pro
 85 90 95
 Thr Gln Ile Leu Gly Ile Lys Asn Leu Ile Ala Ala Val Pro Lys
 100 105 110
 Leu Thr Ile Glu Asn Val Lys Ile Val Asn Glu Asn Gly Glu Ser Ile
 115 120 125
 Gly Glu Gly Asp Ile Leu Glu Asn Ser Lys Glu Leu Ala Leu Glu Gln
 130 135 140
 Leu Arg Tyr Lys Gln Asn Phe Glu Asn Ile Leu Glu Asn Lys Ile Val
 145 150 155 160
 Asn Ile Leu Ala Pro Ile Val Gly Unk Lys Asn Unk Val Val Unk Unk
 165 170 175
 Val Asn Unk Glu Phe Unk Phe Gln Lys Lys Ser Thr Lys Glu Thr
 180 185 190
 Phe Asp Pro Asn Asn Val Gly Lys Glu Arg Ala Lys Phe Arg Arg Lys
 195 200 205
 Lys Arg Arg Arg Ser
 210

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 148 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491

Val Ile Lys Lys Gly Tyr Ile Arg Gly Asp Leu Met Arg Ile Val Arg
 1 5 10 15
 Asn Leu Phe Leu Val Ser Phe Val Ala Tyr Ser Ser Ala Phe Ala Ala
 20 25 30
 Asp Leu Glu Thr Gly Thr Lys Asn Asp Lys Lys Ser Gly Lys Lys Phe

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35	40	45
Tyr Lys Leu His Lys Asn His Gly Ser Glu Thr Glu Thr Lys Asn Asp		
50	55	60
Lys Lys Leu Tyr Asp Phe Thr Lys Asn Ser Gly Leu Glu Gly Val Asp		
65	70	75
Leu Glu Lys Ser Pro Asn Leu Lys Ser His Lys Lys Ser Asp Lys Lys		80
85	90	95
Phe Tyr Lys Gln Leu Ala Lys Asn Asn Ile Ala Glu Gly Val Ser Met		
100	105	110
Pro Ile Val Asn Phe Asn Lys Ala Leu Ser Phe Gly Pro Tyr Phe Glu		
115	120	125
Arg Thr Lys Ser Lys Lys Thr Gln Tyr Met Asp Gly Gly Leu Met Met		
130	135	140
His Ile Arg Phe		
145		

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 281 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492

Val Met Ile Asp Pro Lys Met Val Glu Phe Ser Ile Tyr Ala Asp Ile		
1	5	10
Pro His Leu Leu Thr Pro Ile Ile Thr Asp Pro Lys Lys Ala Ile Gly		15
20	25	30
Ala Leu Gln Ser Val Ala Lys Glu Met Glu Arg Arg Tyr Ser Leu Met		
35	40	45
Ser Glu Tyr Lys Val Lys Thr Ile Asp Ser Tyr Asn Glu Gln Ala Gln		
50	55	60
Ser Asn Asp Val Glu Ala Phe Pro Tyr Leu Ile Val Val Ile Asp Glu		
65	70	75
Leu Ala Asp Leu Met Met Thr Gly Gly Lys Glu Ala Glu Phe Pro Ile		80
85	90	95
Ala Arg Ile Ala Gln Met Gly Arg Ala Ser Gly Leu His Leu Ile Val		
100	105	110
Ala Thr Gln Arg Pro Ser Val Asp Val Val Thr Gly Leu Ile Lys Thr		
115	120	125
Asn Leu Pro Ser Arg Val Ser Phe Arg Val Gly Thr Lys Ile Asp Ser		
130	135	140
Lys Val Ile Leu Asp Thr Asp Gly Ala Gln Ser Leu Leu Gly Arg Gly		
145	150	155
Asp Met Leu Phe Thr Pro Pro Gly Thr Asn Gly Leu Val Arg Leu His		160
165	170	175
Ala Pro Phe Ala Thr Glu Asp Glu Ile Lys Ile Val Asp Phe Ile		
180	185	190
Lys Ala Gln Lys Glu Val Glu Tyr Asp Lys Asp Phe Leu Leu Glu Glu		
195	200	205
Ser Arg Met Pro Leu Asp Thr Pro Asn Tyr Gln Gly Asp Asp Ile Leu		
210	215	220

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Glu Arg Ala Lys Ala Val Ile Leu Glu Lys Lys Ile Thr Ser Thr Ser			
225	230	235	240
Phe Leu Gln Arg Gln Leu Lys Ile Gly Tyr Asn Gln Ala Ala Thr Ile			
245	250	255	
Thr Asp Glu Leu Glu Ala Gln Gly Phe Leu Ser Pro Arg Asn Ala Lys			
260	265	270	
Gly Asn Arg Glu Ile Leu Gln Asn Phe			
275	280		

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493

Met Asn Phe Phe Lys Ile Leu Leu Met Glu Leu Arg Ala Ile Val Ser			
1	5	10	15
His Lys Gly Val Leu Leu Ile Leu Ile Gly Ala Pro Leu Ile Tyr Gly			
20	25	30	
Leu Leu Tyr Pro Leu Pro Tyr Leu Lys Asp Ile Val Thr Gln Gln Lys			
35	40	45	
Ile Ala Leu Val Asp Glu Asp Asn Ser Phe Leu Ser Arg Gln Leu Ala			
50	55	60	
Phe Met Val Gln Ser Ser Asn Glu Leu Glu Ile Ala Phe Phe Ser Pro			
65	70	75	80
Ser Met Leu Glu Ala Lys Lys Leu Leu Lys Glu Glu Lys Ile Tyr Gly			
85	90	95	
Ile Leu His Ile Pro Ser His Phe Glu Ala Asn Ile Tyr Lys Gln Ser			
100	105	110	
Ala Cys Asn Asp Arg Phe Leu Cys Glu Arg Gln Leu Leu Phe Asp Leu			
115	120	125	
Trp Cys Val Ser Glu Cys Gly Gly Glu His Gln Arg Leu Lys Arg			
130	135	140	

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

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(A) NAME/KEY: misc_feature
 (B) LOCATION 1...73

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494

Val Gly Gly Leu Ala Met Leu Gly Phe Phe Tyr Asn Ile Glu Lys Ile
 1 5 10 15
 Ser Leu Ala Thr Ala Thr Ala Phe Ser Gln Cys Ala Pro Unk Tyr Thr
 20 25 30
 Val Leu Leu Ser Pro Leu Leu Lys Glu Lys Leu Lys Arg Ser Ala
 35 40 45
 Leu Ile Ser Ala Cys Ile Gly Leu Val Gly Val Val Leu Ile Ser Asp
 50 55 60
 Pro Ser Val Glu Asn Val Gly Pro Ser
 65 70

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 311 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495

Val Cys Trp Thr Asp Leu Ile Gln Gly Leu Leu Met Met Ser Ala Leu
 1 5 10 15
 Ile Val Val Pro Ile Val Met Ile Ile His Leu Gly Gly Ile Gly Glu
 20 25 30
 Gly Ile Lys Ile Ile Arg Glu Ile Lys Pro Glu Asn Leu Ser Phe Unk
 35 40 45
 Gln Gly Ser Ser Val Val Ala Ile Ile Ser Ser Leu Ala Trp Gly Leu
 50 55 60
 Gly Tyr Phe Gly Gln Pro His Ile Leu Val Arg Phe Met Ser Ile Arg
 65 70 75 80
 Ser Ile Arg Asp Val Pro Lys Ala Thr Thr Ile Gly Ile Ser Trp Met
 85 90 95
 Val Ile Ser Leu Ile Gly Ala Cys Val Met Gly Leu Leu Gly Val Ala
 100 105 110
 Tyr Val His Lys Unk Asp Leu Ser Leu Glu Asp Pro Glu Lys Ile Phe
 115 120 125
 Ile Val Met Ser Gln Leu Leu Phe Asn Pro Trp Ile Thr Gly Ile Leu
 130 135 140
 Leu Ser Ala Ile Leu Ala Ala Val Met Ser Thr Ala Ser Ser Gln Leu
 145 150 155 160
 Leu Val Ser Ser Ser Thr Ile Ala Glu Asp Phe Tyr Ala Thr Ile Phe
 165 170 175
 Asn Lys Asn Ala Pro Gln Lys Leu Val Met Thr Ile Ser Arg Leu Ser
 180 185 190
 Val Leu Gly Val Ala Cys Ile Ala Phe Phe Ile Ser Thr Asp Lys Asn
 195 200 205
 Ala Ser Ile Leu Ser Ile Val Ser Tyr Ala Trp Ala Gly Phe Gly Ala
 210 215 220

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Ser	Phe	Gly	Ser	Val	Ile	Leu	Phe	Ser	Leu	Phe	Trp	Ser	Arg	Met	Thr
225					230				235					240	
Arg	Ile	Gly	Ala	Ile	Ala	Gly	Met	Leu	Ser	Gly	Ala	Ser	Thr	Val	Ile
					245				250					255	
Leu	Tyr	Asp	Lys	Phe	Gly	Lys	Ser	Phe	Leu	Asp	Ile	Tyr	Glu	Ile	Val
					260			265				270			
Pro	Gly	Phe	Ile	Val	Ala	Ser	Val	Ala	Ile	Val	Ala	Phe	Ser	Leu	Phe
					275			280				285			
Ser	Ser	Val	Arg	Ser	Gly	Thr	Lys	Glu	Ala	Phe	Glu	Thr	Met	Leu	Lys
					290			295				300			
Glu	Ile	Glu	Ser	Leu	Lys	His									
					305			310							

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496

Val	Gly	Leu	Phe	Ile	Val	Leu	Phe	Leu	Ile	Ile	Met	Lys	His	Gln	Thr
1					5				10					15	
Ser	Pro	Tyr	Ala	Phe	Thr	His	Asn	Gln	Ala	Leu	Val	Thr	Gln	Thr	Pro
					20			25				30			
Pro	Tyr	Phe	Thr	Gln	Leu	Thr	Ile	Pro	Lys	Pro	Asn	Asp	Ala	Leu	Ser
					35			40				45			
Ala	His	Ala	Ser	Ser	Leu	Ile	Ser	Leu	Pro	Asn	Asp	Asn	Leu	Leu	Ser
					50			55				60			
Ala	Tyr	Phe	Ser	Gly	Thr	Lys	Glu	Gly	Ala	Arg	Asp	Val	Lys	Ile	Ser
					65			70			75			80	
Ala	Asn	Leu	Phe	Asp	Ser	Lys	Thr	Asn	Arg	Trp	Ser	Glu	Ala	Phe	Ile
					85			90				95			
Leu	Leu	Thr	Lys	Glu	Glu	Leu	Ser	His	His	Ser	His	Glu	Tyr	Ile	Lys
					100			105				110			
Lys	Ile	Arg													
		115													

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497

Met Leu Val Gly Pro Thr Gly Val Gly Lys Thr Thr Thr Leu Ala Lys
 1 5 10 15
 Leu Ala Ala Arg Tyr Ser Arg Met Leu Ala Lys Lys Tyr Lys Val Gly
 20 25 30
 Ile Ile Thr Leu Asp Asn Tyr Arg Ile Gly Ala Leu Glu Gln Leu Ser
 35 40 45
 Trp Tyr Ala Asn Lys Met Lys Met Ser Ile Glu Ala Val Ile Asp Ala
 50 55 60
 Lys Asp Phe Ala Lys Glu Ile Glu Ala Leu Glu Tyr Cys Asp Phe Ile
 65 70 75 80
 Leu Val Asp Thr Thr Gly His Ser Gln Tyr Asp Lys Glu Lys Ile Ala
 85 90 95
 Gly Leu Lys Glu Phe Ile Asp Gly Gly Tyr Asn Ile Asp Val Ser Leu
 100 105 110
 Val Leu Ser Val Thr Thr Lys Tyr Glu Asp Met Lys Asp Ile Tyr Asp
 115 120 125
 Ser Phe Gly Val Leu Gly Ile Asp Thr Leu Ile Phe Thr Lys Leu Asp
 130 135 140
 Glu Ser Arg Gly Leu Gly Asn Leu Phe Ser Leu Val His Glu Ser Gln
 145 150 155 160
 Lys Pro Ile Ser Tyr Leu Ser Val Gly Gln Glu Val Pro Met Asp Leu
 165 170 175
 Lys Val Ala Thr Asn Glu Tyr Leu Val Asp Cys Met Leu Asp Gly Phe
 180 185 190
 Ser Asn Pro Asn Lys Glu Gln Ala
 195 200

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498

Val Gly Gly Ala Ser Phe Ile Ser Gly Gly Asn Gly Thr Leu Tyr Gly
 1 5 10 15
 Leu Asn Val Gly Tyr Asp Arg Leu Val Lys Ser Val Ile Leu Gly Gly
 20 25 30
 Tyr Val Ala Tyr Gly Tyr Ser Gly Phe Asn Gly Asn Ile Met His Ser
 35 40 45
 Leu Ala Asn Asn Val Asp Val Gly Met Tyr Ala Arg Ala Phe Leu Lys
 50 55 60
 Arg Asn Glu Phe Thr Leu Ser Ala Asn Glu Thr Tyr Gly Gly Asn Ala
 65 70 75 80

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Ser His Ile Asn Ser Ser Asn Ser Leu Leu Ser Val Leu Asn Gln Arg
 85 90 95
 Tyr Asn Tyr Asn Thr Trp Thr Thr Ser Val Asn Gly Asn Tyr Gly Tyr
 100 105 110
 Asp Phe Met Phe Lys Gln Lys Ser Val Val Leu Lys Pro Gln Val Gly
 115 120 125
 Leu Ser Tyr His Phe Ile Gly Leu Ser Gly Met Lys Gly Lys Met Gln
 130 135 140
 Asn Pro Ala Tyr Gln Gln Phe Val Met His Ser Asn Pro Ser Asn Glu
 145 150 155 160
 Ser Val Leu Thr Leu Asn Met Gly Leu Glu Ser Arg Lys Tyr Phe Gly
 165 170 175
 Lys Asn Ser Tyr Tyr Phe Val Thr Ala Arg Leu Gly Arg Asp Leu Leu
 180 185 190
 Ile Lys Ala Lys Gly Asp Asn Val Val Arg Phe Val Gly Glu Asn Thr
 195 200 205
 Leu Leu Tyr Arg Lys Gly Glu Ile Phe Asn Thr Phe Ala Ser Val Ile
 210 215 220
 Thr Gly Gly Glu Met His Leu Trp Arg Leu Met Tyr Val Asn Ala Gly
 225 230 235 240
 Val Gly Leu Lys Met Gly Leu Gln Tyr Gln Asp Leu Asn Ile Thr Gly
 245 250 255
 Asn Val Gly Met Arg Val Ala Phe
 260

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499

Met Asp Gly Tyr Gly Phe Lys Met Gln Asp Leu Gly Gln Lys Thr Gln
 1 5 10 15
 Val Ile Gln His Ile Phe Ala Gly Asp Asp Val Ser Ala Leu Glu Val
 20 25 30
 Lys Glu Asn Glu Cys Val Lys Ile Met Thr Gly Ala Met Val Pro Lys
 35 40 45
 Gly Ile Glu Thr Ile Val Pro Ile Glu Cys Met Leu Glu Ser His Lys
 50 55 60
 Asp Phe Ala Leu Ala Pro Lys Asp Phe Lys Ile His Ala Asn Ile Arg
 65 70 75 80
 Gln Lys Gly Glu Asn Ala Ser Leu Asn Ser Val Leu Val Pro Lys Asn
 85 90 95
 Thr Arg Leu Asn Tyr Gly His Ile Ala Leu Ile Ala Ser Gln Gly Phe
 100 105 110
 Lys Glu Ile Lys Ala Phe Arg Lys Leu Lys Ile Ala Leu Phe Ser Ser
 115 120 125
 Gly Asp Glu Leu Val Pro Leu Gly Gln Asn Ala Leu Glu Cys Gln Val
 130 135 140
 Tyr Asp Val Asn Ser Val Gly Val Phe Asn Met Leu Lys Asn Tyr Asn

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145	150	155	160
Thr His Phe Leu Gly Val Leu Lys Asp Asp	Lys Asn Leu Gln Leu Lys		
165	170	175	
Ile Leu Glu Leu Gln Gly Tyr Asp Val Ile Leu Ser Ser Ala Gly Val			
180	185	190	
Ser Val Gly Asp Lys Asp Phe Phe Lys Asp Ala Leu Lys Glu Arg Asn			
195	200	205	
Ala Leu Phe Tyr Tyr Glu Lys Val Asn Leu Lys Pro Gly Lys Pro Val			
210	215	220	
Thr Leu Ala Gln Leu Asn Gln Ser Ile Ile Ile Gly Leu Pro Gly Asn			
225	230	235	240
Pro Leu Ser Cys Leu Leu Val Leu Arg Val Leu Ile Leu Pro Leu Leu			
245	250	255	
Glu Arg Leu Ser Leu Asn Lys Asp Phe Lys Leu Lys Pro Phe Lys Ala			
260	265	270	
Gln Ile Asn Ala Pro Leu Lys Leu Asn Asn Lys Arg Thr His Leu Ile			
275	280	285	
Leu Gly Asn Tyr Ser Asn His Gln Phe Ile Pro Tyr Asn Asn Arg Tyr			
290	295	300	
Glu Ser Gly Ala Ile Gln Ala Leu Ala Gln Val Asp Ser Ile Thr Leu			
305	310	315	320
Ile Asp Glu Gly Val Gly Leu Val Gln Gly Glu Ile Glu Ile Leu Arg			
325	330	335	
Phe Glu Asn			

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500

Met Pro Tyr' Ala Leu Arg Lys Arg Phe Phe Lys Arg Leu Leu Leu Phe			
1	5	10	15
Phe Leu Ile Val Cys Met Ile Asn Leu His Ala Lys Ser Tyr Leu Phe			
20	25	30	
Ser Pro Leu Pro Pro Ala His Gln Gln Ile Ile Lys Thr Glu Pro Cys			
35	40	45	
Ser Leu Glu Cys Leu Lys Asp Leu Met Leu Gln Asn Gln Ile Phe Ser			
50	55	60	
Phe Val Ser Gln Tyr Asp Asp Asn Asn Gln Asp Glu Ser Leu Lys Thr			
65	70	75	80
Tyr Tyr Lys Asp Ile Leu Asn Lys Leu Asn Pro Val Phe Ile Ala Ser			
85	90	95	
Gln Thr Pro Ala Lys Glu Ser Tyr Glu Pro Lys Ile Glu Leu Ala Ile			
100	105	110	
Leu Leu Pro Lys Lys Val Val Gly Arg Tyr Ala Ile Leu Val Met Asn			
115	120	125	
Thr Leu Leu Ala Tyr Phe Glu His Gln Lys Gln Arg Phe Gln Tyr Pro			
130	135	140	

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Ser Leu
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(2) INFORMATION FOR SEQ ID NO:501:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - iii) HYPOTHETICAL: YES
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...60
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50

(2) INFORMATION FOR SEQ ID NO:502:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 350 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - iii) HYPOTHETICAL: YES
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...350
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:502

Met	Ala	Leu	Arg	Val	Leu	Leu	Phe	Phe	Cys	Phe	Leu	Phe	Leu	Gln	Ala
1					5				10					15	
Glu	Asp	Lys	Ser	Gln	Glu	Leu	Ser	Ser	Ile	Gln	Lys	Gln	Met	Ala	Leu
							20		25				30		
Val	Asp	Lys	Lys	Leu	Ala	Lys	Asp	Asp	Asn	Val	Trp	Leu	Lys	Lys	Phe
							35		40				45		
Glu	Asn	Tyr	Lys	Ile	Tyr	Asn	Gln	Ile	Tyr	Thr	Glu	Lys	Glu	Ser	Val
							50		55			60			
Arg	Gln	Glu	Leu	Arg	Arg	Leu	Lys	Asn	Lys	Lys	Ser	Lys	Asp	Leu	Leu
							65		70			75			80
Lys	Ile	Ser	Thr	Leu	Glu	His	Thr	Leu	Lys	Ala	Leu	Glu	Ser	Gln	Gln

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Lys	Met	Phe	Glu	Ser	Tyr	Gly	Val	Asn	Pro	Phe	Lys	Asp	Leu	Ile	Glu	
100							105						110			
Arg	Pro	Asn	Ile	Pro	Asn	Ile	Pro	Asn	Ile	Ala	Asn	Pro	Ile	Ala	Ile	
115							120						125			
Ile	Asp	Gly	Ile	Ser	Phe	Ile	Lys	Ser	Met	Arg	Leu	Lys	His	Glu	Asn	
130							135						140			
Leu	Lys	Asn	Asn	Gln	Thr	Ser	Leu	Gly	Glu	Val	Leu	Lys	Leu	Leu	Asp	
145							150				155			160		
Gln	Lys	His	Gln	Leu	Leu	Asn	Gln	Trp	His	Ala	Leu	Asp	Lys	Ser	Ala	
165							170						175			
Lys	Leu	Ser	Asp	Glu	Ile	Tyr	Gln	Thr	Gln	Ala	Lys	Arg	Leu	Glu	Leu	
180							185						190			
Gln	Gly	Ala	Gln	Asn	Ile	Leu	Lys	Thr	Thr	Ile	Gly	Ile	Phe	Gln	Lys	
195							200						205			
Asp	Ser	Asp	Glu	Ala	Ile	Ser	Ile	Val	Lys	Ser	Gln	Val	Lys	Asn	Gln	
210							215						220			
Leu	Phe	Lys	Leu	Val	Tyr	Val	Phe	Leu	Ala	Ala	Leu	Ser	Val	Val		
225							230				235			240		
Phe	Ala	Trp	Ile	Leu	Lys	Ile	Ile	Ser	Ser	Lys	Tyr	Ile	Glu	Asn	Asn	
245							250						255			
Glu	Arg	Val	Tyr	Thr	Val	Asn	Lys	Ala	Ile	Asn	Phe	Val	Asn	Val	Ser	
260							265						270			
Val	Ile	Unk	Unk	Ile	Unk	Leu	Phe	Ser	Tyr	Leu	Glu	Asn	Val	Thr	Tyr	
275							280						285			
Leu	Val	Thr	Val	Leu	Gly	Phe	Ala	Ser	Ala	Gly	Leu	Ala	Ile	Unk	Met	
290							295						300			
Lys	Asp	Leu	Phe	Met	Ser	Leu	Leu	Gly	Trp	Phe	Ile	Ile	Leu	Ile	Gly	
305							310				315			320		
Gly	Ser	Val	His	Val	Gly	Asp	Arg	Val	Arg	Ile	Ala	Lys	Gly	Thr	Asp	
325							330						335			
Ile	Phe	Ile	Gly	Asp	Val	Leu	Asp	Thr	Ser	Asn	Val	Val	His			
340							345						350			

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502

Met	Ala	Leu	Arg	Val	Leu	Leu	Phe	Phe	Cys	Phe	Leu	Phe	Leu	Gln	Ala
1							5		10				15		
Glu	Asp	Lys	Ser	Gln	Glu	Leu	Ser	Ser	Ile	Gln	Lys	Gln	Met	Ala	Leu
							20		25				30		
Val	Asp	Lys	Lys	Leu	Ala	Lys	Asp	Asp	Asn	Val	Trp	Leu	Lys	Lys	Phe
							35		40				45		
Glu	Asn	Tyr	Lys	Ile	Tyr	Asn	Gln	Ile	Tyr	Thr	Glu	Lys	Glu	Ser	Val
							50		55				60		
Arg	Gln	Glu	Leu	Arg	Arg	Leu	Lys	Asn	Lys	Lys	Ser	Lys	Asp	Leu	Leu
							65		70				75		80

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Lys Ile Ser Thr Leu Glu His Thr Leu Lys Ala Leu Glu Ser Gln Gln
 85 90 95
 Lys Met Phe Glu Ser Tyr Gly Val Asn Pro Phe Lys Asp Leu Ile Glu
 100 105 110
 Arg Pro Asn Ile Pro Asn Ile Pro Asn Ile Ala Asn Pro Ile Ala Ile
 115 120 125
 Ile Asp Gly Ile Ser Phe Ile Lys Ser Met Arg Leu Lys His Glu Asn
 130 135 140
 Leu Lys Asn Asn Gln Thr Ser Leu Gly Glu Val Leu Lys Leu Leu Asp
 145 150 155 160
 Gln Lys His Gln Leu Leu Asn Gln Trp His Ala Leu Asp Lys Ser Ala
 165 170 175
 Lys Leu Ser Asp Glu Ile Tyr Gln Thr Gln Ala Lys Arg Leu Glu Leu
 180 185 190
 Gln Gly Ala Gln Asn Ile Leu Lys Thr Thr Ile Gly Ile Phe Gln Lys
 195 200 205
 Asp Ser Asp Glu Ala Ile Ser Ile Val Lys Ser Gln Val Lys Asn Gln
 210 215 220
 Leu Phe Lys Leu Val Tyr Val Phe Leu Ala Ala Leu Leu Ser Val Val
 225 230 235 240
 Phe Ala Trp Ile Leu Lys Ile Ile Ser Ser Lys Tyr Ile Glu Asn Asn
 245 250 255
 Glu Arg Val Tyr Thr Val Asn Lys Ala Ile Asn Phe Val Asn Val Ser
 260 265 270
 Val Ile Unk Unk Ile Unk Leu Phe Ser Tyr Leu Glu Asn Val Thr Tyr
 275 280 285
 Leu Val Thr Val Leu Gly Phe Ala Ser Ala Gly Leu Ala Ile Unk Met
 290 295 300
 Lys Asp Leu Phe Met Ser Leu Leu Gly Trp Phe Ile Ile Leu Ile Gly
 305 310 315 320
 Gly Ser Val His Val Gly Asp Arg Val Arg Ile Ala Lys Gly Thr Asp
 325 330 335
 Ile Phe Ile Gly Asp Val Leu Asp Thr Ser Asn Val Val His
 340 345 350

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503

Met Leu Ser Ala Leu Leu Ser Lys Met Gly Thr Tyr Ala Leu Leu Arg
 1 5 10 15
 Phe Leu Leu Pro Leu Phe Pro Glu Leu Ser Glu Ile Tyr Leu Thr Pro
 20 25 30
 Ile Ala Ile Val Ala Leu Cys Met Ile Ile Tyr Gly Gly Phe Leu Ala
 35 40 45
 Tyr Ala Gln Lys Asp Leu Lys Thr Leu Ile Ala Tyr Ser Ser Phe Ser
 50 55 60
 His Met Gly Val Val Val Leu Gly Val Phe Ser Phe Asn Val Glu Gly

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65	70	75	80
Val Ser Gly Ala Val Phe Met Met Phe Ala His Gly Val Ile Val Met			
85	90	95	
Gly Leu Phe Leu Leu Ala Gly Ile Leu Glu Glu Arg Ala Ser Ser Leu			
100	105	110	
Glu Ile Ala Arg Phe Gly Ser Ile Ala Lys Ser Ala Pro Val Phe Ala			
115	120	125	
Ala Phe Phe Met Ile Val Leu Met Ala Asn Val Gly Met Pro Leu Ser			
130	135	140	
Ile Gly Phe Val Gly Glu Phe Leu Asn Leu Leu Gly Phe Phe Ala Thr			
145	150	155	160
Tyr Pro Leu Leu Ala Ile Ile Ala Gly Thr Ser Leu Ile Leu Ser Ala			
165	170	175	
Val Tyr Ile Leu Thr Ser Tyr Lys Asp Val Phe Phe Gly Asn Leu Lys			
180	185	190	
Thr Gly Asn Asn Gln Ile Ser Val Phe Glu Asp Leu Asn Ala Arg Glu			
195	200	205	
Val Gly Val Leu Ser Val Ile Leu Ala Phe Asp Leu Asn Phe Arg Asp			
210	215	220	
Leu Tyr Lys Ser Ala Phe Lys Thr Asp			
225	230		

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...32

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504

Val	Glu	Leu	Ile	Ser	Asn	Asn	Pro	Asn	Ala	Ser	Gln	Gln	Ser	Ile	Val
1															
							5				10				15
Ile	Pro	Leu	Glu	Thr	Phe	Ala	Leu	Ala	Arg	Ala	Leu	Lys	Gly	Ile	Phe
							20				25				30

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

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(B) LOCATION 1...171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505

Met	Lys	Ile	Phe	Gly	Thr	Asp	Gly	Val	Arg	Gly	Lys	Ala	Gly	Val	Lys
1								5		10					15
Leu	Thr	Pro	Met	Phe	Val	Met	Arg	Leu	Gly	Ile	Ala	Ala	Gly	Leu	Tyr
								20		25					30
Phe	Lys	Lys	His	Ser	Gln	Thr	Asn	Lys	Ile	Leu	Ile	Gly	Lys	Asp	Thr
								35		40					45
Arg	Lys	Ser	Gly	Tyr	Met	Val	Glu	Asn	Ala	Leu	Val	Ser	Ala	Leu	Thr
								50		55					60
Ser	Ile	Gly	Tyr	Asn	Val	Ile	Gln	Ile	Gly	Pro	Met	Pro	Thr	Pro	Ala
								65		70					80
Ile	Ala	Phe	Leu	Thr	Glu	Asp	Met	Arg	Cys	Asp	Ala	Gly	Ile	Met	Ile
								85		90					95
Ser	Ala	Ser	His	Asn	Pro	Phe	Glu	Asp	Asn	Gly	Ile	Lys	Phe	Phe	Asn
								100		105					110
Ser	Tyr	Gly	Tyr	Lys	Leu	Lys	Glu	Glu	Glu	Glu	Arg	Ala	Ile	Glu	Glu
								115		120					125
Ile	Phe	His	Asp	Glu	Glu	Leu	Leu	His	Ser	Ser	Tyr	Lys	Val	Gly	Glu
								130		135					140
Ser	Val	Gly	Ser	Ala	Lys	Arg	Ile	Asp	Asp	Val	Ile	Gly	Pro	Leu	Tyr
								145		150					160
Arg	Ala	Phe	Glu	Ala	Leu	Tyr	Thr	Gln	Thr	Phe					
								165		170					

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506

Val	Arg	Ala	Val	Phe	Val	Phe	Gly	Leu	Lys	Ala	Ala	Phe	Cys	Ile	Gly	
1								5						10		15
Ile	Phe	Phe	Tyr	Gly	Ala	Tyr	Tyr	Phe	Leu	Asp	Glu	Phe	Leu	Ile	Lys	
								20						25		30
Leu																

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507

Met	Lys	Glu	Gln	Glu	Trp	Asp	Leu	Ser	Ala	Leu	Phe	Glu	Asn	Lys	Glu
1		5							10			15			
Ser	Ala	Glu	Glu	Phe	Leu	Lys	Thr	Leu	Gln	Thr	Glu	Val	Gln	Glu	Phe
		20				25				30					
Glu	Asn	Ala	Tyr	Gln	Asn	Asn	Leu	Lys	Asn	Leu	Asp	Ala	Ala	Lys	Phe
	35				40			45							
Ala	Asn	Thr	Leu	Lys	His	Tyr	Glu	Asn	Leu	Ser	Glu	Lys	Ile	Ser	Arg
	50				55			60							
Ala	Met	Ala	Tyr	Ala	Asn	Tyr	Phe	Leu	Pro	Arg	Thr	Leu	Lys	Lys	Arg
	65				70			75		80					
Ser	Phe	Ile	Arg	Asn	Ala	Asn	Gly	Leu	Cys	Lys	Tyr	Pro	Thr	Thr	Pro
					85			90		95					
Phe	Ile	Leu													

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507

Met	Lys	Glu	Gln	Glu	Trp	Asp	Leu	Ser	Ala	Leu	Phe	Glu	Asn	Lys	Glu
1		5			10				15						
Ser	Ala	Glu	Glu	Phe	Leu	Lys	Thr	Leu	Gln	Thr	Glu	Val	Gln	Glu	Phe
		20				25			30						
Glu	Asn	Ala	Tyr	Gln	Asn	Asn	Leu	Lys	Asn	Leu	Asp	Ala	Ala	Lys	Phe
	35				40			45							
Ala	Asn	Thr	Leu	Lys	His	Tyr	Glu	Asn	Leu	Ser	Glu	Lys	Ile	Ser	Arg
	50				55			60							
Ala	Met	Ala	Tyr	Ala	Asn	Tyr	Phe	Leu	Pro	Arg	Thr	Leu	Lys	Lys	Arg
	65				70			75		80					
Ser	Phe	Ile	Arg	Asn	Ala	Asn	Gly	Leu	Cys	Lys	Tyr	Pro	Thr	Thr	Pro
					85			90		95					
Phe	Ile	Leu													

(2) INFORMATION FOR SEQ ID NO:508:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - iii) HYPOTHETICAL: YES
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...78
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50

Leu	Arg	Val	Gly	Met	Tyr	Glu	Val	Cys	Asn	His	Lys	Asp	Gly	Thr	Ala
1				5				10					15		
Tyr	His	Ser	Thr	Arg	Gly	Ser	Lys	Val	Thr	Leu	Ala	Cys	Lys	Thr	Gly
				20				25					30		
Thr	Ala	Gln	Val	Val	Glu	Ile	Ala	Gln	Asn	Ile	Val	Asn	Arg	Met	Lys
				35				40					45		
Glu	Lys	Asp	Met	Glu	Tyr	Phe	His	Unk	Ser	His	Unk	Trp	Ile	Thr	Unk
				50				55				60			
Tyr	Leu	Unk	Pro	Met	Lys	Asn	Pro	Asn	Thr	Leu	Ser	Leu	Phe		
65					70						75				

(2) INFORMATION FOR SEQ ID NO:508:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - iii) HYPOTHETICAL: YES
 - vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
 - ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...78
 - x) SEQUENCE DESCRIPTION: SEQ ID NO:50

```

Leu Arg Val Gly Met Tyr Glu Val Cys Asn His Lys Asp Gly Thr Ala
1           5           10          15
Tyr His Ser Thr Arg Gly Ser Lys Val Thr Leu Ala Cys Lys Thr Gly
20          25          30
Thr Ala Gln Val Val Glu Ile Ala Gln Asn Ile Val Asn Arg Met Lys
35          40          45
Glu Lys Asp Met Glu Tyr Phe His Unk Ser His Unk Trp Ile Thr Unk
50          55          60
Tyr Leu Unk Pro Met Lys Asn Pro Asn Thr Leu Ser Leu Phe
65          70          75

```

(2) INFORMATION FOR SEQ ID NO:509:

- (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 70 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509

Val	Arg	Ser	Gly	Lys	Arg	Leu	Gly	Tyr	Thr	Asn	Gln	Val	Ile	Thr	Asp
1				5				10					15		
Ile	Val	Asn	Ile	Gly	Ile	Gly	Gly	Ser	Asp	Leu	Gly	Ala	Leu	Met	Val
				20				25				30			
Cys	Thr	Ala	Leu	Lys	Arg	Tyr	Gly	His	Pro	Arg	Leu	Lys	Met	His	Phe
				35			40			45					
Val	Ser	Asn	Val	Glu	Trp	His	Ala	Asp	Phe	Arg	Arg	Phe	Gly	Lys	Asn
				50			55			60					
Gln	Pro	Gly	Gln	Arg	Ala										
				65			70								

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510

Met	Asn	Leu	Val	Phe	Leu	Trp	Ala	Ala	Leu	Gly	Gly	Ala	Ile	Gly	Ser
1				5					10			15			
Ser	Leu	Arg	Tyr	Phe	Val	Gly	Lys	Met	Met	Pro	Ser	Lys	Phe	Leu	Met
				20				25			30				
Phe	Glu	Ser	Phe	Pro	Leu	Gly	Thr	Phe	Ser	Val	Asn	Leu	Ile	Gly	Cys
				35			40			45					
Phe	Ile	Ile	Gly	Phe	Met	Gly	His	Leu	Ala	Ala	Lys	Lys	Val	Phe	Gly
				50			55			60					
Asp	Asp	Phe	Gly	Ile	Phe	Phe	Val	Thr	Gly	Val	Leu	Gly	Gly	Phe	Thr
65					70			75			80				
Thr	Phe	Ser	Ser	Tyr	Gly	Leu	Asp	Thr	Leu	Lys	Leu	Gln	Lys	Ser	
								85		90		95			
Gln	Tyr	Leu	Glu	Ala	Ile	Ser	Tyr	Val	Leu	Gly	Thr	Asn	Leu	Gly	
					100			105			110				
Leu	Ile	Gly	Val	Ala	Ile	Gly	Trp	Phe	Leu	Ala	Lys	Asn	Phe	Val	Gly
					115			120			125				

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Val Asn
130

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511

Leu	Gly	Leu	Val	Unk	Gly	Ile	Ser	Leu	Leu	His	Leu	Ser	Leu	Glu	Gln
1				5				10						15	
Lys	Ile	Ser	Val	Phe	Leu	Gly	Unk	Asn	Leu	Met	Leu	Tyr	Pro	Val	Unk
				20				25				30			
Glu	Val	Leu	Phe	Ser	Ile	Leu	Arg	Arg	Lys	Ile	Lys	Arg	Gln	Lys	Ala
				35				40				45			
Thr	His	Ala	Gly												
				50											

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511

Leu	Gly	Leu	Val	Unk	Gly	Ile	Ser	Leu	Leu	His	Leu	Ser	Leu	Glu	Gln
1				5				10						15	
Lys	Ile	Ser	Val	Phe	Leu	Gly	Unk	Asn	Leu	Met	Leu	Tyr	Pro	Val	Unk
				20				25				30			
Glu	Val	Leu	Phe	Ser	Ile	Leu	Arg	Arg	Lys	Ile	Lys	Arg	Gln	Lys	Ala
				35				40				45			
Thr	His	Ala	Gly												
				50											

(2) INFORMATION FOR SEQ ID NO:512:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 79 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512

```

Met Leu Glu Lys Leu Ile Glu Arg Val Leu Phe Ala Thr Arg Trp Leu
1           5           10          15
Leu Ala Pro Leu Cys Ile Ala Met Ser Leu Val Leu Val Val Leu Gly
20          25          30
Tyr Val Phe Met Lys Glu Leu Trp His Met Leu Ser His Leu Asn Thr
35          40          45
Ile Ser Glu Thr Asp Leu Val Leu Ser Ala Leu Gly Leu Val Asp Leu
50          55          60
Leu Val His Gly Arg Ala Cys Phe Asp Gly Ala Ala Arg Gln Leu
65          70          75

```

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513

```

Met His Tyr Gln Leu Thr Ser Phe Asn Ile Ile Gln Asp Leu Phe Ile
1           5           10          15
Thr Cys His Val Leu Arg Ile Lys Met Arg Val Phe Val Cys Phe Leu
20          25          30
Gly Val Phe Val Ser Asn Gly Leu Ala Arg Phe Gly Tyr Val Val Leu
35          40          45
Ile Pro Leu Leu Ile Leu Ser Gly Ser Leu Thr Pro His Gln Ser Phe
50          55          60
Gln Leu Gly Ile Ala Val Leu Met Gly Tyr Val Phe Gly Ser Phe Leu
65          70          75          80
Ile Gln Phe Leu Ser Pro Leu Met Ser Leu Lys Ser Ile Ala Lys Ile
85          90          95
Ser Phe Lys Leu Thr Leu
100

```

(2) INFORMATION FOR SEQ ID NO:514:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...15
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:514

Val	Asp	Met	Lys	Asp	Ala	Val	Gly	Thr	Tyr	Lys	Leu	Unk	Arg	Ala
1					5					10			15	

(2) INFORMATION FOR SEQ ID NO:515:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...377
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:515

Leu	Ala	Gln	Pro	Val	Gln	Val	Arg	Thr	Val	Phe	Met	Ser	Met	Thr	Leu
1						5				10			15		
Asn	Ala	Met	Gly	Gln	Phe	Ala	Tyr	Asn	Phe	Pro	Ala	Asn	Ile	Ser	Lys
						20			25			30			
Asp	Lys	Gln	Leu	Thr	Met	Val	Tyr	Met	Asp	Lys	Asp	Tyr	Gly	Ala	
						35			40			45			
Tyr	Gly	Asn	Ile	Val	Ala	Met	Gly	Gly	Glu	Tyr	Val	Lys	Ile	Glu	Leu
						50			55			60			
Gly	Thr	Asp	Thr	Gly	Leu	Asn	Pro	Phe	Ala	Trp	Ala	Ala	Cys	Val	Gln
						65			70			75			80
Lys	Thr	Asn	Ala	Thr	Met	Glu	Gln	Lys	Gln	Thr	Ala	Ile	Ser	Val	Val
						85			90			95			
Lys	Glu	Leu	Val	Lys	Asn	Leu	Ala	Thr	Lys	Ser	Asp	Glu	Lys	Asp	Glu
						100			105			110			
Asn	Gly	Asn	Ser	Ile	Ser	Phe	Ser	Leu	Ala	Asp	Ser	Asn	Thr	Leu	Ala
						115			120			125			
Ala	Ala	Val	Thr	Asn	Leu	Ile	Thr	Gly	Asp	Met	Asn	Leu	Asp	Tyr	Pro
						130			135			140			
Ile	Thr	Gln	Leu	Ile	Asn	Ala	Phe	Gly	Lys	Asp	His	Asn	Asp	Pro	Asn

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145	150	155	160
Gly Leu Val Ala Arg Leu Ala Pro Phe Cys Lys Ser Thr Asn Gly Glu			
165	170	175	
Phe Gln Trp Leu Phe Asp Asn Lys Ala Thr Asp Arg Leu Asp Phe Ser			
180	185	190	
Lys Thr Ile Ile Gly Val Asp Gly Ser Ser Phe Leu Asp Asn Asn Asp			
195	200	205	
Val Ser Pro Phe Ile Cys Phe Tyr Leu Phe Ala Arg Ile Gln Glu Ala			
210	215	220	
Met Asp Gly Arg Arg Phe Val Leu Asp Ile Asp Glu Ala Trp Lys Tyr			
225	230	235	240
Leu Gly Asp Pro Lys Val Ala Tyr Phe Val Arg Asp Met Leu Lys Thr			
245	250	255	
Ala Arg Lys Arg Asn Ala Ile Val Arg Leu Ala Thr Gln Ser Ile Thr			
260	265	270	
Asp Leu Leu Ala Cys Pro Ile Ala Asp Thr Ile Arg Glu Gln Cys Pro			
275	280	285	
Thr Lys Ile Phe Leu Arg Asn Asp Gly Gly Asn Leu Ser Asp Tyr Gln			
290	295	300	
Arg Leu Ala Asn Val Thr Glu Lys Glu Phe Glu Ile Ile Thr Lys Gly			
305	310	315	320
Leu Asp Arg Lys Ile Leu Tyr Lys Gln Asp Gly Ser Pro Ser Val Ile			
325	330	335	
Ala Ser Phe Asn Leu Arg Gly Ile Pro Lys Glu Tyr Leu Lys Ile Leu			
340	345	350	
Ser Thr Asp Thr Val Phe Val Lys Glu Ile Asp Lys Ile Ile Gln Asn			
355	360	365	
His Ser Ile Ile Asp Lys Tyr Gln Pro			
370	375		

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515

Leu Ala Gln Pro Val Gln Val Arg Thr Val Phe Met Ser Met Thr Leu			
1	5	10	15
Asn Ala Met Gly Gln Phe Ala Tyr Asn Phe Pro Ala Asn Ile Ser Lys			
20	25	30	
Asp Lys Gln Lys Leu Thr Met Val Tyr Met Asp Lys Asp Tyr Gly Ala			
35	40	45	
Tyr Gly Asn Ile Val Ala Met Gly Gly Glu Tyr Val Lys Ile Glu Leu			
50	55	60	
Gly Thr Asp Thr Gly Leu Asn Pro Phe Ala Trp Ala Ala Cys Val Gln			
65	70	75	80
Lys Thr Asn Ala Thr Met Glu Gln Lys Gln Thr Ala Ile Ser Val Val			
85	90	95	
Lys Glu Leu Val Lys Asn Leu Ala Thr Lys Ser Asp Glu Lys Asp Glu			
100	105	110	

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Asn Gly Asn Ser Ile Ser Phe Ser Leu Ala Asp Ser Asn Thr Leu Ala
 115 120 125
 Ala Ala Val Thr Asn Leu Ile Thr Gly Asp Met Asn Leu Asp Tyr Pro
 130 135 140
 Ile Thr Gln Leu Ile Asn Ala Phe Gly Lys Asp His Asn Asp Pro Asn
 145 150 155 160
 Gly Leu Val Ala Arg Leu Ala Pro Phe Cys Lys Ser Thr Asn Gly Glu
 165 170 175
 Phe Gln Trp Leu Phe Asp Asn Lys Ala Thr Asp Arg Leu Asp Phe Ser
 180 185 190
 Lys Thr Ile Ile Gly Val Asp Gly Ser Ser Phe Leu Asp Asn Asn Asp
 195 200 205
 Val Ser Pro Phe Ile Cys Phe Tyr Leu Phe Ala Arg Ile Gln Glu Ala
 210 215 220
 Met Asp Gly Arg Arg Phe Val Leu Asp Ile Asp Glu Ala Trp Lys Tyr
 225 230 235 240
 Leu Gly Asp Pro Lys Val Ala Tyr Phe Val Arg Asp Met Leu Lys Thr
 245 250 255
 Ala Arg Lys Arg Asn Ala Ile Val Arg Leu Ala Thr Gln Ser Ile Thr
 260 265 270
 Asp Leu Leu Ala Cys Pro Ile Ala Asp Thr Ile Arg Glu Gln Cys Pro
 275 280 285
 Thr Lys Ile Phe Leu Arg Asn Asp Gly Gly Asn Leu Ser Asp Tyr Gln
 290 295 300
 Arg Leu Ala Asn Val Thr Glu Lys Glu Phe Glu Ile Ile Thr Lys Gly
 305 310 315 320
 Leu Asp Arg Lys Ile Leu Tyr Lys Gln Asp Gly Ser Pro Ser Val Ile
 325 330 335
 Ala Ser Phe Asn Leu Arg Gly Ile Pro Lys Glu Tyr Leu Lys Ile Leu
 340 345 350
 Ser Thr Asp Thr Val Phe Val Lys Glu Ile Asp Lys Ile Ile Gln Asn
 355 360 365
 His Ser Ile Ile Asp Lys Tyr Gln Pro
 370 375

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1027 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516

Val Cys Leu Asp His Gln Val Gly Ala Gly Lys Thr Leu Cys Ala Ile
 1 5 10 15
 Ala Ser Cys Met Glu Gln Lys Arg Met Gly Leu Val Asn Lys Thr Leu
 20 25 30
 Ile Ala Val Pro Asn His Leu Thr Lys Gln Trp Gly Asp Glu Phe Tyr
 35 40 45
 Lys Ala Tyr Pro Asn Ala Asn Val Leu Val Val Asp Ser Lys Asp Thr
 50 55 60
 Thr Glu Lys Glu Arg Glu Leu Leu Phe Asn Gln Ile Ala Asn Asn

65	70	75	80
Tyr Asp Ala Val Val Ile Ala His Thr His Leu Glu Leu Leu Ser Asn			
85	90	95	
Pro Arg Gly Ile Ile Glu Glu Leu Lys Glu Glu Glu Leu Val Asn Ala			
100	105	110	
Glu Lys Asn Phe Glu Arg Gln Glu Leu Ala Tyr Lys Asn Asn Pro Arg			
115	120	125	
Glu Thr Lys Lys Pro Asn Glu Arg Ala Phe Lys Asn Lys Leu Asp Lys			
130	135	140	
Ile Arg Ala Lys Tyr Asp Ala Ile Leu Glu Lys Gln Gly Ser His Ile			
145	150	155	160
Asp Ile Ser Gln Met Gly Ile Asp Asn Leu Ile Val Asp Glu Ala His			
165	170	175	
Leu Phe Lys Asn Leu Ala Phe Glu Thr Ser Met Glu Lys Ile Ala Gly			
180	185	190	
Leu Gly Asn Gln Gln Gly Ser Asn Arg Ala Arg Asp Leu Phe Ile Lys			
195	200	205	
Thr Arg Tyr Leu His Gln Asn Asp Lys Lys Ile Met Phe Leu Thr Gly			
210	215	220	
Thr Pro Ile Ala Asn Ser Leu Ser Glu Met Tyr His Leu Gln Arg Tyr			
225	230	235	240
Leu Thr Pro Asp Val Leu Lys Glu Arg Gly Leu Glu Phe Phe Asp Asp			
245	250	255	
Trp Ala Lys Thr Tyr Gly Glu Val Val Asn Asp Phe Glu Leu Asp Thr			
260	265	270	
Ser Ala Gln Ser Tyr Lys Met Val Asn Arg Phe Ser Lys Phe Ser Asp			
275	280	285	
Val Gln Gly Leu Ser Thr Met Tyr Arg Ala Phe Ala Asp Ile Val Ser			
290	295	300	
Asn Asp Asp Ile Leu Lys His Asn Pro His Phe Val Pro Lys Val Tyr			
305	310	315	320
Gly Asp Lys Pro Ile Asn Val Val Lys Arg Ser Glu Glu Val Ala			
325	330	335	
Gln Phe Ile Gly Val Ala Leu Glu Asn Gly Lys Tyr Asn Glu Gly Ser			
340	345	350	
Ile Ile Asp Arg Met Gln Lys Cys Glu Gly Lys Lys Ser Gln Lys Gly			
355	360	365	
Gln Asp Asn Ile Leu Ser Cys Thr Thr Asp Ala Arg Lys Val Ala Leu			
370	375	380	
Asp Tyr Arg Leu Ile Asp Pro Asn Ala Lys Val Glu Lys Glu Phe Ser			
385	390	395	400
Lys Ser Tyr Ala Met Ala Lys Asn Ile Tyr Glu Asn Tyr Leu Glu Thr			
405	410	415	
His Ala Thr Lys Gly Thr Gln Leu Gly Phe Ile Gly Leu Ser Thr Pro			
420	425	430	
Lys Thr His Ser Gln Lys Val Ser Leu Glu Ala Leu Asp Asn Ala His			
435	440	445	
Glu Thr Glu Asn Lys Asn Pro Leu Asp Lys Ala Gln Glu Leu Leu Glu			
450	455	460	
Ser Leu Ser Ser Tyr Asp Glu Lys Gly Asn Leu Ile Ala Pro Ser Lys			
465	470	475	480
Lys Glu Leu Glu Asn Glu Leu Lys Glu Lys Glu Ala Lys Ser Val Asn			
485	490	495	
Leu Asp Glu Glu Ile Ala Lys Gly Cys Ser Phe Asp Val Tyr Ser Asp			
500	505	510	
Val Leu Arg His Leu Val Gln Met Gly Ile Pro Gln Asn Glu Ile Ala			
515	520	525	
Phe Ile His Asp Ala Lys Thr Glu Glu Gln Lys Gln Asp Leu Phe Lys			
530	535	540	
Lys Leu Asn Arg Gly Gly Val Arg Val Leu Leu Gly Ser Pro Ala Lys			
545	550	555	560
Met Gly Val Gly Thr Asn Val Gln Glu Arg Leu Val Ala Met His Glu			
565	570	575	
Leu Asp Cys Pro Trp Arg Pro Asp Glu Leu Leu Gln Met Glu Gly Arg			
580	585	590	

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Gly Ile Arg Gln Gly Asn Ile Leu His Gln Asn Asp Pro Glu Asn Phe
 595 600 605
 Arg Met Lys Ile Tyr Arg Tyr Ala Thr Glu Lys Thr Tyr Asp Ser Arg
 610 615 620
 Met Trp Gln Ile Ile Glu Thr Lys Ser Lys Gly Ile Glu Gln Phe Arg
 625 630 635 640
 Asn Ala His Lys Leu Gly Leu Asn Glu Leu Glu Asp Phe Asn Met Gly
 645 650 655
 Ser Ser Asn Ala Ser Glu Met Lys Ala Glu Ala Thr Gly Asn Pro Leu
 660 665 670
 Ile Ile Glu Glu Val Lys Leu Arg Ala Glu Ile Lys Ser Glu Glu Ser
 675 680 685
 Lys Tyr Lys Ala Phe Asn Lys Glu His Tyr Phe Asn Glu Glu Ser Leu
 690 695 700
 Lys Asn Asn Ala Ser Lys Leu Asp Tyr Leu Lys Gln Glu Leu Lys Asp
 705 710 715 720
 Leu Glu Thr Leu Gln Arg Ser Val Ile Ile Pro Thr His Thr Glu Ile
 725 730 735
 Lys Leu Tyr Asp Leu Lys Asn Glu Glu Ser Lys Asp Tyr Glu Leu Ile
 740 745 750
 Lys Val Lys Glu Val Glu Pro Leu Lys Glu Asn Ala Ser Met Ser Glu
 755 760 765
 Glu Leu Thr His Lys Lys Leu Lys Glu Gln Asn Lys Gln Ile Ala Glu
 770 775 780
 Gln Asn Lys Glu Lys Leu Asp Ala Ile Lys Lys Gln Phe Ala Ser Asn
 785 790 795 800
 Leu Asn Thr Leu Phe Val Asn Glu Glu Asp Tyr Lys Leu Leu Glu
 805 810 815
 Tyr Lys Gly Phe Val Val Asn Ala Tyr Lys Thr Lys Tyr Gln Val Glu
 820 825 830
 Phe Ser Leu Ser Pro Lys Asp Asn Pro Asn Ile Ala Tyr Ser Pro Ser
 835 840 845
 Asn Met Val Tyr Lys Asn Asp Thr Ile Asn Met Phe Ser Ser Tyr Asn
 850 855 860
 Phe Cys Ala Glu Ile Lys Phe Asp Gly Phe Leu Lys Arg Leu Asp Asn
 865 870 875 880
 Ala Ile Thr Lys Leu Pro Glu Lys Ile Lys Glu Leu Glu Asn Ser Ile
 885 890 895
 Glu Ile Thr Lys Lys Asn Ile Ala Lys Tyr Thr Arg Leu Val Glu Gln
 900 905 910
 Lys Pro Ser Tyr Pro Arg Leu Glu Tyr Leu Gln Ala Leu Lys Trp Asp
 915 920 925
 His Lys Thr Leu Ile Asp Asp Leu Ala Lys Met Ser Lys Asp Arg Asn
 930 935 940
 Tyr Lys Pro Ala Phe Asn Pro Lys Ser Lys Glu Val Leu Lys Asn Leu
 945 950 955 960
 Asn Ala Glu Lys Arg Ala Ser Leu Glu Asn Glu Arg Glu Glu Gln Gly
 965 970 975
 Val Lys Gly Asn Thr Lys Ser His Asp Glu Ile Glu Pro Ala Thr Glu
 980 985 990
 Gln Val Ile Glu Lys Glu Ile Glu Lys Gly Asp Glu Ile Ala Asn Asn
 995 1000 1005
 Val Asp Tyr Tyr Glu Asn Glu Gln Glu Val Glu Ile Thr Lys Ser Met
 1010 1015 1020
 Gly Arg Arg
 1025

(2) INFORMATION FOR SEQ ID NO:517:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 154 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517

Met	Lys	Leu	Val	Ser	Leu	Ile	Val	Ala	Leu	Val	Phe	Cys	Cys	Phe	Leu
1								5		10				15	
Gly	Ala	Val	Glu	Leu	Pro	Gly	Val	Tyr	Gln	Thr	Gln	Glu	Phe	Leu	Tyr
								20		25			30		
Met	Lys	Ser	Ser	Phe	Val	Glu	Phe	Phe	Glu	His	Asn	Gly	Lys	Phe	Tyr
								35		40			45		
Ala	Tyr	Gly	Ile	Ser	Asp	Val	Unk	Unk	Ser	Lys	Ala	Lys	Lys	Asp	Lys
							50		55		60				
Leu	Asn	Pro	Asn	Pro	Lys	Leu	Arg	Asn	Arg	Ser	Asp	Lys	Gly	Val	Val
							65		70		75		80		
Phe	Leu	Ser	Asp	Leu	Ile	Lys	Val	Gly	Glu	Gln	Ser	Tyr	Lys	Gly	Gly
							85		90			95			
Lys	Ala	Unk	Asn	Phe	Unk	Asp	Gly	Lys	Thr	Unk	His	Val	Arg	Val	Thr
							100		105			110			
Gln	Unk	Ser	Asn	Gly	Asp	Leu	Unk	Phe	Thr	Ser	Ser	Tyr	Unk	Lys	Trp
							115		120			125			
Gly	Tyr	Val	Gly	Lys	Thr	Phe	Thr	Trp	Lys	Arg	Leu	Ser	Asp	Glu	Glu
							130		135			140			
Ile	Lys	Asn	Leu	Lys	Leu	Lys	Arg	Phe	Asn						
							145		150						

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517

Met	Lys	Leu	Val	Ser	Leu	Ile	Val	Ala	Leu	Val	Phe	Cys	Cys	Phe	Leu
1								5		10			15		
Gly	Ala	Val	Glu	Leu	Pro	Gly	Val	Tyr	Gln	Thr	Gln	Glu	Phe	Leu	Tyr
								20		25			30		
Met	Lys	Ser	Ser	Phe	Val	Glu	Phe	Phe	Glu	His	Asn	Gly	Lys	Phe	Tyr
								35		40			45		
Ala	Tyr	Gly	Ile	Ser	Asp	Val	Unk	Unk	Ser	Lys	Ala	Lys	Lys	Asp	Lys
							50		55		60				
Leu	Asn	Pro	Asn	Pro	Lys	Leu	Arg	Asn	Arg	Ser	Asp	Lys	Gly	Val	Val
							65		70		75		80		

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Phe Leu Ser Asp Leu Ile Lys Val Gly Glu Gln Ser Tyr Lys Gly Gly
 85 90 95
 Lys Ala Unk Asn Phe Unk Asp Gly Lys Thr Unk His Val Arg Val Thr
 100 105 110
 Gln Unk Ser Asn Gly Asp Leu Unk Phe Thr Ser Ser Tyr Unk Lys Trp
 115 120 125
 Gly Tyr Val Gly Lys Thr Phe Thr Trp Lys Arg Leu Ser Asp Glu Glu
 130 135 140
 Ile Lys Asn Leu Lys Leu Lys Arg Phe Asn
 145 150

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518

Met Ala Glu Glu Glu Lys Thr Glu Leu Pro Ser Ala Lys Lys Ile Gln
 1 5 10 15
 Lys Ala Arg Glu Glu Gly Asn Val Pro Lys Ser Met Glu Val Val Gly
 20 25 30
 Val Phe Arg Val Ile Gly Trp Ala Asn Glu Tyr Phe Cys Phe Phe Tyr
 35 40 45
 Met Val Gly Gly Met Ala Leu Ala Arg Cys Ile Ala Met Cys
 50 55 60

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 237 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519

Met Lys Thr Leu Val Lys Asn Thr Ile Tyr Ser Phe Leu Leu Ser
 1 5 10 15
 Val Leu Met Ala Glu Asp Ile Thr Ser Gly Leu Lys Gln Leu Asp Asn

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20	25	30
Thr Tyr Gln Glu Thr Asn Gln Gln Val Leu Lys Asn Leu Asp Glu Ile		
35	40	45
Phe Ser Thr Thr Ser Pro Ser Ala Asn Asn Lys Ile Gly Gln Glu Asp		
50	55	60
Ala Leu Asn Ile Lys Lys Ala Ala Ile Ala Leu Arg Gly Asp Leu Ala		
65	70	75
Leu Leu Lys Ala Asn Phe Glu Ala Asn Glu Leu Phe Phe Ile Ser Glu		80
85	90	95
Asp Val Ile Phe Lys Thr Tyr Met Ser Ser Pro Glu Leu Leu Leu Thr		
100	105	110
Tyr Met Lys Ile Asn Pro Leu Asp Gln Lys Thr Ala Glu Gln Gln Cys		
115	120	125
Gly Ile Ser Asp Lys Val Leu Val Leu Tyr Cys Glu Gly Lys Leu Lys		
130	135	140
Ile Glu Gln Glu Lys Gln Asn Ile Arg Glu Arg Leu Glu Thr Ser Leu		
145	150	155
Lys Ala Tyr Gln Ser Asn Ile Gly Gly Thr Ala Ser Leu Ile Thr Ala		160
165	170	175
Ser Gln Thr Leu Val Glu Ser Leu Lys Asn Lys Asn Phe Ile Lys Gly		
180	185	190
Ile Lys Lys Leu Met Leu Ala His Asn Lys Val Phe Leu Asn Tyr Leu		
195	200	205
Glu Glu Leu Asp Ala Leu Glu Arg Ser Leu Glu Gln Ser Lys Arg Gln		
210	215	220
Tyr Leu Gln Glu Arg Gln Ser Ser Lys Ile Ile Val Lys		
225	230	235

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520

1	5	10	15
Asp Tyr Val Val Val Phe Gly Glu Asp Thr Pro Ile Lys Leu Ile Gln			
20	25	30	
Ala Leu Lys Pro Asp Ile Leu Val Lys Gly Ala Asp Tyr Leu Asn Lys			
35	40	45	
Glu Val Ile Gly Ser Glu Leu Ala Lys Glu Thr Arg Leu Ile Glu Phe			
50	55	60	
Glu Glu Gly Tyr Ser Thr Ser Ala Ile Ile Glu Lys Ile Lys Arg Thr			
65	70	75	80
His Asn Asp			

(2) INFORMATION FOR SEQ ID NO:521:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...7
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521

Leu Glu Thr Leu Phe Leu Val
1 5

(2) INFORMATION FOR SEQ ID NO:521:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...7
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521

Leu Glu Thr Leu Phe Leu Val
1 5

(2) INFORMATION FOR SEQ ID NO:522:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...64
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:522

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Val	Tyr	Asp	Lys	Ser	Leu	Cys	Lys	Thr	Met	Ala	Leu	Ala	Leu	Lys	Ala
1									5					10	15
Leu	Gly	Val	Lys	Arg	Ala	Met	Val	Val	Asn	Gly	Gly	Gly	Thr	Gly	Glu
										20	25			30	
Ile	Val	Leu	His	Asp	Ile	Thr	His	Ala	Cys	Glu	Leu	Lys	Asn	Asn	Glu
									35	40			45		
Ile	Leu	Glu	Tyr	Asp	Leu	Ser	Ala	Lys	Asp	Phe	Asp	Leu	Pro	Pro	Ser
									50	55			60		

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523

Met	Leu	Val	Glu	Ile	Glu	Asn	Leu	Thr	Lys	Thr	Tyr	Gly	Ser	Leu	Lys
1									5	10				15	
Ala	Leu	Asp	Asn	Ile	Ser	Leu	Lys	Leu	Pro	Lys	Gln	Gln	Phe	Ile	Gly
									20	25			30		
Leu	Leu	Gly	Pro	Asn	Gly	Ala	Gly	Lys	Thr	Thr	Leu	Leu	Lys	Ile	Leu
									35	40			45		
Ala	Gly	Leu	Asn	Leu	Asn	Tyr	Gln	Gly	Glu	Val	Lys	Ile	Leu	Asn	Gln
						50	55		60						
Lys	Ile	Gly	Ile	Glu	Thr	Lys	Lys	Ser	Val	Ala	Phe	Leu	Ser	Asp	Gly
						65	70		75				80		
Asp	Phe	Leu	Asp	Pro	Lys	Leu	Thr	Pro	Leu	Lys	Ala	Ile	Ala	Phe	Tyr
						85	90		95						
Lys	Asp	Phe	Phe	Ser	Asp	Phe	Asp	Glu	Ser	Lys	Ala	Leu	Asn	Leu	Leu
						100	105		110						
Lys	Arg	Phe	Ser	Val	Pro	Leu	Lys	Arg	Glu	Phe	Lys	Ala	Leu	Ser	Lys
						115	120		125						
Gly	Met	Arg	Glu	Lys	Leu	Gln	Leu	Ile	Leu	Thr	Leu	Ser	Arg	Asn	Ala
						130	135		140						
Ser	Leu	Tyr	Leu	Phe	Asp	Glu	Pro	Val	Ala	Gly	Ile	Asp	Pro	Ile	Ala
						145	150		155				160		
Arg	Glu	Glu	Ile	Phe	Glu	Leu	Ile	Ala	Lys	Glu	Phe	Ser	Gln	Asn	Ala
						165	170		175						
Ser	Leu	Leu	Val	Ser	Thr	His	Leu	Val	Val	Asp	Val	Glu	Lys	Tyr	Leu
						180	185		190						
Asp	Ser	Ala	Ile	Phe	Leu	Lys	Glu	Ala	Lys	Val	Val	Ala	Phe	Gly	Asp
						195	200		205						
Val	Gly	Glu	Leu	Lys	Lys	Gly	Tyr	Ser	Ser	Leu	Glu	Ala	Ala	Tyr	Lys
						210	215		220						
Glu	Arg	Leu	Lys												
						225									

(2) INFORMATION FOR SEQ ID NO:524:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 273 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524

Met	Asn	Lys	Leu	Phe	Leu	Ala	Phe	Ile	Val	Gly	Gly	Met	Leu	Leu	Ser
1				5					10			15			
Ala	Asp	Ala	Leu	Asn	Asp	Lys	Ile	Glu	Asn	Leu	Met	Gly	Glu	Arg	Ser
						20		25			30				
Tyr	His	Met	Asn	Lys	Leu	Phe	Leu	Glu	Arg	Leu	Phe	Lys	Asn	Arg	Lys
						35		40			45				
Asp	Phe	Tyr	Glu	Met	Gly	Arg	Leu	Asp	Ser	Leu	Lys	Leu	Leu	Asn	Thr
						50		55			60				
Leu	Lys	Glu	Asn	Gly	Leu	Leu	Ser	Phe	Asn	Phe	Asp	Lys	Pro	Ser	Val
						65		70			75		80		
Leu	Lys	Ile	Thr	Phe	Lys	Ala	Ser	Ser	Asn	Pro	Leu	Ala	Phe	Ala	Lys
						85			90			95			
Ser	Ile	Asn	Asn	Ser	Leu	Asn	Met	Met	Gly	Tyr	Ser	Tyr	Val	Leu	Pro
						100		105			110				
Ile	Arg	Met	Gln	Ser	Ser	Ser	Gly	Glu	Asn	Val	Phe	Ser	Tyr	Glu	Leu
						115		120			125				
Lys	Thr	Glu	Tyr	Val	Leu	Asp	Pro	Asn	Ile	Leu	Ile	Glu	Thr	Met	Lys
						130		135			140				
Arg	His	Gly	Phe	Asp	Phe	Met	Asp	Ile	Arg	Arg	Val	Ser	Leu	Lys	Glu
						145		150			155		160		
Trp	Glu	Tyr	Asp	Phe	Ala	Leu	Gln	Lys	Ile	Lys	Leu	Pro	Asn	Ala	Arg
						165			170			175			
Ala	Leu	Val	Leu	Ser	Ser	Asp	Pro	Val	Glu	Phe	Lys	Glu	Ala	Ser	Gly
						180			185			190			
Lys	Tyr	Trp	Leu	Ser	Val	Asn	Gln	Asn	Ala	Tyr	Leu	Lys	Ile	Ser	Ser
						195			200			205			
Asn	Asn	Pro	Leu	Trp	Gln	Pro	Lys	Ile	Ile	Phe	Tyr	Asp	Glu	Asn	Leu
						210		215			220				
Lys	Ile	Ile	Gln	Ile	Ile	Ala	Lys	Glu	Asn	Arg	Gln	Gln	Glu	Ile	Ala
						225		230			235		240		
Leu	Asn	Leu	Leu	Asp	Gly	Val	Arg	Phe	Ile	His	Ile	Thr	Asp	Ala	Lys
						245			250			255			
Asn	Pro	Ile	Ile	Leu	Lys	Asn	Gly	Ile	Ser	Val	Val	Phe	Asp	Ala	Met
						260			265			270			
Pro															

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525

Val	Ser	Arg	Pro	Phe	Lys	Thr	Ile	Lys	Lys	Pro	Pro	Gln	Pro	Pro
1				5				10				15		

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526

Met	Unk	Thr	His	Asp	Arg	Arg	Lys	Leu	Arg	Ile	Unk	Leu	Thr	Gln	Thr
1				5				10				15			
Thr	Thr	Leu	Val	Ala	Thr	Ile	Gly	Ser	Asn	Ala	Pro	Tyr	Ile	Gly	Leu
				20			25				30				
Leu	Gly	Thr	Val	Met	Gly	Ile	Met	Leu	Thr	Phe	Met	Asp	Leu	Gly	Ser
	35				40			45							
Ala	Ser	Gly	Ile	Asp	Thr	Lys	Ala	Ile	Met	Thr	Asn	Leu	Ala	Leu	Ala
	50				55			60							
Leu	Lys	Ala	Thr	Gly	Met	Gly	Leu	Leu	Val	Ala	Ile	Pro	Ala	Ile	Val
	65			70			75			80					
Ile	Tyr	Asn	Leu	Leu	Val	Arg	Lys	Ser	Glu	Ile	Leu	Val	Thr	Lys	Trp
					85			90			95				
Asp	Ile	Phe	His	His	Pro	Val	Asp	Thr	Gln	Ser	His	Glu	Val	Tyr	Ser
					100			105			110				
Lys	Ala														

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526

Met	Unk	Thr	His	Asp	Arg	Arg	Lys	Leu	Arg	Ile	Unk	Leu	Thr	Gln	Thr
1															15
Thr	Thr	Leu	Val	Ala	Thr	Ile	Gly	Ser	Asn	Ala	Pro	Tyr	Ile	Gly	Leu
															30
Leu	Gly	Thr	Val	Met	Gly	Ile	Met	Leu	Thr	Phe	Met	Asp	Leu	Gly	Ser
															45
Ala	Ser	Gly	Ile	Asp	Thr	Lys	Ala	Ile	Met	Thr	Asn	Leu	Ala	Leu	Ala
															50
Leu	Lys	Ala	Thr	Gly	Met	Gly	Leu	Leu	Val	Ala	Ile	Pro	Ala	Ile	Val
															65
Ile	Tyr	Asn	Leu	Leu	Val	Arg	Lys	Ser	Glu	Ile	Leu	Val	Thr	Lys	Trp
															80
															85
Asp	Ile	Phe	His	His	Pro	Val	Asp	Thr	Gln	Ser	His	Glu	Val	Tyr	Ser
															95
100															110
Lys	Ala														

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...67

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527

Met	Ile	Ala	Val	Leu	Pro	Pro	Leu	Phe	Ser	Met	Gly	Ser	Phe	Asp	Glu
1															15
Trp	Ile	Tyr	Arg	Gly	Leu	Val	Ala	Leu	Met	Val	Ser	Cys	Pro	Cys	Ala
															30
Leu	Val	Ile	Ser	Val	Pro	Leu	Gly	Tyr	Phe	Gly	Gly	Val	Gly	Ala	Ala
															45
Ser	Arg	Lys	Gly	Ile	Leu	Met	Lys	Gly	Val	His	Val	Leu	Glu	Gly	Ala
															50
Tyr	Pro	Asn													60
65															

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528

Val	Gln	His	Phe	Asn	Phe	Leu	Tyr	Lys	Asp	Ser	Leu	Phe	Ser	Ile	Ala
1			5					10						15	
Leu	Phe	Thr	Phe	Ile	Ile	Ala	Leu	Val	Ile	Leu	Leu	Glu	Gln	Ala	Arg
				20					25					30	
Ala	Tyr	Phe	Thr	Arg	Lys	Arg	Asn	Lys	Phe	Leu	Gln	Lys	Phe	Ala	
	35				40							45			
Gln	Asn	Gln	Asn	Ala	Tyr	Ala	Ser	Ser	Glu	Asn	Leu	Asp	Glu	Leu	Leu
	50					55				60					
Lys	His	Ala	Lys	Ile	Ser	Ser	Leu	Met	Phe	Leu	Ala	Arg	Ala	Tyr	Ser
	65				70				75			80			
Lys	Ala	Asp	Val	Glu	Met	Ser	Ile	Glu	Ile	Leu	Lys	Gly	Leu	Leu	Asn
					85				90			95			
Arg	Pro	Leu	Lys	Asp	Glu	Glu	Lys	Ile	Ala	Val	Leu	Asp	Leu	Leu	Ala
		100				105						110			
Lys	Asn	Tyr	Phe	Ser	Val	Gly	Tyr	Leu	Gln	Lys	Thr	Lys	Asp	Thr	Val
	115					120					125				
Lys	Glu	Ile	Leu	Arg	Phe	Ser	Pro	Arg	Asn	Val	Glu	Ala	Leu	Leu	Lys
	130					135					140				
Leu	Leu	His	Ala	Tyr	Glu	Leu	Glu	Lys	Asp	Tyr	Ser	Lys	Ala	Leu	Glu
	145				150					155			160		
Thr	Leu	Glu	Cys	Leu	Glu	Glu	Leu	Glu	Val	Pro	Lys	Ile	Glu	Thr	Ile
					165				170			175			
Lys	Asn	Tyr	Leu	Tyr	Leu	Met	His	Leu	Ile	Glu	Asn	Lys	Glu	Asp	Ala
	180					185				190					
Ala	Lys	Ile	Leu	His	Val	Ser	Lys	Ala	Ser	Leu	Asp	Leu	Lys	Ile	
	195					200				205					
Ala	Leu	Asn	His	Leu	Lys	Ser	His	Asp	Glu	Asn	Leu	Phe	Trp	Gln	Glu
	210					215				220					
Ile	Asp	Thr	Thr	Glu	Arg	Leu	Glu	Asn	Val	Ile	Asp	Leu	Leu	Trp	Asp
	225				230					235			240		
Met	Asn	Ile	Pro	Ala	Phe	Ile	Leu	Glu	Lys	His	Ala	Leu	Leu	Gln	Asp
					245				250			255			
Ile	Ala	Arg	Ser	Gln	Gly	Leu	Leu	Leu	Asp	His	Lys	Pro	Cys	Gln	Ile
					260			265			270				
Phe	Glu	Leu	Glu	Val	Leu	Arg	Ala	Leu	Leu	His	Ser	Pro	Ile	Lys	Ala
					275			280			285				
Ser	Leu	Thr	Phe	Glu	Tyr	Arg	Cys	Lys	His	Cys	Lys	Gln	Ile	Phe	Pro
	290					295				300					
Phe	Glu	Ser	His	Arg	Cys	Pro	Val	Cys	Tyr	Gln	Leu	Ala	Phe	Met	Asp
	305					310				315			320		
Met	Val	Ala													

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...10
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:529

Met Glu His Leu Thr Arg Gly Ile Lys His
1 5 10

(2) INFORMATION FOR SEQ ID NO:530:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...12
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:530

Val Val Ile Leu Gly Ser His Gly Lys Glu Glu Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:531:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 79 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...79
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:531

Met Lys Lys Val Ile Val Ala Leu Gly Val Leu Ala Phe Ala Asn Val
1 5 10 15
Leu Met Ala Thr Asp Val Lys Ala Leu Val Lys Gly Cys Ala Ala Cys
20 25 30
His Gly Val Lys Phe Glu Lys Ala Leu Gly Lys Ser Lys Ile Val

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35	40	45
Asn Met Met Ser Glu Lys	Glu Ile Glu Glu Asp Leu Met Ala Phe Lys	
50	55	60
Ser Gly Ala Asn Lys Asn Pro Val Met Thr Arg Lys Leu Lys Asn		
65	70	75

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532

Met Gly Ile Ala Thr Ser Leu Ile Ser Glu Val Ser Lys Phe Tyr Tyr			
1	5	10	15
Ala Leu Lys Tyr His Ala Lys Phe Met Ser Leu Gly Glu Leu Gly Cys			
20	25	30	
Tyr Ala Ser His Tyr Ser Leu Trp Gln Lys Cys Ile Glu Leu Asn Glu			
35	40	45	
Ala Ile Cys Ile Leu Glu Asp Asp Ile Thr Leu Lys Glu Asp Phe Lys			
50	55	60	
Glu Gly Leu Asp Phe Leu Glu Lys His Ile Gln Glu Leu Gly Tyr Ala			
65	70	75	80
Arg Leu Met His Leu Leu Tyr Asp Ala Ser Val Lys Ser Glu Pro			
85	90	95	

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533

Met His Ile Lys Ser Gly Ala Val Phe Ile Ser Asp Ala His Phe Leu			
1	5	10	15
Pro Lys Ser Pro His Leu Ile His Thr Leu Lys Glu Leu Leu Ser Ala			
20	25	30	

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Lys Pro Pro Gln Val Phe Phe Met Gly Asp Ile Phe His Val Leu Val
 35 40 45
 Gly Tyr Leu Pro Leu Asp Lys Glu Gln Gln Lys Ile Ile Asp Leu Ile
 50 55 60
 His Ala Leu Ser Glu Ile Ser Gln Val Phe Tyr Phe Glu Gly Asn His
 65 70 75 80
 Asp Phe Ser Met Arg Phe Val Phe Asn Ser Lys Val Met Val Phe Glu
 85 90 95
 Arg Gln Asn Gln Pro Ala Leu Phe Gln Tyr Asp Asn Lys Arg Phe Leu
 100 105 110
 Leu Ala His Gly Asp Leu Phe Ile Thr Lys Ala Tyr Glu Phe Tyr Ile
 115 120 125
 Thr Gln Leu Thr Ser Thr Trp Ala Arg Phe Phe Leu Thr Phe Leu Asn
 130 135 140
 Leu Leu Ser Phe Lys Thr Leu Tyr Pro Phe
 145 150

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...67

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534

Met Gln Asp Leu Asp Asn Asn Met Ser Leu Asp Thr Ala His Asn Thr
 1 5 10 15
 Leu Ser Ser Asn Gly Lys Asn Ile Thr Ile Ala Gly Val Val Lys Ala
 .20 25 30
 Leu Gln Lys Ile Gly Val Ser Ala Lys Gly Met Val Ser Ile Leu Gln
 35 40 45
 Ala Leu Lys Lys Ser Gly Ala Ile Ser Ala Lys Trp Arg Tyr Tyr Asp
 50 55 60
 Lys Gln Gln
 65

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

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(A) NAME/KEY: misc_feature
 (B) LOCATION 1...67

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534

```

Met Gln Asp Leu Asp Asn Asn Met Ser Leu Asp Thr Ala His Asn Thr
1           5          10          15
Leu Ser Ser Asn Gly Lys Asn Ile Thr Ile Ala Gly Val Val Lys Ala
20          25          30
Leu Gln Lys Ile Gly Val Ser Ala Lys Gly Met Val Ser Ile Leu Gln
35          40          45
Ala Leu Lys Lys Ser Gly Ala Ile Ser Ala Lys Trp Arg Tyr Tyr Asp
50          55          60
Lys Gln Gln
65
  
```

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535

```

Val Gln Pro Met Lys Ser Lys Lys Leu Tyr Leu Ala Leu Ile Ile Gly
1           5          10          15
Val Leu Leu Ala Phe Leu Thr Leu Ser Ser Trp Leu Gly Asn Ser Gly
20          25          30
Leu Val Gly Arg Phe Gly Val Trp Phe Ala Ala Ile Asn Lys Lys Tyr
35          40          45
Phe Gly Tyr Leu Ser Leu Ile Asn Leu Pro Tyr Leu Ala Trp Val Leu
50          55          60
Phe Leu Leu Tyr Arg Ala Lys Asn Pro Phe Thr Glu Ile Val Leu Glu
65          70          75          80
Lys Thr Leu Gly His Leu Leu Gly Ile Leu Ser Leu Leu Phe Leu Gln
85          90          95
Ser Ser Leu Leu Asn Gln Gly Glu Ile Gly Asn Ser Ala Arg Leu Phe
100         105         110
Leu His Pro Phe Ile Gly Asp Phe Gly Leu Tyr Val Leu Ile Met Leu
115         120         125
Met Val Val Ile Ser Tyr Leu Ile Leu Phe Lys Leu Pro Pro Lys Ser
130         135         140
Val Phe Tyr Pro Tyr Met Asn Lys Thr Gln Ser Leu Leu Lys Glu Ile
145         150         155         160
Tyr Lys Gln Cys Leu Gln Ala Phe Ser Pro Asn Phe Ser Leu Lys Lys
165         170         175
Glu Gly Phe Glu Asn Thr Pro Ser Asp Ser Gln Lys Lys Glu Thr Asn
180         185         190
Asn Asp Lys Glu Lys Glu Asn Leu Lys Glu Asn Pro Ile Asp Glu Asn
195         200         205
His Asn Thr Pro Asn Glu Glu Ser Phe Leu Ala Ile Pro Thr Pro Tyr
210         215         220
  
```

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Asn	Thr	Thr	Leu	Asn	Asn	Ser	Glu	Pro	Gln	Glu	Gly	Leu	Val	Gln	Ile
225				230			235					240			
Ser	Pro	His	Pro	Pro	Thr	His	Tyr	Thr	Ile	Tyr	Pro	Lys	Arg	Asn	Arg
				245			250					255			
Phe	Asp	Asp	Leu	Thr	Asn	Pro	Thr	Leu	Lys	Glu	Pro	Lys	Gln	Glu	Thr
				260			265					270			
Lys	Glu	Arg	Glu	Pro	Thr	Leu	Lys	Lys	Glu	Thr	Pro	Thr	Thr	Leu	Lys
				275			280					285			
Pro	Ile	Met	Pro	Ile	Ser	Ala	Ser	Thr	Gln	Lys	Ile	Met	Thr	Lys	Gln
	290				295						300				
Lys	Thr	Thr	Lys	Pro	Leu	Thr	Thr	Pro							
	305				310										

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536

Val	Met	Leu	Ser	Arg	Asp	Ile	Val	Gln	Tyr	Ser	Lys	Ile	Arg	Thr	Glu
1						5			10			15			
Leu	Tyr	Ala	Tyr	Leu	Thr	Tyr	Leu	Phe	Ser	His	Asn	Ile	Arg	Asn	His
						20			25			30			
Leu	Pro	Glu	Ile	Thr	Leu	Asp	Tyr	Leu	Asn	Arg	Gln	Ile	Ser	Lys	Met
						35			40			45			
Gln	Ala	Glu	Ile	Lys	Met	Ala	Lys	Ser	Phe	Phe	Val	Leu	Asp	Ala	Lys
						50			55			60			
Gly	Met	Leu	Met	Leu	Lys	Pro	Ser	Gln	Phe	Lys	Gln	Gly	His	Lys	
						65			70			75			80
Glu	Gly	Leu	Leu	Glu	His	Asp	Leu	Thr	Glu	Gly	Ile	Glu	Leu	Glu	Ser
						85			90			95			
His	Val	Ser	Phe	Ser	Asp	Lys	Tyr	Tyr	Phe	Tyr	Gln	Ala	Val	Asn	Glu
						100			105			110			
Lys	Arg	Cys	Ile	Leu	Thr	Asp	Pro	Tyr	Pro	Ser	Lys	Lys	Gly	Asn	His
						115			120			125			
Leu	Val	Val	Ser	Ala	Ser	Tyr	Pro	Val	Tyr	Asp	Gln	Asn	Asn	Asp	Leu
						130			135			140			
Ala	Phe	Val	Val	Cys	Leu	Gln	Ile	Pro	Leu	Arg	Val	Ala	Ile	Glu	Ile
						145			150			155			160
Ser	Ser	Pro	Ser	Lys	Tyr	Phe	Lys	Thr	Phe	Ser	Glu	Gly	Ser	Met	Val
						165			170			175			
Met	Tyr	Phe	Met	Ile	Ser	Ile	Met	Leu	Thr	Leu	Val	Ser	Leu	Leu	Leu
						180			185			190			
Phe	Val	Lys	Cys	Ile	Ser	Ser	Phe	Trp	Thr	Ala	Ile	Val	His	Phe	Ser
						195			200			205			
Ser	Phe	Asp	Ile	Lys	Glu	Val	Phe	His	Pro	Ile	Val	Leu	Thr	Leu	
						210			215			220			
Ala	Leu	Ala	Thr	Phe	Asp	Leu	Val	Lys	Ala	Ile	Phe	Glu	Glu	Val	
						225			230			235			240
Leu	Gly	Lys	Asn	Ser	Gly	Asp	Asn	His	His	Ala	Ile	His	Arg	Thr	Met

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